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O'Bryen, Barbara

From: Yu, Misook
Sent: Monday, September 29, 2003 2:35 PM
To: O'Bryen, Barbara
Subject: RE: 09402713

Barb, would you please add oligo-search for DNA encoding SEQ ID NO:7 in US issued nucleic acid data base also as we discussed over the phone. Thank you.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

-----Original Message-----

Fr m: O'Bryen, Barbara
Sent: Monday, September 29, 2003 2:30 PM
T : Yu, Misook
Subject: RE: 09402713

Misook,
Results 16-45 are not saved anywhere (this is true of *all* searches). In order to get those extra results, the search has to be rerun. That will take at least 24 hours. I will contact you when the new results are ready.
Barb

-----Original Message-----

From: Yu, Misook
Sent: Monday, September 29, 2003 2:23 PM
To: O'Bryen, Barbara
Subject: RE: 09402713

Barb, would you please print out the Result NO. 16-45 of SEQ ID NOs 1, 3, 4, 6 and DNA encoding SEQ ID NO:2 from Issued Patent NA only. Review of the search result indicates 1-15 is from two patents that are not prior art. Thank you.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

-----Original Message-----

From: O'Bryen, Barbara
Sent: Monday, September 29, 2003 1:57 PM
To: Yu, Misook
Cc: Hale, Mary
Subject: RE: 09402713

Misook,
This search is finished. You can pick it up from the table outside the door to the 6th floor STIC cluster.
Barb

-----Original Message-----

From: Yu, Misook
Sent: Monday, September 29, 2003 1:45 PM
To: O'Bryen, Barbara
Subject: FW: 09402713
Importance: High

Barb, is the search result ready to be pick up?

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

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-----Original Message-----

From: Hale, Mary
Sent: Monday, September 29, 2003 1:38 PM
To: Yu, Misook
Subject: FW: 09402713
Importance: High

You search has been completed by Barb. You can call her at 308-4291

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Monday, September 29, 2003 1:24 PM
To: Hale, Mary
Subject: FW: 09402713
Importance: High

I thought I should send this to you..Linda

-----Original Message-----

From: Yu, Misook
Sent: Monday, September 29, 2003 1:23 PM
To: STIC-Biotech/ChemLib
Subject: FW: 09402713
Importance: High

Is there any hope that I could get the search result of this case by tomorrow morning (9/30)?

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

-----Original Message-----

From: Page, Thurman
Sent: Friday, September 26, 2003 9:42 AM
To: STIC-Biotech/ChemLib
Cc: Yu, Misook
Subject: FW: 09402713
Importance: High

RUSH SEARCH APPROVED

Thurman K. Page
SPE Art Units 1615 & 1616
Technology Center 1600

-----Original Message-----

From: Yu, Misook
Sent: Friday, September 26, 2003 9:40 AM
To: Page, Thurman
Subject: 09402713

Please approve rush Oligo-search for SEQ ID NOs 1, 3, 4, 6 and DNA encoding SEQ ID NO:2. It is due this biweek.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:01:08 ; Search time 13035.4 Seconds

(without alignments)
11241.524 Million cell updates/sec

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Perfect score: 3582

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Searched: 2888711 seqs, 20454813386 residues

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Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3582	100.0	3582	6	BD082485	BD082485 PCA3, PCA
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16	1357	37.9	2426	6	AX267494	AX267494 Sequence
17	1357	37.9	2426	6	AX261038	AX261038 Sequence
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ALIGNMENTS

RESULT 1
BD082485
LOCUS
DEFINITION
BD082485
ACCESSION
BD082485.1 GI:22628095
VERSION
JP 2001522240-A/4.
KEYWORDS
SOURCE
ORGANISM
Mastadenovirus
viruses; dsDNA viruses, no RNA stage; Adenoviridae.
REFERENCE
1 (bases 1 to 3582)
AUTHORS
Bussemakers,M.J.G.
TITLE
PCA3, PCA3 genes, and methods of use
Patent: JP 2001522240-A 4 13-NOV-2001;
JOURNAL
DIAGNOCURE INC

COMMENT

PN JP 2001522240-A/4
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G. BUSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC
C1201/68,
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CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 401..553. Location/Qualifiers

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/organism="Mastadenovirus"
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/db_xref="taxon:10509"

BASE COUNT 1052 a 787 c 680 g 1063 t

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GGCTGACGCCGAGGAGACACAGAAATCTGCATGTTGGGAAGACCTGATGATACAG 120
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Oy	1861	CACGAATTCCTGCGAGTGCAAATCCCGAAAGATACCTTTATGCCATTTTCATAGTGAGTGC	1920
Db	1861	CACGAANTTCATGCGAGTGCAAATCCCGAAAGATACCTTTATGCCATTTTCATAGTGAGTGC	1920
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Oy	1981	TTTGAGTTAAATGGAAGAAATAGGGCACTCTGTGAGCCACTTTAGAGTTCACTCTGGC	2040
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Oy	2041	AATTAAGAAATTTACAAAGAGCTACTGCAGGACCAATTTGTTAAGACTCTGTGTGTGTGT	2100
Db	2041	AATTAAGAAATTTACAAAGAGCTACTGCAGGACCAATTTGTTAAGACTCTGTGTGTGTGT	2100
Oy	2101	GTCGTGTGTGAGTGTACATGCCAAAGTGTCCCTCTCTCTTGAACCCATTAATTTCAAGC	2160
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Db	2221	CTCATTTATCTCCAGTAAATGTGATTAATATGTCATCTGTTACATATAAAAAAGTTTGAC	2280
Oy	2281	TTCCAAAAAGCAGCTGGAAATGAGCAACACACAAATATGCAATTAATCTAACTCCTACATCA	2340
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Db	2401	AAATPACTGATTAAGGTCTCAGCTGGGGGCGTGCATCAGCGGGTTTGAGAAATATTCAA	2460
Oy	2461	TTCTCAGAGAAAGCAGAAATTTGAAATTCCTCCATCTTTTAGAAATCAATTTACAGGTTTG	2520
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Oy	2521	GAGAGGATTCAGACAGCTCAGGTCTTCACTAATATCTCGAATCTTGTCCCTCTTG	2580
Db	2521	GAGAGGATTCAGACAGCTCAGGTCTTCACTAATATCTCGAATCTTGTCCCTCTTG	2580
Oy	2581	TGTTCAATGGAATGACCAATTAATATGTTATCTTGAACGATGCTCATAGAGAGATA	2640
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Oy	2881	GACACATATTAAGCTTTCAGCTTGGCTTCCACGACTTTATCTTTCTCCAAACATGCG	2940
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QY	3121	TCTAAGAGGTTCAAAAATCCAACTATTATCTTCTCTTCTTCACTCCCTGCTCCTCT	3180		
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QY	3421	CTAATTTTGAGAAATTTCCAAATTAGAGACTCACATGTTTATCTGCTTATCAATTTTAA	3480		
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QY	3541	TCTTGCCATCTATATCAACTTTGATTTGTTTACAACTTT	3582		
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RESULT 2	AR261166	3923 bp	DNA	linear	PAT 29-JAN-2003
LOCUS	AR261166				
DEFINITION	Sequence 690 from patent US 6321716.				
ACCESSION	AR261166				
VERSION	AR261166.1	GI:28071929			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 3923)				
AUTHORS	Mashiki,Z. and Harada,J.				
TITLE	Negative pressure control apparatus for engine mounted in vehicle				
JOURNAL	Patent: US 6321716-A 690 27-NOV-2001;				
FEATURES	Location/Qualifiers				
	1..3923				
BASE COUNT	1157 a	840 c	740 g	1186 t	
ORIGIN					
Query Match	84.8%;	Score 3036;	DB 6;	Length 3923;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 3036;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	ACAGAGAAATAGCAAGTCCGAGAGAGCTGGCATCAGAAAAACAGAGGGAGATTTGTGT	60		
DB	1	ACAGAGAAATAGCAAGTCCGAGAGAGCTGGCATCAGAAAAACAGAGGGAGATTTGTGT	60		

QY	61	GGCTGCACCCGAGGGAGACCCAGGAAGATTCATGTGTGGGAAGACCTGATCATACAG	120
Db	61	GGCTGCACCCGAGGGAGACCCAGGAAGATTCGATGTGTGGGAAGACCTGATCATACAG	120
QY	121	GAATTACACACATATATCTAGTTGTTTCAATGACACCCAGATTAATATGTAAGACGTA	180
Db	121	GAATTACACACATATATCTAGTTGTTTCAATGACACCCAGATTAATATGTAAGACGCTA	180
QY	181	GTCCGCTGTGACTCTCTCAGTGACACAGGGCTGGATCCATCGACGGCACTTTCTGAG	240
Db	181	GTCCGCTGTGACTCTCTCAGTGACACAGGGCTGGATCCATCGACGGCACTTTCTGAG	240
QY	241	TACGTAGTGCACAAAGAAAGACTACAGCATCTCAATGCGAGGGGTGAAATTAAGAA	300
Db	241	TACGTAGTGCACAAAGAAAGACTACAGCATCTCAATGCGAGGGGTGAAATTAAGAA	300
QY	301	GGCTGCTGACTTTACCATCTGAGGCGACACATCTGCTGAATGAGAGATTAATACATC	360
Db	301	GGCTGCTGACTTTACCATCTGAGGCGACACATCTGCTGAATGAGAGATTAATACATC	360
QY	361	TAGAAACACAGACATGACATTAATGTTCTAAGTACATGTTTTCACATTTCCAG	420
Db	361	TAGAAACACAGACATGACATTAATGTTCTAAGTACATGTTTTCACATTTCCAG	420
QY	421	CCCCCTTTAAATTCACACACACAGAGAACAAAAAGGACACAGATCCCTGGGAGA	480
Db	421	CCCCCTTTAAATTCACACACACAGAGAACAAAAAGGACACAGATCCCTGGGAGA	480
QY	481	AATGCCGCGCCGCTCTGTGGTCTCATGATGACCTCGCCCTCTGCTCCCTCTGT	540
Db	481	AATGCCGCGCCGCTCTGTGGTCTCATGATGACCTCGCCCTCTGCTCCCTCTGT	540
QY	541	GAGGGAAGACATTGAAAAATGAATTGATGTTCTCTTAAGGATGGCGAGAAAAACGA	600
Db	541	GAGGGAAGACATTGAAAAATGAATTGATGTTCTCTTAAGGATGGCGAGAAAAACGA	600
QY	601	TCCCTTTGGGATTTATTTATTTAAAGGGATTACATTTGAAATGAAGTCAACAAAGTAG	660
Db	601	TCCCTTTGGGATTTATTTATTTAAAGGGATTACATTTGAAATGAAGTCAACAAAGTAG	660
QY	661	CATTACCAATGAGAGAAAAACAGACGAGAAAAATCTTGATGGCTTCACAAGACATGACA	720
Db	661	CATTACCAATGAGAGAAAAACAGACGAGAAAAATCTTGATGGCTTCACAAGACATGACA	720
QY	721	AACAAATATGGAATATCTGTGATGACATGAGCGACCAAGCTGGGGAGGAGATPACACGG	780
Db	721	AACAAATATGGAATATCTGTGATGACATGAGCGACCAAGCTGGGGAGGAGATPACACGG	780
QY	781	GCAGAGGGTCAAGATTCTGGCCCTGCTCCTTAACTGTGCGTTCTAAACCAAAATCATTT	840
Db	781	GCAGAGGGTCAAGATTCTGGCCCTGCTCCTTAACTGTGCGTTCTAAACCAAAATCATTT	840
QY	841	ATATTTCTAACCCCTCAAAAAAAGCTGTTGTAATATCGATCTACAGGTTCTCTTCGG	900
Db	841	ATATTTCTAACCCCTCAAAAAAAGCTGTTGTAATATCGATCTACAGGTTCTCTTCGG	900
QY	901	CCCAACATTTCTCCATATATCCAGCCACACTCATTTTAAATTAATTTAGTTCCAGATCTGTA	960
Db	901	CCCAACATTTCTCCATATATCCAGCCACACTCATTTTAAATTAATTTAGTTCCAGATCTGTA	960
QY	961	CTGTGACCTTTCTACACTGTAGAAATACATTAATCTCATTTTCTCAAAACCCCTTCGT	1020
Db	961	CTGTGACCTTTCTACACTGTAGAAATACATTAATCTCATTTTCTCAAAACCCCTTCGT	1020
QY	1021	GCTGCTTAATATGTAGCTGTGTTTCTTAAGGAGTTCCTGGCCAGGGAGATCTGTG	1080
Db	1021	GCTGCTTAATATGTAGCTGTGTTTCTTAAGGAGTTCCTGGCCAGGGAGATCTGTG	1080
QY	1081	AACAGGCTGGGAAGCATCTCAAGATCTTTCAGGGTTATACTTACGACACAGCATGA	1140
Db	1081	AACAGGCTGGGAAGCATCTCAAGATCTTTCAGGGTTATACTTACGACACAGCATGA	1140

QY	1144	TCATTAACGAGAGTAATTA	CTAATATCAACATCATCTCTAGTGTCTTGCCCACTAGCAAT	1200
Db	1141	TCATTAACGAGAGTAATTA	CTAATATCAACATCATCTCTAGTGTCTTGCCCACTAGCAAT	1200
QY	1201	TCATTTCCCACTTTTGTGGCCATTC	CTCAAGACCTCAAAATGTCATTCATTAATATACCA	1266
Db	1201	TCATTTCCCACTTTTGTGGCCATTC	CTCAAGACCTCAAAATGTCATTCATTAATATACCA	1266
QY	1261	GGATTAACCTTTTTTTTTTAA	CCGTGAAGAAATTCATGTTACATGCACTATGGGAATTTA	1320
Db	1261	GGATTAACCTTTTTTTTTTAA	CCGTGAAGAAATTCATGTTACATGCACTATGGGAATTTA	1320
QY	1321	ATTACATATTTTGTGTTTCC	AGTGCACAAATGACTATAGTCCTTTATACCTCCCTTTGTT	1380
Db	1321	ATTACATATTTTGTGTTTCC	AGTGCACAAATGACTATAGTCCTTTATACCTCCCTTTGTT	1380
QY	1381	GATTTTTTTTTCCAGATATA	AGGTTAAAGTTCAGTCCGTGTACTGAGGCTGTATACAGAC	1440
Db	1381	GATTTTTTTTTCCAGATATA	AGGTTAAAGTTCAGTCCGTGTACTGAGGCTGTATACAGAC	1440
QY	1441	AGCCTTCGCCCATCCCTC	CAGCCTTATCTGTATCACCATCAACCCCTCCCATACACCT	1500
Db	1441	AGCCTTCGCCCATCCCTC	CAGCCTTATCTGTATCACCATCAACCCCTCCCATACACCT	1500
QY	1501	AAACAAATCTPACTCTGT	TAATTCCTTGAAACATGTCAGACATTAATTCCTCTGTGCT	1560
Db	1501	AAACAAATCTPACTCTGT	TAATTCCTTGAAACATGTCAGACATTAATTCCTCTGTGCT	1560
QY	1561	GAGAAGCTCTTCCTGTCT	CTTAAATCTAGAAATGATGTAAGTTTGAATTAAGTTGACTA	1620
Db	1561	GAGAAGCTCTTCCTGTCT	CTTAAATCTAGAAATGATGTAAGTTTGAATTAAGTTGACTA	1620
QY	1621	TCCTACTTCATGCAAA	AGGAGACATATGAGATTCTATCACCATGAGACAGCAATTA	1680
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QY	1681	CTAAAGGCTAATTTGAT	TATTAAGGTTTAACATAATATATGAATATGCAAGGCCACAGA	1740
Db	1681	CTAAAGGCTAATTTGAT	TATTAAGGTTTAACATAATATATGAATATGCAAGGCCACAGA	1740
QY	1741	GGGAATGTTTATGGG	CACGTTTGTGACCTGGGATGTGAAGCAAAAGGCAGGAACTCA	1800
Db	1741	GGGAATGTTTATGGG	CACGTTTGTGACCTGGGATGTGAAGCAAAAGGCAGGAACTCA	1800
QY	1801	TAGTATCTTAATATA	TATTAATCTTCATTTCTATCTATCACAATATTCACAAGCTTTT	1860
Db	1801	TAGTATCTTAATATA	TATTAATCTTCATTTCTATCTATCACAATATTCACAAGCTTTT	1860
QY	1861	CACAGAAATTCATG	CAGTGCACAAATCCCAAGGTAACCTTTATCCATTTTCATGTGATGC	1920
Db	1861	CACAGAAATTCATG	CAGTGCACAAATCCCAAGGTAACCTTTATCCATTTTCATGTGATGC	1920
QY	1921	GCTTATAGAAATTTGG	CAATATCACTGTGCTACTATTCACAACTTTGAGATGTGTTGTC	1980
Db	1921	GCTTATAGAAATTTGG	CAATATCACTGTGCTACTATTCACAACTTTGAGATGTGTTGTC	1980
QY	1981	TTGTAGTAAATTTGA	AAAGAAATAGGCGACTCTTGAGAGCACTTTTAGGGTTCACTCCGCG	2040
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Db	2041	AATAAAGAAATTTAC	AAAGAGCTACTCAGGACCAAGTTGTAAAGACCTCTGTGTGTGTGT	2100
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RESULT 3
AR278697 3923 bp DNA linear PAT 10-APR-2003
LOCUS AR278697
DEFINITION Sequence 690 from patent US 6512094.
ACCESSION AR278697
VERSION AR278697.1 GI:29712943
KEYWORDS
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3923)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
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Vedrick,T.S., Garter,D., Li,S.X., Wang,A., Skelley,Y.A.W.,
Hepler,W.T., and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

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BASE COUNT 1157 a 840 c 740 g 1186 t
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Query Match 84.8%; Score 3036; DB 6; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
AX200988
LOCUS AX200988 3923 bp DNA linear PAT 29-AUG-2001

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Db	1021	GCTGCTAATATGTAGCTGACTGTTTTTCTTAAGAGAGTGTCTGGCCAGGGATCTGTG	1080
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QY	1321	ATTACATATTTTGTGTTTCCAGTGCAGAAAGTAACTAAAGTCTTAAATCCCTCCCTTGT	1380
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QY	1381	GATTTTTTCCAGTATAAAGTTAAATGCTTAAAGCTGTACGAGGCTGTATACAGCAC	1440
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Db	1441	AGCCTCTCCCATCCCTCCAGCCTTATCTGTGCATACACCATTAACCCCTCCCATACACCT	1500
QY	1501	AAACAAATCAACTGTAAATTCCTGTAACATGTCAGAGACATTAATTTCTTCTGCT	1560
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QY	1561	GAGAAGCTCTCTGCTCTTAAATCTAGAATGATGTAAAGTTTGAATAGTTGACTA	1620
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Db	1621	TCTTACTTCATGCAAGAGGAGACATATAGATTCTATCTCATATGACACACAATA	1680
QY	1681	CTAAAGGTAAATTTGATTAATAGGTTAGATAAATATTAAGAAATGCAAGGACACAGA	1740
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Db 1741 GGGATGTTTATGGGCGACGTTTGTAAGCTGGGATGTGAAGCAAGGCGAGGAACCTCA 1800
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Qy 2881 GACACATATTAAGCTTTCAGCTTTGCTTCCAGAGACTTTTATCTTTTCCAAACATGCG 2940
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RESULT 5
AX267716
LOCUS AX267716 690 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 690 from Patent WO0173032.
ACCESSION AX267716
VERSION AX267716.1 GI:16516388
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kaios,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITILE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 690 04-OCT-2001;
CORIXA CORPORATION (US)
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SOURCE
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BASE COUNT 1157 a 840 c 740 g 1186 t
ORIGIN

Query Match 84.8%; Score 3036; DB 6; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GGCCTGACGCGAGGAGACAGCAAGATCTGCATGTGGAGAGGACTGATGATACAGAG 120
Qy 121 GAATTACACACATATATCTTATGTTTCAATGAACACCAAGATTAATTAAGTGAAGCTTA 180
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Qy 361 TAGAAACAGCAAGATGACATATATATGCTTAAGTAGAGATGTTTGGACATTTCCAG 420
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Db	421	CCCCTTTAAATATCCACACACAGGAACCAAAAGGAAACACAGATCCTGGAGA	480
OY	481	AATCCCGGCCGCATCTGGGTATGATGATGAGCTGGCCCTGGCTGGTCGGCTTG	540
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OY	541	GAGGGAAGGACATTAGAAAATGAAATGATGTGTCTCTTAAAGGATGGGACGAAACAAGA	600
Db	541	GAGGGAAGGACATTAGAAAATGAAATGATGTGTCTCTTAAAGGATGGGACGAAACAAGA	600
OY	601	TCCCTGTGTGATATTATTTTGAACGGGATTACAGATTTGAATGAAGTCAACAAATGAC	660
Db	601	TCCCTGTGTGATATTATTTTGAACGGGATTTACAGATTTGAATGAAGTCAACAAATGAG	660
OY	661	CATTACCATAAGAGAAAAACAGACGAGAAAATTTATGGCTTCACACAGCATGCAACA	720
Db	661	CATTACCATAAGAGAAAAACAGACGAGAAAATTTGATGGCTTCACACAGCATGCAACA	720
OY	721	AACAAAATGCAATCTGTGATGACATGAGCCAAAGCTGGGAGAGATAACCGGG	780
Db	721	AACAAAATGCAATCTGTGATGACATGAGCGCAAGCTGGGAGAGATAACCGGG	780
OY	781	GCAAGAGGTCCGAAATCTGGCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840
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OY	841	ATATTTCTAACCCTCAAACAAAGCTGTGTAAATATGTATCTGATCTGACGGTCTCTGGG	900
Db	841	ATATTTCTAACCCTCAAACAAAGCTGTGTAAATATGTATCTGATCTGACGGTCTCTGGG	900
OY	901	CCCACAAATTCCTCCATATATCCAGCACACTATTTTAATTTTAATTTTCCAGATCTGTA	960
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Db	961	CTGTGACCTTCTACACTGTGAAATTAACATTTACTTTGTTTCAAGACCTTCGTGT	1020
OY	1021	GCTGCTTAATATGATGACTGCTTTTTCTTAAGAGTGTCTGGCCAGGGATCTGTG	1080
Db	1021	GCTGCTTAATATGATGACTGCTTTTTCTTAAGAGTGTCTGGCCAGGGATCTGTG	1080
OY	1081	AACAGGCTGGGAACCATCTCAAGATCTTCCAGGGTATACTTCTGACACAGCATGA	1140
Db	1081	AACAGGCTGGGAACCATCTCAAGATCTTCCAGGGTATACTTCTGACACAGCATGA	1140
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Db	1141	TCATTACGAGATTAATCTAATCAACATCATCTCAGTGTCTTGGCCACTAGTAAT	1200
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OY	1261	GGATTAACCTTTTTTTTAAACCTGGAAGAAATTCATGTACATCAGCTATGGAATTTA	1320
Db	1261	GGATTAACCTTTTTTTTAAACCTGGAAGAAATTCATGTACATCAGCTATGGAATTTA	1320
OY	1321	ATTACATATTTTGTTTTCCAGTGCAGAAAGATGATCTTTATCCCTCCCTTTGTTT	1380
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Db	1381	GATTTTTTTTCCAGTAAATGTTAAATGCTTACCTTTGCTAGAGGTGATPACAGAC	1440
OY	1441	AGCCTTCCCATCTCCAGCCTTATCTGTCAATCACCATCAACCCCTCCCATACACT	1500
Db	1441	AGCCTTCCCATCTCCAGCCTTATCTGTCAATCACCATCAACCCCTCCCATACACT	1500

OY	1501	AAACAAATCTAACTTGTGAATTCCTTGAACATGTCAGACATACATTATTCCTTCGCT	1560
Db	1501	AAACAAATCTAACTTGTGAATTCCTTGAACATGTCAGACATACATTATTCCTTCGCT	1560
OY	1561	GAGAAAGCTTCCTTCGCTCTCTTAATAGACATGATGAAAGTTTGAAATAGTTGACTA	1620
Db	1561	GAGAAAGCTTCCTTCGCTCTCTTAATAGACATGATGAAAGTTTGAAATAGTTGACTA	1620
OY	1621	TCTTACTTTCATGCAAGAGGAGACACATATAGATTCATCTCATGAGACAGACAATA	1680
Db	1621	TCTTACTTTCATGCAAGAGGAGACACATATAGATTCATCTCATGAGACAGACAATA	1680
OY	1681	CTAAAGTGTAATTTGATTATAGAGTTTAGATAAATATATAGAAATGCAAGAGCCACAGA	1740
Db	1681	CTAAAGTGTAATTTGATTATAGAGTTTAGATAAATATATAGAAATGCAAGAGCCACAGA	1740
OY	1741	GGGAATGTTTATGGGGCACTTTTGAAGCCTGGGATGTAAGCAAGAGGAGGAACTCA	1800
Db	1741	GGGAATGTTTATGGGGCACTTTTGAAGCCTGGGATGTAAGCAAGAGGAGGAACTCA	1800
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OY	2101	GTCGTGTGTAGGTACATGCCAAAGTGTCCCTCTCTCTTGAACCATTAATTTTCAGAC	2160
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OY	2221	CTCATTTATTCGCCAGTAATGTGATTAATATGTATCATCTGTTAACATATAAAAAAGTTTGAC	2280
Db	2221	CTCATTTATTCGCCAGTAATGTGATTAATATGTATCATCTGTTAACATATAAAAAAGTTTGAC	2280
OY	2281	TTCACAAAAGCAGCTGGAAATGACAAACACATATGCAATATCTAATCTCTACATCA	2340
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Db	2341	GCTACACACGCTTGACATATATGTTGTAAGAGCAACCTGCACTTGTGGGTCTCTTAAGC	2400
OY	2401	AAATATCTTGCATTAGGTCACGTGGGGCTGTGCATCAGCGGTTTGAGAAATATTCAA	2460
Db	2401	AAATATCTTGCATTAGGTCACGTGGGGCTGTGCATCAGCGGTTTGAGAAATATTCAA	2460
OY	2461	TTCTCAGCAGAGCCAGAAATTTGAATTCCTCATCTTTTAGGAATCATTTTACAGGTTTG	2520
Db	2461	TTCTCAGCAGAGCCAGAAATTTGAATTCCTCATCTTTTAGGAATCATTTTACAGGTTTG	2520
OY	2521	GAGAGAAATTCAGACGTCAGAGCTCTTCACTAATATGTCGAACTTCCTCTCTTGG	2580
Db	2521	GAGAGAAATTCAGACGTCAGAGCTCTTCACTAATATGTCGAACTTCCTCTCTTGG	2580
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RESULT 6
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ACCESSION AF103907.1 GI:6165973
VERSION
KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE Bussemakers,M.J., van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
AUTHORS Kattihus,H.F., Schalken,J.A., Debruyne,F.M., Ru,N. and Isaacs,W.B.
DD3: a new prostate-specific gene, highly overexpressed in prostate
TITLE Cancer
JOURNAL Cancer Res. 59 (23), 5975-5979 (1999)
MEDLINE 20072260
PUBMED 10606244
REFERENCE 2 (bases 1 to 3923)
AUTHORS Bussemakers,M.J.G., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Kattihus,H.F.M., Schalken,J.A., Debruyne,F.M.J., Ru,N. and
Isaacs,W.B.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) Urology Research Laboratory, University
Hospitaal Nijmegen, P.O. Box 9101, Nijmegen 6500 HB, Netherlands
FEATURES
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Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 5435)
AUTHORS Bussemakers,M.J., Van Bokhoven,A., Verheegh,G.W., Smit,F.P.,
Kathaus,H.F., Schalken,J.A., Debruyne,F.M., Ru,N. and Isaacs,W.B.
DD3: a new prostate-specific gene, highly overexpressed in prostate
cancer
JOURNAL Cancer Res. 59 (23), 5975-5979 (1999)
MEDLINE 20072260
PUBMED 10606244
REFERENCE 2 (bases 1 to 5435)
AUTHORS Bussemakers,M.J.G., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Kathaus,H.F.M., Schalken,J.A., Debruyne,F.M.D., Ru,N. and
Isaacs,W.B.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) Urology Research Laboratory, University
Hospital Nijmegen, P.O. Box 9101, Nijmegen 6500 HB, Netherlands
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Matches 2570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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VERSION
KEYWORDS
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AR261036 3112 bp DNA linear PAT 29-JAN-2003
LOCUS AR261036
DEFINITION Sequence 468 from patent US 6321716.
ACCESSION AR261036
VERSION AR261036.1 GI:28071799
KEYWORDS
SOURCE Unknown.

ORGANISM		Unknown.	
REFERENCE		Unclassified.	
AUTHORS		1 (bases 1 to 3112)	
TITLE		Mashiki, Z., and Harada, J.	
JOURNAL		Negative pressure control apparatus for engine mounted in vehicle	
FEATURES		Patent: US 6321716-A 468 27-NOV-2001.	
SOURCE		Location/Qualifiers	
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DB	2333	CAGCTATGGAATTTAATTAATATTTGTTTCCAGTGAAGATGATGATGCTTTA	2392
QY	1365	TCCCTCCCTTTGTTGATTTTTCACAGATTAAGTTAAATGCTTACGCTGTACTG	1424
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QY	1425	AGGCTGTATACAG-CACAGCCTCCGCCATCCCTCCAGCCTTATCTGTATCACCATCA	1483
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QY	1484	CCCTCCCATACACCTTAACAAATCTTAACTGTATTTCTTGAACATGTACGACATTA	1543
DB	2513	CCCTCCCAT-CAACCTTAACAAATCTTAACTGTATTTCTTGAACATGTACAG-CATA	2570
QY	1544	CATTATTCCTTCGCTGAGAGGCTCTCTGCTGCTCTTAAATGAGAAATGTAAGT	1603
DB	2571	CATTATTCCTTCGCTGAGAGGCTCTCTGCTGCTCTTAAATGAGAAATGTAAGT	2630
QY	1604	TTTGAATTAAGTTGAATCTTACTTCAATGCAAGAGGAGACATATGATGATTCATC	1663
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QY	1664	ACATGAGACAGCAATTAATTAAGTATTTGATTAATAGATTTAGATTAATATATGA	1723
DB	2691	ACATGAGACAGCAATTAATTAAGTATTTGATTAATAGATTTAGATTAATATATGA	2750
QY	1724	AATGCAAGAGCAGAGAGAGATTTTATGAGGACGTTTAAAGCTGGGATGGAAGC	1783
DB	2751	AATGCAAGAGCAGAGAGAGATTTTATGAGGACGTTTAAAGCTGGGATGGAAGC	2810
QY	1784	AAAGCAGAGAACTCATATATCTTATATATATCTTCAATTTCTATCTATACACA	1843
DB	2811	AAAGCAGAGAACTCATATATCTTATATATATCTTCAATTTCTATCTATACACA	2870
QY	1844	ATATCCAAACAGCTTTTACAGATTCATGCAAGTGAATCCCAAGGTAACTTTATC	1903
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QY	2024	TAGGTTCACTCTCGGCAATTAAGATTTTCAAAAGAGC	2061
DB	3051	TAGGTTCACTCTCGGCAATTAAGATTTTCAAAAGAGC	3088

RESULT 11
AR278567
LOCUS AR278567 3112 bp DNA linear PAT 10-Apr-2003
DEFINITION Sequence 468 from patent US 6512094.
ACCESSION AR278567
VERSION AR278567.1 GI:29712813
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 3112)

AUTHORS

Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.

Query Match	38.18;	Score 1364;	DB 6;	Length 3112;
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QY	525	GCCCTGTCGCCCTTGTGAGGGAGAGACATTGAAAATGAATTGATGTCTCTTAAAGA				584
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Db	2333	CAGCTATGGGAATTTAAATTACATATTTTTGTTTCCAGTGCAGGAAGATGACTAATGCTTTTA	2392
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Db	2453	AGGCTGTATATACAGCACAGCCCTCCGCCATCCCTCCAGCCCTTAATCTGTGCATCACATCAA	2512
QY	1484	CCCCCTCCCATPACCACTTAACAAATATCTAATCTTCCCTGTAACATGTCAAGACATA	1543
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QY	1544	CATTATTTCTTCTGCTCGAGAAAGCTCTTCTGCTCTTAAATCTAAGATATGTAAAGT	1603
Db	2571	CATTATTTCTTCTGCTCGAGAAAGCTCTTCTGCTCTTAAATCTAAGATATGTAAAGT	2630
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QY	1784	AAAGGCAAGGGAACCTCATGATATCTTATATATATPACTTCATTTCTCATCTATATCA	1843
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RESULT 12			
AX106204			
LOCUS	AX106204	3112 bp	DNA
DEFINITION	Sequence	342 from Patent WO0125273.	Linear
ACCESSION	AX106204		
VERSION	AX106204.1	GI:13921893	

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 Skelky,Y.A., Xu,J., Cheever,M.A. and Reed,S.G.
AUTHORS Compositions and methods for wli specific immunotherapy
TITLE Patent: WO 0125273-A 342 12-APR-2001;
JOURNAL CORIXA CORPORATION (US)
FEATURES
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BASE COUNT 975 a 587 c 624 g 926 t
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Query Match 38.1%; Score 1364; DB 6; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
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OY 465 AGAGATCCCTGGGAGAAATGCCCCGCCGCATCTTGGGTCATGATGAGCCGCGCTGT 524
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DB 2333 CAGCTATGGAATTTAATTAACATATTTTGTTCAGTGAAGAGATGATGATCTTTA 2392
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RESULT 13
AX106687 3112 bp DNA linear PAT 30-APR-2001
LOCUS

DEFINITION Sequence 468 from Patent WO0125272.
ACCESSION AX106687
VERSION AX106687.1 GI:13922352
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
AUTHOR Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0125272-A 468 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
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BASE COUNT 975 a 587 c 624 g 926 t
ORIGIN
Query Match 38.1%; Score 1364; DB 6; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
QY 285 GGTGAATAAAGAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 344
DB 1313 GGTGAATAAAGAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 1372
QY 345 AGATATTTAACTACTAGAAACAGACAGATGACAAATATATGTCTAAGTAGACATGT 404
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RESULT 14
AXI40978 3112 bp DNA linear PAT 31-MAY-2001
LOCUS Sequence 468 from Patent WO0134802.
DEFINITION AXI40978
ACCESSION AXI40978
VERSION AXI40978.1 GI:14281075
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skeiky,Y.A. and Wang,A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 468 17-MAY-2001.
CORIXA CORPORATION (US)
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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			Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE			
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0151633-A 468 19-JUL-2001;		
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Best Local Similarity	99.8%; Pred. No. 0;		
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ALIGNMENTS

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; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solt, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
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; SEQ ID NO: 470
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; ORGANISM: Homo sapiens
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RESULT 2

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; Sequence 470, Application US/09352616a
; Patient No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jlang, Yuqul
; APPLICANT: Xu, Jlangchun

APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.42768
; CURRENT APPLICATION NUMBER: US/09/352,616a
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616a-470
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 323 AGATAATTAACATCTAGTAAAGACAGATGACATATATGTCTTAAGTATGACATGT 382
Db 1709 AGATAATTAACATCTAGTAAAGACAGATGACATATATGTCTTAAGTATGACATGT 1650
QY 383 TTTTGACATTTCCAGCCCTTTAAATATTCACACACAGAGAACCAAAAGAAAGACAC 442
Db 1649 TTTTGACATTTCCAGCCCTTTAAATATTCACACACAGAGAACCAAAAGAAAGACAC 1590
QY 443 AGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTATCATGATGAGCTGCCCTGT 502
Db 1589 AGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTATCATGATGAGCTGCCCTGT 1530
QY 503 GCCCTGTCGCCCTTGTGAGGAGAGACATTAAGAAATGAATGATGTGCTTAAAGGA 562
Db 1529 GCCCTGTCGCCCTTGTGAGGAGAGACATTAAGAAATGAATGATGTGCTTAAAGGA 1470
QY 563 TGGCGAGAAAAGATCTGTGTGATATTTTGAACGGGATTAACGATTTGAAT 622
Db 1469 TGGCGAGAAAAGATCTGTGTGATATTTTGAACGGGATTAACGATTTGAAT 1410
QY 623 GAAGTCACAAAGATGAGATTAACCAATGAGAGAAAAGACAGAAAATCTGTGAT 682
Db 1409 GAAGTCACAAAGATGAGATTAACCAATGAGAGAAAAGACAGAAAATCTGTGAT 1350
QY 683 CACAAAGCATGCAACAAACAAATGCAATCTGTGATGACATGAGCCAGCCAGCTGGG 742
Db 1349 CACAAAGCATGCAACAAACAAATGCAATCTGTGATGACATGAGCCAGCCAGCTGGG 1290
QY 743 AGGAGATACACAGGGGCGAGAGGATCTGTGAGGCTGCTGCTTAACCTGTGCTTC 802
Db 1289 AGGAGATACACAGGGGCGAGAGGATCTGTGAGGCTGCTGCTTAACCTGTGCTTC 1230
QY 803 ATAAACCAATCATTTTCAATTTTCTAACCCCTCAAAAACAAGCTGTGTAAATCTGATCTC 862
Db 1229 ATAAACCAATCATTTTCAATTTTCTAACCCCTCAAAAACAAGCTGTGTAAATCTGATCTC 1170
QY 863 TACGGTTCTCTTGTGGGCCCAACATTTCTCCATATATCCAGCCAGCTCATTTTAAATTT 922
Db 1169 TACGGTTCTCTTGTGGGCCCAACATTTCTCCATATATCCAGCCAGCTCATTTTAAATTT 1110
QY 923 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGATTAACATTAATCTGATCTTC 982
Db 1109 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGATTAACATTAATCTGATCTTC 1050
QY 983 AAAGACCTTCGTGTGTCTGCTCCCTAATATGTAGCTGACTGTTTTTCTTAAGAGTGTCTG 1042
Db 1049 AAAGACCTTCGTGTGTCTGCTCCCTAATATGTAGCTGACTGTTTTTCTTAAGAGTGTCTG 990
QY 1043 GCCCAGGGGATCTGTGAACAGGCTGGGAGAGATCTCAAGATCTTCCAGGGTTTACTTFA 1102
Db 989 GCCCAGGGGATCTGTGAACAGGCTGGGAGAGATCTCAAGATCTTCCAGGGTTTACTTFA 930

Db	1493	AGAAATCCCTGGGAAATAGCCCGCCGCACTCTGGGTCAATGCATAGACCTGCCTGT	1552
Qy	503	GCCGTGTCGGCTTGTGAGGGAGGACATTAGAAATGAATTGATGTCTTAAAGA	562
Db	1553	GCCGTGTCGGCTTGTGAGGGAGGACATTAGAAATGAATTGATGTCTTAAAGA	1612
Qy	563	TGGGCAGGAAACGATTCCTGTGTGTGATATTATTGAAACGGATTACGATTTGAAAT	622
Db	1613	TGGGCAGGAAACGATTCCTGTGTGTGATATTATTGAAACGGATTACGATTTGAAAT	1672
Qy	623	GAATTCACAAAGTAGACTTACAAATGAGAGAAACAGACGAAAAATCTTGATGCTT	682
Db	1673	GAATTCACAAAGTAGACTTACCAATGAGAGAAACAGACGAAAAATCTTGATGCTT	1732
Qy	683	CACAAGACATGCACAAACAAATGGAATAGTATGATGACATGAGGACGCCAACCTGGG	742
Db	1733	CACAAGACATGCACAAACAAATGGAATAGTATGATGACATGAGGACGCCAACCTGGG	1792
Qy	743	AGGAGATTAACACGGGGCAGAGGTCAGAGATTCTGGCCCTGTCTTAACCTGTGCTTC	802
Db	1793	AGGAGATTAACACGGGGCAGAGGTCAGAGATTCTGGCCCTGTCTTAACCTGTGCTTC	1852
Qy	803	ATAACCAAATCATTTCAATTTCTAACCTCAAAACAAAGCTGTGTGAATATCGATCTC	862
Db	1853	ATAACCAAATCATTTCAATTTCTAACCTCAAAACAAAGCTGTGTGAATATCGATCTC	1912
Qy	863	TACGGTTCCTTCTGGGCCAACAATCTTCATATATCCAGCCACACTATTTTAAATTTT	922
Db	1913	TACGGTTCCTTCTGGGCCAACAATCTTCATATATCCAGCCACACTATTTTAAATTTT	1972
Qy	923	AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTACTATTTGTTC	982
Db	1973	AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTACTATTTGTTC	2032
Qy	983	AAAAACCTTCGTGTGTGCTGCTCAATATATATAGCTGACTGTTTTTCTTAAGAGTGTCTG	1042
Db	2033	AAAAACCTTCGTGTGTGCTGCTCAATATATATAGCTGACTGTTTTTCTTAAGAGTGTCTG	2092
Qy	1043	GCCGAGGGGATCTGTGAACAGGCTGGGAGAGCATCTCAAGATCTTCCAGGGTTATCTTA	1102
Db	2093	GCCGAGGGGATCTGTGAACAGGCTGGGAGAGCATCTCAAGATCTTCCAGGGTTATCTTA	2152
Qy	1103	CTAGCACACAGCATGATCATTTACGAGTGAAATATCTAATCAACATCATCTCAGTGCT	1162
Db	2153	CTAGCACACAGCATGATCATTTACGAGTGAAATATCTAATCAACATCATCTCAGTGCT	2212
Qy	1163	TTGGCCCACTAGGAATTCATTTCCCACTTTGTGTGCCATCTCTCAAGCTCCAAATGTCA	1222
Db	2213	TTGGCCCACTAGGAATTCATTTCCCACTTTGTGTGCCATCTCTCAAGCTCCAAATGTCA	2272
Qy	1223	TTCCATTAAATTCACAGGATTAACCTTTTAACTGGGAAGAAATTCATAGTTACATG	1282
Db	2273	TTCCATTAAATTCACAGGATTAACCTTTTAACTGGGAAGAAATTCATAGTTACATG	2332
Qy	1283	CAGCTATGGGAATTTAATACATATTTTGTTCACGTGCAAGAGATGACTAAGTCTTTTA	1342
Db	2333	CAGCTATGGGAATTTAATACATATTTTGTTCACGTGCAAGAGATGACTAAGTCTTTTA	2392
Qy	1343	TCCTCTCCCTTTGTTTGATTTTTTTCACGATATAAGTTAAATGCTTAGCTGTACTG	1402
Db	2393	TCCTCTCCCTTTGTTTGATTTTTTTCACGATATAAGTTAAATGCTTAGCTGTACTG	2452
Qy	1403	AGGCTGTATACAGC 1416	
Db	2453	AGGCTGTATACAGC 2466	
RESULT 4			
US-09-352-616A-468			
; Sequence 468, Application US/09352616A			
; Patent No. 6395278			
; GENERAL INFORMATION:			
; APPLICANT: Dillon, Davin C.			

APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, JIANGCHUN
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.42708
CURRENT APPLICATION NUMBER: US/09/352.616A
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616A-468

Query Match 56.7%: Score 1154; DB 4; Length 3112;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

263 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACATCTGCTGAATGG 322
1313 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACATCTGCTGAATGG 1372
323 AGATTAATTAACATCACTAGAACACGACATGACATATATATGTTCTAAGTAGACATGT 382
1373 AGATTAATTAACATCACTAGAACACGACATGACATATATATGTTCTAAGTAGACATGT 1432
383 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAAGCAAAAGAAACAC 442
1433 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAAGCAAAAGAAACAC 1492
443 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTGATGATGAGCCCTGCGCTGT 502
1493 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTGATGATGAGCCCTGCGCTGT 1552
503 GCGTGTGCTCCGCTTGTGAGGAGGAGACATTAGAAATGATGATGCTTTAAAGGA 562
1553 GCGTGTGCTCCGCTTGTGAGGAGGAGACATTAGAAATGATGATGCTTTAAAGGA 1612
563 TGGGCGAGAAACAGATCTGTTGTGATATTTGAACGGGATTACAGATTTGAAT 622
1613 TGGGCGAGAAACAGATCTGTTGTGATATTTGAACGGGATTACAGATTTGAAT 1672
623 GAAGTCAAAAGTGAGCATTTACCAATGAGAGAAACAGAGAAATCTTGATGGCTT 682
1673 GAAGTCAAAAGTGAGCATTTACCAATGAGAGAAACAGAGAAATCTTGATGGCTT 1732
683 CACAAGCATGCAACAAACAAATGGAATCTGTGATGATGAGGAGCCAAAGCTGGGG 742
1733 CACAAGCATGCAACAAACAAATGGAATCTGTGATGATGAGGAGCCAAAGCTGGGG 1792
743 AGGAGATTAACGAGGGGCGAGAGGTCAGATTCGCGCCGCTCAAACTGCGCTTC 802
1793 AGGAGATTAACGAGGGGCGAGAGGTCAGATTCGCGCCGCTCAAACTGCGCTTC 1852
803 ATACCAAAATCATTTATTTCTAACCCTCAAAACAAAGCTGTTGAATATGATCTC 862
1853 ATACCAAAATCATTTATTTCTAACCCTCAAAACAAAGCTGTTGAATATGATCTC 1912
863 TACGGTCTCTTGGGCCCAACATTCCTCATATATCAGGACACATCATTTTAAATTT 922
1913 TACGGTCTCTTGGGCCCAACATTCCTCATATATCAGGACACATCATTTTAAATTT 1972
923 AGTTCCCAATCTGTACTGTGACTTTCTACATCTGAGATTAACATTTACATTTGTTTC 982
1973 AGTTCCCAATCTGTACTGTGACTTTCTACATCTGAGATTAACATTTACATTTGTTTC 2032
983 AAAGACCTTCTGTGCTGCTTAATATGATGATGATGATGATGATGATGATGATGATG 1042
2033 AAAGACCTTCTGTGCTGCTTAATATGATGATGATGATGATGATGATGATGATGATG 2092

1043 GCCCAGGAGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATACCTTA 1102
2093 GCCCAGGAGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATACCTTA 2152
1103 CTAGCAGACAGCATGATCATTTAGGAGTGAATATCTAATCAACATCATCTGAGTGTCT 1162
2153 CTAGCAGACAGCATGATCATTTAGGAGTGAATATCTAATCAACATCATCTGAGTGTCT 2212
1163 TTGCCCATCTGAATTCATTTCCCATTTTGTGCCCATTCTCAAGACCTCAAAATGTCA 1222
2213 TTGCCCATCTGAATTCATTTCCCATTTTGTGCCCATTCTCAAGACCTCAAAATGTCA 2272
1223 TTCCATTAATATGACAGATTAACCTTTTAACTGGAAGAAATTCAGTTACATG 1282
2273 TTCCATTAATATGACAGATTAACCTTTTAACTGGAAGAAATTCAGTTACATG 2332
1283 CACCTATGGAATTAATATCATATTTGTTTCCAGTGAAGATGACATACCTGCTTA 1342
2333 CACCTATGGAATTAATATCATATTTGTTTCCAGTGAAGATGACATACCTGCTTA 2392
1343 TCCCTCCCTTGTGATTTTTCAGATATAAGTTAAATGCTTACCTTACTG 1402
2393 TCCCTCCCTTGTGATTTTTCAGATATAAGTTAAATGCTTACCTTACTG 2452
1403 AGGCTGATACAC 1416
2453 AGGCTGATACAC 2466

RESULT 5

US-09-439-313-469/C
Sequence 469, Application US/09439313

Patent No. 6329505
GENERAL INFORMATION:

APPLICANT: Xu, JIANGCHUN
APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise

APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.

APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary

APPLICANT: Retter, Mark
APPLICANT: Solik, John

APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42709

CURRENT APPLICATION NUMBER: US/09/439, 313
NUMBER OF SEQ ID NOS: 575

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 469

LENGTH: 2229
TYPE: DNA

ORGANISM: Homo sapiens
US-09-439-313-469

Query Match 50.7%: Score 1033; DB 4; Length 2229;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;

Matches 1153; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

263 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACATCTGCTGAATGG 322
1775 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACATCTGCTGAATGG 1716
323 AGATTAATTAACATCACTAGAACACGACATGACATATATATGTTCTAAGTAGACATGT 382
1715 AGATTAATTAACATCACTAGAACACGACATGACATATATATGTTCTAAGTAGACATGT 1656
383 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAAGCAAAAGAAAGACAC 442
1655 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAAGCAAAAGAAAGACAC 1596

|||||
Db 1055 AAGACCTTGGTGTCTGCTTAATATGATGAGTGTGTTTCCTAAGAGGTTCTG 996
QY 1043 GCCCAGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTTACTTA 1102
Db 995 GCCCAGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTTACTTA 936
QY 1103 CTAGACACACAGCATGATCATTTACGGAGTAATTAATCAATCAATCATCTCTAGTCT 1162
Db 935 CTAGACACACAGCATGATCATTTACGGAGTAATTAATCAATCAATCATCTCTAGTCT 876
QY 1163 TTGGCCATCTGAATTCATTTCCACTTTTGCCCATCTCTCAAGCCCAAAATGTCA 1222
Db 875 TTGGCCATCTGAATTCATTTCCACTTTTGCCCATCTCTCAAGCCCAAAATGTCA 816
QY 1223 TTCCATTAATATCACAGATTTAACTTTTAACTGGAAGAAATTCATGTTACATG 1282
Db 815 TTCCATTAATATCACAGATTTAACTTTTAACTGGAAGAAATTCATGTTACATG 757
QY 1283 CAGCATAGGAATTTAATTAATTAATTTGTTTCCAGTGCAGAGATGACTAAGTCTTTA 1342
Db 756 CAGCATAGGAATTTAATTAATTAATTTGTTTCCAGTGCAGAGATGACTAAGTCTTTA 697
QY 1343 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATGCTTAGCCTGTACTG 1402
Db 696 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATGCTTAGCCTGTACTG 637
QY 1403 AGGCTGTATACAGC 1416
Db 636 AGGCTGTATACAGC 623

RESULT 7

US-09-439-313-471/c
: Sequence 471, Application US/09439313
: Patent No. 6329505
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang Yugu
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael
: APPLICANT: Fanger, Gary
: APPLICANT: Retter, Mark
: APPLICANT: Solk, John
: APPLICANT: Day, Craig
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C9
: CURRENT APPLICATION NUMBER: US/09/439, 313
: CURRENT FILING DATE: 1999-11-12
: NUMBER OF SEQ ID NOS: 575
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 471
: LENGTH: 812
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-439-313-471

Query Match 35.3%; Score 720; DB 4; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGGAATGG 322
Db 720 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGGAATGG 661
QY 323 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATGTCTAAGTAGTACATGT 382
Db 660 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATGTCTAAGTAGTACATGT 601

QY 383 TTTTGCACATTTCCAGCCCTTTTAATATCCACACACAGCAAGCAACAAAGAGACAC 442
Db 600 TTTTGCACATTTCCAGCCCTTTTAATATCCACACACAGCAAGCAACAAAGAGACAC 541
QY 443 AGAGATCCCTGGGGAATGCCCCGCCATCTGGGTCATGATGATGAGCTGGCCCTGT 502
Db 540 AGAGATCCCTGGGGAATGCCCCGCCATCTGGGTCATGATGATGAGCTGGCCCTGT 481
QY 503 GCCTGTCCCGCTTGTGAGGGAAGACATTTAGAAATGAATGATGTCTTTAAAGGA 562
Db 480 GCCTGTCCCGCTTGTGAGGGAAGACATTTAGAAATGAATGATGTCTTTAAAGGA 421
QY 563 TGGGCGAGAAACAGATCTGTGTGATTTTATTTTGAACCGGATTTACGATTTGAAT 622
Db 420 TGGGCGAGAAACAGATCTGTGTGATTTTATTTTGAACCGGATTTACGATTTGAAT 361
QY 623 GAAGTCACAAAGTAGCATTCACAAATGAGAGGAAACAGCAGAAATTTGATGGCTT 682
Db 360 GAAGTCACAAAGTAGCATTCACAAATGAGAGGAAACAGCAGAAATTTGATGGCTT 301
QY 683 CACAAGCATGCAACAAACAAATGGAATCTGTGATGACATGAGCGAGCAAGCTGGGG 742
Db 300 CACAAGCATGCAACAAACAAATGGAATCTGTGATGACATGAGCGAGCAAGCTGGGG 241
QY 743 AGGAGATTAACACAGGGGCGACAGGCTCAGGATTTGGCCCTGCTCTAACTGGCTTC 802
Db 240 AGGAGATTAACACAGGGGCGACAGGCTCAGGATTTGGCCCTGCTCTAACTGGCTTC 181
QY 803 ATTAACCAATCATTTTCATTTTCTAACCCTCAACAAACAGCTGTGATATGATCTC 862
Db 180 ATTAACCAATCATTTTCATTTTCTAACCCTCAACAAACAGCTGTGATATGATCTC 121
QY 863 TACGGTTCCTTGTGGGCCCAACATTCATATATCCAGCCACATCATTTTAAATATT 922
Db 120 TACGGTTCCTTGTGGGCCCAACATTCATATATCCAGCCACATCATTTTAAATATT 61
QY 923 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATTAACATTTGTTCTC 982
Db 60 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATTAACATTTGTTCTC 1

RESULT 8

US-09-352-616A-471/c
: Sequence 471, Application US/09352616A
: Patent No. 6395278
: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang, Yugu
: APPLICANT: Xu, Jiangchun
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
: FILE REFERENCE: 210121.427C8
: CURRENT APPLICATION NUMBER: US/09/352, 616A
: CURRENT FILING DATE: 1999-07-13
: NUMBER OF SEQ ID NOS: 472
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 471
: LENGTH: 812
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-352-616A-471

Query Match 35.3%; Score 720; DB 4; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGGAATGG 322
Db 720 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGGAATGG 661
QY 323 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATGTCTAAGTAGTACATGT 382

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Db 660 AGATATTTACATCTCTGAAACAGCAGATGACATATTAATGTTAGTAGTGACATGT 601
Qy 383 TTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAGAACACAAAAGAGACAC 442
Db 600 TTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAGAACACAAAAGAGACAC 541
Qy 443 AGAGATCCCTGGGAGAAATGCCCCGGCCCATCTTGGGTGATGAGCCCTCGCCCTGT 502
Db 540 AGAGATCCCTGGGAGAAATGCCCCGGCCCATCTTGGGTGATGAGCCCTCGCCCTGT 481
Qy 503 GCTGTGTCCTGCTGTGAGGAGAGACATTGAAAATGAATTGATGTTCTTCCTTAAAGA 562
Db 480 GCTGTGTCCTGCTGTGAGGAGAGACATTGAAAATGAATTGATGTTCTTCCTTAAAGA 421
Qy 563 TGGGAGAGAAACAGATCCTGTGTGATATTTATTTAGCGGATTAACAGATTTGAAT 622
Db 420 TGGGAGAGAAACAGATCCTGTGTGATATTTATTTAGCGGATTAACAGATTTGAAT 361
Qy 623 GAAGTCAAAAGTGAGCATTTACCAATGAGAGAAACAGAGAAATCTTGATGCGTT 682
Db 360 GAAGTCAAAAGTGAGCATTTACCAATGAGAGAAACAGAGAAATCTTGATGCGTT 301
Qy 683 CACAAGACATGCAACAAACAAATGGAATGATGATGATGATGAGGACAGCCAGCTGGGG 742
Db 300 CACAAGACATGCAACAAACAAATGGAATGATGATGATGATGAGGACAGCCAGCTGGGG 241
Qy 743 AGGAGATACACAGGGGAGAGGATGAGATTTGCGCCCTGCTCTTAACGTGCGCTTC 802
Db 240 AGGAGATACACAGGGGAGAGGATGAGATTTGCGCCCTGCTCTTAACGTGCGCTTC 181
Qy 803 ATACCAAAATGATTTGATTTTCTTAACCTCAAAACAAAGCGTTGTAATTCGATGTC 862
Db 180 ATACCAAAATGATTTGATTTTCTTAACCTCAAAACAAAGCGTTGTAATTCGATGTC 121
Qy 863 TAGGTTCTCTTGGGCCCCAATTTCCATATATCCAGCACACTATTTTAAATATT 922
Db 120 TAGGTTCTCTTGGGCCCCAATTTCCATATATCCAGCACACTATTTTAAATATT 61
Qy 923 AGTTCCGAGATCTGTACTGTGACCTTTTACACGTGAAATTAACATTTCTCTTTGTC 982
Db 60 AGTTCCGAGATCTGTACTGTGACCTTTTACACGTGAAATTAACATTTCTCTTTGTC 1

RESULT 9
US-09-439-313-313
; Sequence 313, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT FILING DATE: 1999-11-12
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature

```

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; LOCATION: (1)...(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-313

Query Match
Best Local Similarity 9.9%; Score 201; DB 4; Length 718;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 263 GGTGAGAAATAGAAAGGCTGCTGACTTTTACCATCTGAGGCGACACATCTGCTGAATGG 322
Db 73 GGTGAGAAATAGAAAGGCTGCTGACTTTTACCATCTGAGGCGACACATCTGCTGAATGG 132
Qy 323 AGATATTTACATCTCTGAAACAGCAGATGACATATTAATGTTAGTAGTGACATGT 382
Db 133 AGATATTTACATCTCTGAAACAGCAGATGACATATTAATGTTAGTAGTGACATGT 192
Qy 383 TTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAGAACACAAAAGAGACAC 442
Db 193 TTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAGAACACAAAAGAGACAC 252
Qy 443 AGAGATCCCTGGGAGAAATGCCCCGGCCCATCTTGGGTGATGAGCCCTCGCCCTGT 502
Db 253 AGAGATCCCTGGGAGAAATGCCCCGGCCCATCTTGGGTGATGAGCCCTCGCCCTGT 312
Qy 503 GCTGTGTCCTGCTGTGAGGAGAGACATTGAAAATGAATTGATGTTCTTCCTTAAAGA 562
Db 313 GCTGTGTCCTGCTGTGAGGAGAGACATTGAAAATGAATTGATGTTCTTCCTTAAAGA 372
Qy 563 TGG 565
Db 373 TGG 375

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RESULT 10
US-09-352-616A-313
; Sequence 313, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jlangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc_feature
; LOCATION: (1)...(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-313

Query Match
Best Local Similarity 9.9%; Score 201; DB 4; Length 718;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 263 GGTGAGAAATAGAAAGGCTGCTGACTTTTACCATCTGAGGCGACACATCTGCTGAATGG 322
Db 73 GGTGAGAAATAGAAAGGCTGCTGACTTTTACCATCTGAGGCGACACATCTGCTGAATGG 132
Qy 323 AGATATTTACATCTCTGAAACAGCAGATGACATATTAATGTTAGTAGTGACATGT 382
Db 133 AGATATTTACATCTCTGAAACAGCAGATGACATATTAATGTTAGTAGTGACATGT 192
Qy 383 TTTTGACATTTCCAGCCCTTTTAAATATCCACACACAGAGAACACAAAAGAGACAC 442

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Db 193 TTTTGCATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAAGGAACAC 252
QY 443 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGTATCATGAGCCTCGCCCTGT 502
Db 253 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGTATCATGAGCCTCGCCCTGT 312
QY 503 GCCTGGTCCCGCTTTGGAGGAAGGACATTAGAAAATGAATGTGTCTTAAAGA 562
Db 313 GCCTGATCCCGCTTTGGAGGAAGGACATTAGAAAATGAATGTGTCTTAAAGA 372
QY 563 TGG 565
Db 373 TGG 375

RESULT 11
US-09-232-149A-313
; Sequence 313, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-313

Query Match
Best Local Similarity 99.3%; Score 201; DB 4; Length 718;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 263 GGTGAGAAATAGAAAGGCTGCTACCTTACATCTGAGGCCACACATCTGTGAATGG 322
Db 73 GGTGAGAAATAGAAAGGCTGCTACCTTACATCTGAGGCCACACATCTGTGAATGG 132
QY 323 AGTAAATTAACATCACTAGAAACAGCAAGATGACATATATGTCTTAAGTAGACATGT 382
Db 133 AGTAAATTAACATCACTAGAAACAGCAAGATGACATATATGTCTTAAGTAGACATGT 192
QY 383 TTTTGCATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAAGGAACAC 442
Db 193 TTTTGCATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAAGGAACAC 252
QY 443 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGTATCATGAGCCTCGCCCTGT 502
Db 253 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGTATCATGAGCCTCGCCCTGT 312
QY 503 GCCTGGTCCCGCTTTGGAGGAAGGACATTAGAAAATGAATGTGTCTTAAAGA 562
Db 313 GCCTGATCCCGCTTTGGAGGAAGGACATTAGAAAATGAATGTGTCTTAAAGA 372
QY 563 TGG 565
Db 373 TGG 375

RESULT 12
US-09-439-313-287/C
; Sequence 287, Application US/09439313
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Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Rietter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 287
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-287

Query Match
Best Local Similarity 99.6%; Score 179; DB 4; Length 301;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 637 AGCATTAACATGAGGAGAAACAGACGAGAAATCTTGATGGCTTCACAGCATGCAA 656
Db 301 AGCATTAACATGAGGAGAAACAGACGAGAAATCTTGATGGCTTCACAGCATGCAA 242
QY 697 CAACAAAATGGAATACCTGATGATGACATGAGGAGCAACCTGGGAGGATTAACACG 756
Db 241 CAACAAAATGGAATACCTGATGATGACATGAGGAGCAACCTGGGAGGATTAACACG 182
QY 757 GGGCAGAGGGTCAAGATTTCTGGCCCTGCTCAAACTGCGTTCATAACCAATCAT 816
Db 181 GGGCAGAGGGTCAAGATTTCTGGCCCTGCTCAAACTGCGTTCATAACCAATCAT 122
QY 817 TCATATTTCACCCCTCAAAACAAAGCTGTTGTAATATCGATCTAGC 866
Db 121 TCATATTTCACCCCTCAAAACAAAGCTGTTGTAATATCGATCTAGC 72

RESULT 13
US-09-352-616A-287/C
; Sequence 287, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 287
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-287

Query Match
Best Local Similarity 99.6%; Score 179; DB 4; Length 301;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 637 AGCATTTACCAATGAGAGGAAAAACAGACGAGAAATCTTGATGGCTTCAAGACATGCAA 696
    |||||||
DB 301 AGCATTTACCAATGAGAGGAAAAACAGACGAGAAATCTTGATGGCTTCAAGACATGCAA 242
QY 697 CAACCAAAATGGAATACTGTGTATGACATGAGGACGACCAAGCTGGGAGAGATAACCAAG 756
    |||||||
DB 241 CAACCAAAATGGAATACTGTGTATGACATGAGGACGACCAAGCTGGGAGAGATAACCAAG 182
QY 757 GGGCAGAGGCTCAGAGATTCTGGCCCTGCTTAACCTGTGCTTCAATACCAATTCATT 816
    |||||||
DB 181 GGGCAGAGGCTCAGAGATTCTGGCCCTGCTTAACCTGTGCTTCAATACCAATTCATT 122
QY 817 TCATATTTCTAACCTCAAAACAAAGCTGTATATCTATCTATCTCTACG 866
    |||||||
DB 121 TCATATTTCTAACCTCAAAACAAAGCTGTATATCTATCTATCTCTACG 72

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RESULT 14

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US-09-232-149A-287/C
; Sequence 287, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Jennifer Lynn
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232.149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 287
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-149A-287

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Query Match      8.8%; Score 179; DB 4; Length 301;
Best Local Similarity 99.6%; Pred. No. 3e-77;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 637 AGCATTTACCAATGAGAGGAAAAACAGACGAGAAATCTTGATGGCTTCAAGACATGCAA 696
    |||||||
DB 301 AGCATTTACCAATGAGAGGAAAAACAGACGAGAAATCTTGATGGCTTCAAGACATGCAA 242
QY 697 CAACCAAAATGGAATACTGTGTATGACATGAGGACGACCAAGCTGGGAGAGATAACCAAG 756
    |||||||
DB 241 CAACCAAAATGGAATACTGTGTATGACATGAGGACGACCAAGCTGGGAGAGATAACCAAG 182
QY 757 GGGCAGAGGCTCAGAGATTCTGGCCCTGCTTAACCTGTGCTTCAATACCAATTCATT 816
    |||||||
DB 181 GGGCAGAGGCTCAGAGATTCTGGCCCTGCTTAACCTGTGCTTCAATACCAATTCATT 122
QY 817 TCATATTTCTAACCTCAAAACAAAGCTGTATATCTATCTATCTCTACG 866
    |||||||
DB 121 TCATATTTCTAACCTCAAAACAAAGCTGTATATCTATCTATCTCTACG 72

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RESULT 15

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US-09-620-312D-791
; Sequence 791, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom

```

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; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620.312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552.317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488.725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PL_FL_genes Version 1.0
; SEQ ID NO 791
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(789)
US-09-620-312D-791

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Query Match      1.3%; Score 26; DB 4; Length 1379;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 120.911 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2003, 19:58:56 ; Search time 69 seconds
(without alignments)
326.240 Million cell updates/sec

Title: US-09-402-713A-2

Perfect score: 51

Sequence: 1 MFLHISPFKPHPTQEAQKE.....HLGSSMLALCLVPLVREGH 51

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	Xgapop 60.0 , Ygapext 60.0
	Fgapop 6.0 , Fgapext 7.0
	Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135271

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCCALIGN=200 -THR.SCORE=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptlo -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09402713.ecgn.1.1.56.0runat_26092003_143100_16996 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEOUVERY -NEG.SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

- 1: Issued.Patents.NA.*
- 2: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/Backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	51	100.0	812	4	US-09-439-313-471
C 2	51	100.0	812	4	US-09-352-616A-471
C 3	51	100.0	2229	4	US-09-439-313-469
C 4	51	100.0	2229	4	US-09-352-616A-469
C 5	51	100.0	2426	4	US-09-439-313-470
C 6	51	100.0	2426	4	US-09-352-616A-470
C 7	51	100.0	3112	4	US-09-439-313-468
C 8	51	100.0	3112	4	US-09-352-616A-468
C 9	43	84.3	718	4	US-09-439-313-313
C 10	43	84.3	718	4	US-09-352-616A-313
C 11	43	84.3	718	4	US-09-232-149A-313
C 12	8	15.7	30001	1	US-08-125-468-1

C 13	8	15.7	30001	2	US-08-474-933-1	Sequence 1, Appl1
C 14	7	13.7	490	4	US-09-495-050A-219	Sequence 219, App
C 15	7	13.7	547	4	US-09-702-705-65	Sequence 65, Appl
C 16	7	13.7	547	4	US-09-736-457-65	Sequence 65, Appl
C 17	7	13.7	588	3	US-09-129-030-27	Sequence 27, Appl
C 18	7	13.7	745	4	US-09-581-001B-20	Sequence 20, Appl
C 19	7	13.7	1335	4	US-09-107-532A-298	Sequence 298, App
C 20	7	13.7	1376	2	US-08-868-288A-2	Sequence 2, Appl1
C 21	7	13.7	1376	3	US-09-235-372-2	Sequence 2, Appl1
C 22	7	13.7	1376	3	US-09-388-993-2	Sequence 2, Appl1
C 23	7	13.7	1467	4	US-09-252-991A-1331	Sequence 1331, Ap
C 24	7	13.7	1578	3	US-09-044-404A-1	Sequence 1, Appl1
C 25	7	13.7	1578	4	US-09-586-924-1	Sequence 1, Appl1
C 26	7	13.7	1621	4	US-09-996-243-147	Sequence 147, App
C 27	7	13.7	2163	4	US-09-328-352-639	Sequence 639, App
C 28	7	13.7	2268	4	US-09-620-312D-909	Sequence 909, App
C 29	7	13.7	2329	4	US-09-411-977-1	Sequence 1, Appl1
C 30	7	13.7	2437	1	US-07-795-859B-5	Sequence 5, Appl1
C 31	7	13.7	2437	1	US-08-457-616-5	Sequence 5, Appl1
C 32	7	13.7	2437	4	US-09-235-538-1	Sequence 1, Appl1
C 33	7	13.7	2538	4	US-09-252-991A-1285	Sequence 1285, Ap
C 34	7	13.7	2571	4	US-09-147-949A-1	Sequence 1279, Ap
C 35	7	13.7	2600	1	US-08-147-949A-1	Sequence 1, Appl1
C 36	7	13.7	2798	4	US-09-484-970B-90	Sequence 90, Appl1
C 37	7	13.7	3023	4	US-09-203-453-4	Sequence 4, Appl1
C 38	7	13.7	3023	4	US-09-900-236-4	Sequence 4, Appl1
C 39	7	13.7	3063	3	US-09-086-912-1	Sequence 1, Appl1
C 40	7	13.7	3066	4	US-09-203-453-1	Sequence 1, Appl1
C 41	7	13.7	3066	4	US-09-900-236-1	Sequence 1, Appl1
C 42	7	13.7	3218	4	US-09-221-017B-255	Sequence 255, App
C 43	7	13.7	13188	4	US-08-961-527-70	Sequence 70, Appl
C 44	7	13.7	31328	4	US-09-215-694-19	Sequence 19, Appl
C 45	7	13.7	36651	4	US-09-738-894A-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-439-313-471/C
Sequence 471, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqun
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 471
LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-471

Alignment Scores:
Pred. No.: 1.59e-44
Score: 51.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 812
Matches: 51
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
DB: 4

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US-09-402-713a-2 (1-51) x US-09-439-313-471 (1-812)
QY 1 MetPheLeuHisIleSerSerProPheLysTyPProHisThrGlnGluAlaGlnLysGlu 20
Db 604 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 545
QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCGCCGCATCTTGTCATCGATGAGCCCTCGCC 485
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 484 CTGTGCTGTGCTCCGCTTGAGGAGGAGGACAT 452

RESULT 2
US-09-352-616a-471/c
; Sequence 471, Application US/09352616a
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqun
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616a
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616a-471

Alignment Scores:
Pred. No.: 1,59e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x US-09-352-616a-471 (1-812)
QY 1 MetPheLeuHisIleSerSerProPheLysTyPProHisThrGlnGluAlaGlnLysGlu 20
Db 604 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 545
QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCGCCGCATCTTGTCATCGATGAGCCCTCGCC 485
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 484 CTGTGCTGTGCTCCGCTTGAGGAGGAGGACAT 452

RESULT 3
US-09-439-313-469/c
; Sequence 469, Application US/09439313
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqun
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
```

```
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS OF METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-469

Alignment Scores:
Pred. No.: 4.16e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x US-09-439-313-469 (1-2229)
QY 1 MetPheLeuHisIleSerSerProPheLysTyPProHisThrGlnGluAlaGlnLysGlu 20
Db 1659 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 1600
QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 1599 GCACAGAGATCCCTGGGAGAAATGCCGCCGCATCTTGTCATCGATGAGCCCTCGCC 1540
QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 1539 CTGTGCTGTGCTCCGCTTGAGGAGGAGGACAT 1507

RESULT 4
US-09-352-616a-469/c
; Sequence 469, Application US/09352616a
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqun
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616a
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616a-469

Alignment Scores:
Pred. No.: 4.16e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x US-09-352-616a-469 (1-2229)
QY 1 MetPheLeuHisIleSerSerProPheLysTyPProHisThrGlnGluAlaGlnLysGlu 20
Db 1 MetPheLeuHisIleSerSerProPheLysTyPProHisThrGlnGluAlaGlnLysGlu 20
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Db      1659 ATGTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAAGGAA 1600
Oy      21 AlAGlnArSerLeuGlUmEtProGlyArGhISleuGlySerSerMetSerLeuA 40
        |||||||
Db      1599 GCACAGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTATCATGATGAGCTCGCC 1540
Oy      41 LeuCysLeuValProLeuValArGluGlyHis 51
        |||||||
Db      1539 CTGTGCTGTGTCGCCGCTTGTGAGGGAAGACAT 1507

RESULT 5
US-09-439-313-470/c
; Sequence 470, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439, 313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-470

Alignment Scores:
Pred. No.:      4.5e-44      Length:      2426
Score:          51.00      Matches:      51
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             4           Gaps:          0

US-09-402-713A-2 (1-51) x US-09-439-313-470 (1-2426)
Oy      1 MetPheLeuHISleSerSerProPheLysTyrProHISThrGlnGluAlaGlnLysGlu 20
        |||||||
Db      1653 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAAGGAA 1594
Oy      21 AlAGlnArSerLeuGlUmEtProGlyArGhISleuGlySerSerMetSerLeuA 40
        |||||||
Db      1593 GCACAGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTATCATGATGAGCTCGCC 1534
Oy      41 LeuCysLeuValProLeuValArGluGlyHis 51
        |||||||
Db      1533 CTGTGCTGTGTCGCCGCTTGTGAGGGAAGACAT 1501

RESULT 6
US-09-352-616A-470/c
; Sequence 470, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
```

```
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352, 616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-470

Alignment Scores:
Pred. No.:      4.5e-44      Length:      2426
Score:          51.00      Matches:      51
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             4           Gaps:          0

US-09-402-713A-2 (1-51) x US-09-352-616A-470 (1-2426)
Oy      1 MetPheLeuHISleSerSerProPheLysTyrProHISThrGlnGluAlaGlnLysGlu 20
        |||||||
Db      1653 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAAGGAA 1594
Oy      21 AlAGlnArSerLeuGlUmEtProGlyArGhISleuGlySerSerMetSerLeuA 40
        |||||||
Db      1593 GCACAGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTATCATGATGAGCTCGCC 1534
Oy      41 LeuCysLeuValProLeuValArGluGlyHis 51
        |||||||
Db      1533 CTGTGCTGTGTCGCCGCTTGTGAGGGAAGACAT 1501

RESULT 7
US-09-439-313-468
; Sequence 468, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439, 313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-468

Alignment Scores:
Pred. No.:      5.71e-44      Length:      3112
Score:          51.00      Matches:      51
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             4           Gaps:          0

US-09-402-713A-2 (1-51) x US-09-439-313-468 (1-3112)
Oy      1 MetPheLeuHISleSerSerProPheLysTyrProHISThrGlnGluAlaGlnLysGlu 20
```

```
Db      1429 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 1488
Qy      21 AlaglnArgSerLeuGlyMetProGlyArgHisLeuGlySerMetSerLeuAla 40
Db      1489 GCACAGAGATCCCTGGGAGAAATGCCGCGCCCACTTGGGTATCATGATGAGCCTCGCC 1548
Qy      41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db      1549 CTGTGCTGTGCTCCGCTTGTGAGGAGGAGACAT 1581

RESULT 8
US-09-352-616A-468
; Sequence 468, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-468

Alignment Scores:
Pred. No.:      5 71e-44      Length:      3112
Score:          51.00      Matches:      31
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             4          Gaps:      0

US-09-402-713A-2 (1-51) x US-09-352-616A-468 (1-3112)
Qy      1 MetPheLeuHisIleSerSerProPheIleTyProHisThrGlnGluAlaGlnGly 20
Db      1429 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 1488
Qy      21 AlaglnArgSerLeuGlyMetProGlyArgHisLeuGlySerMetSerLeuAla 40
Db      1489 GCACAGAGATCCCTGGGAGAAATGCCGCGCCCACTTGGGTATCATGATGAGCCTCGCC 1548
Qy      41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db      1549 CTGTGCTGTGCTCCGCTTGTGAGGAGGAGACAT 1581

RESULT 9
US-09-439-313-313
; Sequence 313, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
```

```
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-313

Alignment Scores:
Pred. No.:      3.06e-36      Length:      718
Score:          43.00      Matches:      43
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    84.31%      Indels:      0
DB:             4          Gaps:      0

US-09-402-713A-2 (1-51) x US-09-439-313-313 (1-718)
Qy      1 MetPheLeuHisIleSerSerProPheIleTyProHisThrGlnGluAlaGlnGly 20
Db      189 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGGAGCAAAAGGAA 248
Qy      21 AlaglnArgSerLeuGlyMetProGlyArgHisLeuGlySerMetSerLeuAla 40
Db      249 GCACAGAGATCCCTGGGAGAAATGCCGCGCCCACTTGGGTATCATGATGAGCCTCGCC 308
Qy      41 LeuCysLeu 43
Db      309 CTGTGCTGTG 317

RESULT 10
US-09-352-616A-313
; Sequence 313, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-313

Alignment Scores:
Pred. No.:      3.06e-36      Length:      718
Score:          43.00      Matches:      43
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    84.31%      Indels:      0
DB:             4          Gaps:      0
```

US-09-402-713A-2 (1-51) x US-09-352-616A-313 (1-718)

QY 1 MetpHeuHsIleSerSerProPhelyTyrProHsIstHnGlnGluAlaGlnysGlu 20
|||||
Db 189 ATGTTTGGCATTTCAGCCCTTTTAATATCCACACACAGAAACAAAGAA 248

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHsIleGlySerMetSerLeuAla 40
|||||
Db 249 GCACAGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTATCATGATGAGCTCGCC 308

QY 41 LeuGlySer 43
|||||
Db 309 CTGTGCTG 317

RESULT 11
US-09-232-149A-313
; Sequence 313, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-313

Alignment Scores:
Pred. No.: 3,06e-36 Length: 718
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.31% Indels: 0
Gaps: 0
DB: 4

US-09-402-713A-2 (1-51) x US-09-232-149A-313 (1-718)

QY 1 MetpHeuHsIleSerSerProPhelyTyrProHsIstHnGlnGluAlaGlnysGlu 20
|||||
Db 189 ATGTTTGGCATTTCAGCCCTTTTAATATCCACACACAGAAACAAAGAA 248

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHsIleGlySerMetSerLeuAla 40
|||||
Db 249 GCACAGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTATCATGAGCTCGCC 308

QY 41 LeuGlySer 43
|||||
Db 309 CTGTGCTG 317

RESULT 12
US-08-125-468-1/C
; Sequence 1, Application US/08125468
; Patent No. 5589385
; GENERAL INFORMATION:
; APPLICANT: Ryan, Michael J.
; APPLICANT: Lotvin, Jason A.
; APPLICANT: Strathy, Nancy
; APPLICANT: Fantini, Susan E.
; TITLE OF INVENTION: Cloning of the biosynthetic pathway for
; TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmid
; TITLE OF INVENTION: useful therein

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,255-02
TELEPHONE: (201)831-3241
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-125-468-1

Alignment Scores:
Pred. No.: 316 Length: 30001
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.69% Indels: 0
Gaps: 0
DB: 1

US-09-402-713A-2 (1-51) x US-08-125-468-1 (1-30001)

QY 39 LeuAlaLeuGlySerLeuValProLeu 46
|||||
Db 19783 CTGGCGCTGTGGCTGTGCGCTG 19760

RESULT 13
US-08-474-993-1/C
; Sequence 1, Application US/08474933
; Patent No. 5866410
; GENERAL INFORMATION:
; APPLICANT: Ryan, Michael J.
; APPLICANT: Lotvin, Jason A.
; APPLICANT: Strathy, Nancy
; APPLICANT: Fantini, Susan E.
; TITLE OF INVENTION: Cloning of the biosynthetic pathway for
; TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmid
; TITLE OF INVENTION: useful therein
; NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

```

: APPLICATION NUMBER: US/08/474,933
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/125,468
: FILING DATE: 22-SEP-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Tsevdos, Estelle J
: REGISTRATION NUMBER: 31,145
: REFERENCE/DOCKET NUMBER: 31,255-02
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201)831-3241
: TELEFAX: (201)831-3305
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30001 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-474-933-1

```

```

Alignment Scores:
Pred. No.: 316 Length: 30001
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.69% Indels: 0
DB: 2 Gaps: 0

```

US-09-402-713A-2 (1-51) x US-08-474-933-1 (1-30001)

```

QY 39 LeuAlaLeuCySLeuValProLeu 46
DB 19783 CTGGCCCTCTGCTGCTGCTGCTG 19760

```

```

RESULT 14
US-09-495-050A-219/C
: Sequence 219, Application US/09495050A
: Patent No. 6492505
: GENERAL INFORMATION:
: APPLICANT: Roopa, Reddy
: APPLICANT: Guegler, Karl, J.
: APPLICANT: Au-Young, Janice
: TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
: FILE REFERENCE: PA-0013 US
: CURRENT APPLICATION NUMBER: US/09/495,050A
: PRIORITY FILING DATE: 2000-01-31
: PRIOR APPLICATION NUMBER: 60/118,318
: NUMBER OF SEQ ID NOS: 305
: SOFTWARE: PERL Program
: SEQ ID NO 219
: LENGTH: 490
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No. 6492505 2553280CT1
US-09-495-050A-219

```

```

Alignment Scores:
Pred. No.: 69.2 Length: 490
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.73% Indels: 0
DB: 4 Gaps: 0

```

US-09-402-713A-2 (1-51) x US-09-495-050A-219 (1-490)

```

QY 3 LeuHisIleSer*SerProPhe 9
|||||

```

DB 346 TTACATATTTCTTCCTTTT 326

```

RESULT 15
US-09-702-705-65/C
: Sequence 65, Application US/09702705
: Patent No. 6504010
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Iodes, Michael A.
: APPLICANT: Panger, Gary
: APPLICANT: Vedvick, Tom
: APPLICANT: Carter, Darrick
: APPLICANT: Retter, Marc
: APPLICANT: Mannion, Jane
: APPLICANT: Pan, Liqun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.478C14
: CURRENT APPLICATION NUMBER: US/09/702,705
: PRIORITY FILING DATE: 2000-10-30
: NUMBER OF SEQ ID NOS: 1833
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 65
: LENGTH: 547
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (1)...(547)
: OTHER INFORMATION: n = A,T,C or G
US-09-702-705-65

```

```

Alignment Scores:
Pred. No.: 76.9 Length: 547
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.73% Indels: 0
DB: 4 Gaps: 0

```

US-09-402-713A-2 (1-51) x US-09-702-705-65 (1-547)

```

QY 5 IleSerSerProPheLysTyr 11
|||||
DB 164 ATCTCTCTCTCTTCAATAT 144

```

Search completed: September 26, 2003, 21:39:29
Job time : 76 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:01:08 : Search time 7412.95 Seconds
(without alignments)
11241.524 Million cell updates/sec

Title: US-09-402-713a-1
Perfect score: 2037
Sequence: 1 agaagctgcacacgaataa.....caataagaattacaaga 2037

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues
Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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22: em_ov:*
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32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rod:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlg_hum:*
40: em_hlg_mus:*
41: em_hlg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2037	100.0	2037	6	BD082482
2	1775	87.1	1872	6	BD082483
3	1629	80.0	3582	6	BD082485
4	1629	80.0	3923	6	AR261166
5	1629	80.0	3923	6	AR278697
6	1629	80.0	3923	6	AX200988
7	1629	80.0	3923	6	AX267716
8	1629	80.0	3923	6	AF103907
9	1185	58.2	5435	9	AF103908
10	1154	56.7	2426	6	AR261038
11	1154	56.7	2426	6	AR278569
12	1154	56.7	2426	6	AX106206
13	1154	56.7	2426	6	AX106689
14	1154	56.7	2426	6	AX140980
15	1154	56.7	2426	6	AX200840
16	1154	56.7	2426	6	AX267496
17	1154	56.7	3112	6	AR261036
18	1154	56.7	3112	6	AR278567
19	1154	56.7	3112	6	AX106204
20	1154	56.7	3112	6	AX106687
21	1154	56.7	3112	6	AX140978
22	1154	56.7	3112	6	AX200838
23	1154	56.7	3112	6	AX267494
24	1033	50.7	2229	6	AR261037
25	1033	50.7	2229	6	AR278568
26	1033	50.7	2229	6	AX106205
27	1033	50.7	2229	6	AX106688
28	1033	50.7	2229	6	AX140979
29	1033	50.7	2229	6	AX200839
30	1033	50.7	2229	6	AX267495
31	972	47.7	128480	9	AL359314
32	723	35.5	820	6	BD082484
33	720	35.3	812	6	AR261039
34	720	35.3	812	6	AR278570
35	720	35.3	812	6	AX106207
36	720	35.3	812	6	AX106690
37	720	35.3	812	6	AX140981
38	720	35.3	812	6	AX200841
39	720	35.3	812	6	AX267497
40	473	23.2	597	6	BD078456
41	276	13.5	129109	9	AL390239
42	241	11.8	481	6	BD119166
43	233	11.4	359	6	AX018075
44	233	11.4	359	6	BD134961
45	210	10.3	278	6	AX107858

ALIGNMENTS

RESULT 1
BD082482
LOCUS: BD082482 2037 bp. DNA linear PART 27-AUG-2002
DEFINITION: PCA3, PCA3 genes, and methods of use.
ACCESSION: BD082482
VERSION: BD082482.1 GI:22628092
KEYWORDS: JP 2001522240-A/1.
SOURCE: JP 2001522240-A/1.
ORGANISM: Mastadenovirus
Mastadenovirus
Viruses; dsDNA viruses, no RNA stage; Adenoviridae.
1 (bases 1 to 2037)
REFERENCE: Bussemakers, M.J.G.
TITLE: PCA3, PCA3 genes, and methods of use
JOURNAL: Patent: JP 2001522240-A 1 13-NOV-2001;
DIAGNOCURE INC SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES

COMMENT JP 2001522240-A/1
PN 13-NOV-2001
PD 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC
C1201/68,
PC G01N33/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 379..531.
Location/Qualifiers
1..2037
/organism="Mastadenovirus"
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BASE COUNT 622 a 426 c 406 g 575 t 8 others
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Query Match 100.0%; Score 2037; DB 6; Length 2037;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2037; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AGAAGCTGGCATCGAAGAAACAGAGGGGAGATTGTGTGGCTGCAGCCGAGGAGACCAG 60
QY 61 GAAGATCGCATGGTGGGAAGAGACCTGATGATACAGAGAAATTACACACATTAATCTTAG 120
Db 61 GAAGATCGCATGGTGGGAAGAGACCTGATGATACAGAGAAATTACACACATTAATCTTAG 120
QY 121 TGTTCATGAAACCCAGATTAATTAAGTGAAGAGCTAGTCCGTGTGAGTCTCCAGT 180
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Db 1081 GATCTTTCCAGGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1140
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Db 1201 TTCTCAAGACCTCAAAATGTCATTCATTAATTAATTAATTAATTAATTAATTAATTA 1260
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Db 1321 GCAAGATGACTAAGCTTATTCCTTATCCCTGCTTGTGTTGTTTTCAGATTAATTA 1380
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QY 1501 CCTTGAACATGTCAGGNCATCATTTTCTTCTGCTGAGAAAGCTTCTGCTGCTT 1560
Db 1501 CCTTGAACATGTCAGGNCATCATTTTCTTCTGCTGAGAAAGCTTCTGCTGCTT 1560
QY 1561 AANTCTGAATGATGTAAGTTTGAATTAAGTTGACTATCTTCTTCTGAGAAAGG 1620
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Db 1801 CATTTCTATCTATCTATCAACAATATATCAACAAGCTTTTTCACAGATTCATGACGTCAAA 1860
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Db 1861 TCCCAAGGTAACCTTTATCCATTTCAATGAGTACGCGCTTGAATTTTGGCAATCA 1920
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Db 1921 TACTGTCTACTATCTCACTTGAAGTGTGCTTGTGCTTGTAGTAATTTGAAGAATA 1980
OY 1981 GGGCAGCTTGTGAGGCACTTTAGGCTTCACTCTCGCAATAAAGATTTTACAAAGA 2037
Db 1981 GGGCAGCTTGTGAGGCACTTTAGGCTTCACTCTCGCAATAAAGATTTTACAAAGA 2037

RESULT 2

BD082483 1872 bp DNA linear PAT 27-AUG-2002
LOCUS BD082483
DEFINITION PCA3, PCA3 genes, and methods of use.
ACCESSION BD082483
VERSION BD082483.1 GI:22628093
KEYWORDS JP 2001522240-A/2.
SOURCE Mastadenovirus
ORGANISM Mastadenovirus

REFERENCE 1 (bases 1 to 1872)
Virus; dsDNA viruses, no RNA stage; Adenoviridae.

AUTHORS Bussemakers, M.J.G.
TITLE PCA3, PCA3 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 2 13-NOV-2001;
DIAGNOCURE INC

COMMENT

PN JP 2001522240-A/2
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC
C1201/68,
PC GOIN13/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.

FEATURES
source 1..1872 Location/Qualifiers
BASE COUNT 567 a 389 c 369 g 539 t 8 others
ORIGIN

Query Match 87.1%; Score 1775; DB 6; Length 1872;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1883	ATTTCANCGTAGAGCCGTTTAGAATTTTGGCAAAATCATATGCGTCACTTATTCACACTT	1942
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QY	1943	TGAGATGTGTTTGTCTCTGTAGTAATTTGAAGAAGAAATAGGCGACTCTGTGAGCACACTT	2002
Db	1778	TGAGATGTGTTTGTCTCTGTAGTAATTTGAAGAAGAAATAGGCGACTCTGTGAGCACACTT	1837
QY	2003	AGGCTTCACTCCTGGCAATTAAGAATTTACAAAGA	2037
Db	1838	AGGCTTCACTCCTGGCAATTAAGAATTTACAAAGA	1872

RESULT 3				
LOCUS	BD082485			
DEFINITION	BD082485	3582 bp	DNA	Linear
ACCESSION	BD082485			
VERSION	BD082485.1	GI:22628095		
KEYWORDS	JP 2001522240-A/4.			
SOURCE	Mastadenovirus			
ORGANISM	Mastadenovirus			
REFERENCE	Virus(es); dsDNA virus(es), no RNA stage; Adenoviridae.			
AUTHORS	I (bases 1 to 3582)			
TITLE	Bussemakers, M.J.G.			
JOURNAL	PCAT3, PCAT3 genes, and methods of use			
	Patent: JP 2001522240-A 4.13-NOV-2001;			

COMMENT	DIAGNOCURE INC
PN	JP 2001522240-A/4
PD	13-NOV-2001
PF	09-APR-1998 JP 1998542194
PR	10-APR-1997 US 60/041836
PI	MARION J G BUSSEMAKERS
PC	C12N15/00,C12N15/12,C12N5/12,C07K14/47,C07K16/18, FC C12Q1/68,
PC	G01N33/577,A61K39/395,A01K67/027
CC	Strandedness: Double;
CC	Topology: Linear;
CH	
EH	Key
FT	CDS 401..553.
FEATURES	Location/Qualifiers
source	1..3582
	/organism="Mastadenovirus"
	/mol_type="genomic DNA"
	/db_xref="taxon:10509"
BASE COUNT	1052 a 787 c 680 g 1063 t
ORIGIN	

Query Match	80.0%;	Score 1629;	DB 6;	Length 3582;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 2029;	Conservative	0;	Mismatches 8;	Indels 0;
				Gaps 0;
QY	1	AGAAGCTGGCATCGAATAACAGAGGAGATTTGTGTGGCTGCGACCCGAGGAGACCCAG	60	
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QY	61	GAGATCTGCATGTTGGGAGACCTGTATGATACAGAGAAATTACACATATATCTTAA	120	

Dp	83	GAAGATCTGCATGCTGGGGAAGGACCTGATGATACAGAGGAATTTACAAACATATACCTAG	142
QY	121	TGTTTCATGAACACCCAGATTAATTAAGTGAAGACCTAGTCCGCTGTGAGTCTCTCACT	180
Dp	143	TGTTTCATGAACACCCAGATTAATTAAGTGAAGACCTAGTCCGCTGTGAGTCTCTCACT	202
QY	181	GACACAGGGCTGAGTACCATCGACGAGGACCTTCTGAGTACTGACATGAGCAAAAGAA	240
Dp	203	GACACAGGGCTGAGTACCATCGACGAGGACCTTCTGAGTACTGACATGAGCAAAAGAA	262
QY	241	CTACAGACATCTCAATGGCAGGGGTGAGAAATAGAAGAGCTGCTGACTTTACATCTGA	300
Dp	263	CTACAGACATCTCAATGGCAGGGGTGAGAAATAGAAGAGCTGCTGACTTTACATCTGA	322
QY	301	GGCCACACATCTGCTGGAATGGAGTAATTAACATCATTAGAAAGAGCAAGATGACATA	360
Dp	323	GGCCACACATCTGCTGGAATGGAGTAATTAACATCATTAGAAAGAGCAAGATGACATA	382
QY	361	TAATGCTPAAGTAGTACATGTTTTGGACATTTCCAGCCCTTAAATATTCACACACA	420
Dp	383	TAATGCTPAAGTAGTACATGTTTTGGACATTTCCAGCCCTTAAATATTCACACACA	442
QY	421	CAGSAGACAAAAGSAGACAGAGATCCCGGGAGAAATCCCGCGGCATCTGGG	480
Dp	443	CAGSAGACAAAAGSAGACAGAGATCCCGGGAGAAATCCCGCGGCATCTGGG	502
QY	481	TCATCGATGAGCCCTGCCCTGTGCTCCGCTTGTGAGGGAGAGCATTAGAAAATG	540
Dp	503	TCATCGATGAGCCCTGCCCTGTGCTCCGCTTGTGAGGGAGAGCATTAGAAAATG	562
QY	541	AATGATGTCGTTCTTAAAGATGGGCGAGAAAACAGATCCTGTTGTGATATTTATTTG	600
Dp	563	AATGATGTCGTTCTTAAAGATGGGCGAGAAAACAGATCCTGTTGTGATATTTATTTG	622
QY	601	AACGGATATACAGATTTGAAATGAAGTACAAAGTACACATTTACCATAGAGAGAAACA	660
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QY	661	GACGAGAAAATCTTGATGGCTTCACAGACATGCACAAACAAAATGGAATACTGTGATG	720
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Dp	743	ACATGAGGACGACAACTGGGGAGAGATAACCAAGGGGCGAGAGGTGAGATTTCTGGCC	802
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Dp	803	CTGCTGCCTTAAACTGTGGCTTCATPACCAAAATCATTTTCATATTTCTCAACCTCAAAACA	862
QY	841	AGCTGTGTAAATATCTGATCTCTACGGTTCCTTGTGGGCCCAACATTTCTCATATATCCA	900
Dp	863	AGCTGTGTAAATATCTGATCTCTACGGTTCCTTGTGGGCCCAACATTTCTCATATATCCA	922
QY	901	GCCACACATCTTAAATATTTAGTCTCCCAATCTGTAAGTCTGACCTTTACACTGTAG	960
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QY	961	AATAACATTAATCTATTTTGTCCAAAGACCTTTCGTGTTGCTGCTAATATAGTACTACT	1020
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QY	1021	GTTTTTCTTAAGSAGTGTTCGGCCACAGGGATCTGTGAACAGGCTGGGAAGCATCTCAA	1080
Dp	1043	GTTTTTCTTAAGSAGTGTTCGGCCACAGGGATCTGTGAACAGGCTGGGAAGCATCTCAA	1102
QY	1081	GATCTTTCCAGGAGTATCTACTACTAGACACACAGATGATCATTACGAGAGTAAATATCTA	1140
Dp	1103	GATCTTTCCAGGAGTATCTACTACTAGACACACAGATGATCATTACGAGAGTAAATATCTA	1162
QY	1141	ATCAACATCATCTCAGTCTGTTCGCCATACAGTGAATTCATTTCCACTTTTGTGCCCA	1200
Dp	1163	ATCAACATCATCTCAGTCTGTTCGCCATACAGTGAATTCATTTCCACTTTTGTGCCCA	1222

1201 TTCTCAGACCTCAAAATGTCATTTCATTAATATCAGAGATTAACTTTTTTTTAAACC 1260
1223 TTCTCAGACCTCAAAATGTCATTTCATTAATATCAGAGATTAACTTTTTTTTAAACC 1282
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1343 GCAAGAGTACATAAGTCTTTATCCCTCCCTTTGTTTATTTTTTTTCCAGTAAAGT 1402
1381 TAAATAGTCTTACCTTTGTCAGAGCTGTATACAGACAGCCCTCCCATCCCTCCAGC 1440
1403 TAAATAGTCTTACCTTTGTCAGAGCTGTATACAGACAGCCCTCCCATCCCTCCAGC 1462
1441 CTATTCGTGATCACCATCAACCCCTCCCATNYSMACCTAAACAAATCTAAGTTGAAT 1500
1463 CTATTCGTGATCACCATCAACCCCTCCCATNYSMACCTAAACAAATCTAAGTTGAAT 1522
1501 CCTTGAACATGTCAGACATACATATTTCTCTGCTGAGAGAGCTCTCTCTCTCTCT 1560
1523 CCTTGAACATGTCAGACATACATATTTCTCTGCTGAGAGAGCTCTCTCTCTCTCT 1582
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1621 ACACATATGATGATCATCATCATGAGACAGCAAAATCTAAAGTGAATTTGATTA 1680
1643 ACACATATGATGATCATCATCATGAGACAGCAAAATCTAAAGTGAATTTGATTA 1702
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1763 TGTAAAGCTGTGATGTAAGMAAGGACAGAGAACTCATAGTATCTTATATATATCT 1822
1801 CATTTCTCTATCTATCATCAATATCCAAAGCTTTTCCAGAGATTCATGCAAGTCAAA 1860
1823 CATTTCTCTATCTATCATCAATATCCAAAGCTTTTCCAGAGATTCATGCAAGTCAAA 1882
1861 TCCCAAGAGTAACTTTTCAATTCATGAGGAGGCTTGAATTTTGGCAATCA 1920
1883 TCCCAAGAGTAACTTTTCAATTCATGAGGAGGCTTGAATTTTGGCAATCA 1942
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1943 TACTGTCACCTATCTCAACTTTGAGATGTTTGTCTTGTAGTAAATGGAAGAAAT 2002
1981 GGGCAGCTCTTGTGAGGCACTTTAGGCTTCACTCCCTGGCAATAAAGAAATTTACAAAGA 2037
2003 GGGCAGCTCTTGTGAGGCACTTTAGGCTTCACTCCCTGGCAATAAAGAAATTTACAAAGA 2059

RESULT 4
LOCUS AR261166 3923 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 690 from patent US 6321716.
ACCESSION AR261166
VERSION AR261166.1 GI:28071929
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3923)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 690 27-NOV-2001;
FEATURES Location/Qualifiers

	source	1..3923	/organism="unknown"
	BASE COUNT	1157 a	840 c 740 g 1186 t
	ORIGIN		
Query Match	80.0%; Score 1629; DB 6; Length 3923;		
Best Local Similarity	99.6%; Pred. No. 0;		
Matches 2029; Conservative	0; Mismatches 8; Indels 0; Gaps 0;		
1	AGAGCTGGCATCAGAAAAACAGAGGGGAGATTTGTGTGGCTGACGCCAGGAGACCG 60		
23	AGAGCTGGCATCAGAAAAACAGAGGGGAGATTTGTGTGGCTGACGCCAGGAGACCG 82		
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83	GAGATCTGCATGTTGGGAGAGACCTGATGATPACAGAGAAATTTACACATPACTTTG 142		
121	TGTTCAATGAACACCAAGATTAATTAAGTGAAGAGCTAGTCCGCTGTGAGTCTCTCA 180		
143	TGTTCAATGAACACCAAGATTAATTAAGTGAAGAGCTAGTCCGCTGTGAGTCTCTCA 202		
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203	GACACAGGCTGGATACCATGACGGGCACTTTCTAGTACTGACGACAAAGAAAGA 262		
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LOCUS AR278697				
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ACCESSION AR278697				
VERSION AR278697.1				
KEYWORDS GI:29712943				
SOURCE Unknown.				
ORGANISM Unknown.				
REFERENCE 1 (bases 1 to 3923)				
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,I.A.W., Hepler,W.T. and Henderson, R.A.				
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer				
JOURNAL Patent: US 6512094-A 690 28-JAN-2003;				
FEATURES Location/Qualifiers				
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Query Match 80.0%; Score 1629; DB 6; Length 3923;				
Best Local Similarity 99.6%; Pred. No. 0;				
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VERSION			
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ORGANISM			
Homo sapiens (human)			
REFERENCE			
AUTHORS			
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XU, J., DILLON, D. C., MITCHEM, J. L., HAZLOCKER, S. L., JIANG, Y.,			
REED, S. G., KALOS, M. D., FANGER, G. R., DAY, C. H., RETTER, M. W.,			
STOLK, J. A., SKEELLY, Y. A., WANG, A. and MEAGHER, M. J.			
TITLE			
Compositions and methods for the therapy and diagnosis of prostate			
cancer			
JOURNAL			
PATENT: WO 0151633-A 618 19-JUL-2001;			
CORIXA CORPORATION (US)			
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ACCESSION	AX267716		
VERSION	AX267716.1	GI:16516388	
KEYWORDS			
SOURCE			
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REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
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	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Rether,M.W., Stolk,J.A., Day,C.H., Vedvik,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T. and Henderson,R.A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate Cancer		
JOURNAL	Patent: WO 0173032-A 690 04-OCT-2001;		
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 VERSION AF103907.1 GI:6165973
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 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 3923)
Bussemakers,M.J., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Kerthaus,H.F., Schalken,J.A., Debruyne,F.M., Ru,N. and Isaacs,W.B.
DD3: a new prostate-specific gene, highly overexpressed in prostate
cancer
JOURNAL Cancer Res. 59 (23), 5975-5979 (1999)
MEDLINE 20072260
PUBMED 10606244
2 (bases 1 to 3923)
Bussemakers,M.J.G., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Kerthaus,H.F.M., Schalken,J.A., Debruyne,F.M.J., Ru,N. and
Isaacs,W.B.
Direct Submission
Submitted (28-OCT-1998) Urology Research Laboratory, University
Hospital Nijmegen, P.O. Box 9101, Nijmegen 6500 HB, Netherlands
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QY	1921	TACTGTCATCTATCTCAACTCAACTTGAAGATGTGTTGTCTCTTACTTAAATGAAGAATA	1980
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QY	1981	GGGCACTCTGTGTGAGCCACTTTAGGGTTCACCTCTCGGCATATAAAGAAATTTACAAAGA	2037
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DEFINITION	Homo sapiens non-coding RNA DD3 gene, exons 2, 3, and 4.		
ACCESSION	AF103908		
VERSION	AF103908.1	GI:6165974	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Bussemakers,M.J., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P., Katthaus,H.F., Schalken,J.A., Debruyne,F.M., Ru,N. and Isaacs,W.B.		
TITLE	DD3: a new prostate-specific gene, highly overexpressed in prostate Cancer		
JOURNAL	Cancer Res. 59 (23), 5975-5979		(1999)
MEDLINE	20072260		
PUBMED	10606244		
REFERENCE	2 (bases 1 to 5435)		
AUTHORS	Bussemakers,M.J.G., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P., Katthaus,H.F.M., Schalken,J.A., Debruyne,F.M.J., Ru,N. and Isaacs,W.B.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-OCT-1998) Urology Research Laboratory, University Hospital Nijmegen, P.O. Box 9101, Nijmegen 6500 HB, Netherlands		
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DEFINITION
ACCESSION
AR261038
Sequence 470 from patent US 6321716.
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VERSION AR261038.1 GI:28071801
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
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1409 GAACTCAAAAGTGAGCATTAACCAATGAGAGAAAGACAGAGAAATCTTGATGGCTT 1350
683 CACAGACATGCAACAAACAAATGGAATCTGTGATGATGATGATGATGATGATGATGATGATGAT 742
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743 AGGAGATTAACAGGAGGAGGAGGAGGATGAGATTTGCGCTGCTGCTAAACCTGAGCTTTC 802
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RESULT 11
AR278569/c 2426 bp DNA linear PAT 10-APR-2003
LOCUS AR278569
DEFINITION Sequence 470 from patent US 6512094.
ACCESSION AR278569
VERSION AR278569.1 GI:29712815
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2426)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer.
JOURNAL Patent: US 6512094-A 470 28-JAN-2003;
FEATRES Location/Qualifiers
source 1..2426
BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN

Query Match 56.7%; Score 1154; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 263 GGTGGAATATAGAAAGGCTGCTTACCATGTGAGGCACATCTGCTGAATGG 322
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Db 1709 AGATTAATTACATCTAGAAACAGAGATGACATATATGTCTAAGTAGTGACATGT 1650
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Qy 1403 AGCGTATACAGC 1416
Db 629 AGCGTATACAGC 616

RESULT 12
AX106206/c 2426 bp DNA linear PAT 30-APR-2001
LOCUS AX106206
DEFINITION Sequence 344 from Patent W00125273.
ACCESSION AX106206
VERSION AX106206.1 GI:13921895
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
AUTHORS Skeiky,Y.A., Xu,J., Cheever,M.A. and Reed,S.G.
TITLE Compositions and methods for wli specific immunotherapy
JOURNAL Patent: WO 0125273-A 344 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
SOURCE 1. 2426
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN
Query Match 56.7%; Score 1154; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAGAAATTAAGAAAGGCTGCTGCTTACATCTGAGCCACACATCTGCTGAATGG 322
DB 1769 GGTGAGAAATTAAGAAAGGCTGCTGCTTACATCTGAGCCACACATCTGCTGAATGG 1710
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DB 1709 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATACTGCTAGTAGACATGT 1650
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DB 689 TCCTCCCTCTTGTGATTTTTCCTAGATTAAGTTAAATGCTTACGCTTGTACTG 630
QY 1403 AGGCTGTATACAGC 1416
DB 629 AGGCTGTATACAGC 616
RESULT 13
AX106689/c 2426 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 470 from Patent WO0125272.
DEFINITION AX106689
ACCESSION AX106689
VERSION AX106689.1 GI:13922354
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
REFERENCE 1
AUTHORS Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0125273-A 470 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
SOURCE 1. 2426
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN
Query Match 56.7%; Score 1154; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAGAAATTAAGAAAGGCTGCTGCTTACATCTGAGCCACACATCTGCTGAATGG 322
DB 1769 GGTGAGAAATTAAGAAAGGCTGCTGCTTACATCTGAGCCACACATCTGCTGAATGG 1710
QY 323 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATACTGCTAGTAGACATGT 382
DB 1709 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATACTGCTAGTAGACATGT 1650
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DB 1649 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAAAGCAAAAGAGAGAC 1590
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Db 1349 CACAAGACATCAACAAACAAATGGAATCTGTGATGATGATGAGCCAGCTGGGG 1290
QY 743 AGGAGATACACAGGGGAGAGGGGATGCTGAGGATTCGCTGCTAAGCTGCTGCTC 802
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RESULT 14

AX140980/c 2426 bp DNA linear PAT 31-MAY-2001
LOCUS AX140980
DEFINITION Sequence 470 from Patent WO0134802.
ACCESSION AX140980
VERSION AX140980.1 GI:14281077
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1. Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y.,
Reed S.G., Kaios M.D., Retter M.W., Stolk D.A., Day C.H.,
Skelly Y.A. and Wang A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 470 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1..2426
/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN
Query Match 56.7%; Score 1154; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAAGAAATGAAGAGGCTGCTGATCTTACCATGTGAGGCCACACATCTGCTGAATGG 322
Db 1769 GGTGAAGAAATGAAGAGGCTGCTGATCTTACCATGTGAGGCCACACATCTGCTGAATGG 1710
QY 323 AGATTAATTAATCAATCAATGAAGAACAGAGATGATGATTAATGCTAAGTAGTACATGT 382
Db 1709 AGATTAATTAATCAATCAATGAAGAACAGAGATGATGATTAATGCTAAGTAGTACATGT 1650
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QY 863 TACGGTCTCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 922
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Db 629 AGGCTGTATACAGC 616

RESULT 15
AX200840/c 2426 bp DNA linear PAT 29-AUG-2001
LOCUS AX200840
DEFINITION Sequence 470 from Patent WO0151633.
ACCESSION AX200840
VERSION AX200840.1 GI:15390743
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
XU,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skelky,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: WO 0151633-A 470 19-JUL-2001;
JOURNAL CORIAX CORPORATION (US)
TITLE Location/Qualifiers
FEATURES
source
1.2426
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Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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Run on: September 26, 2003, 20:07:52 ; Search time 533.821 Seconds
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Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2037	100.0	2037	19	AAV62427
2	1775	87.1	1872	19	AAV62428
3	1629	80.0	3923	22	AAV64026
4	1629	80.0	3923	22	AAH93861
5	1629	80.0	3923	24	ABK92196
6	1629	80.0	3923	24	ABL95397
7	1629	80.0	3923	25	ACA59834
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C	10	1154	56.7	2426	22	AAH93805	Human prostate-spe
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C	12	1154	56.7	2426	22	AAH02870	Prostate tumour an
C	13	1154	56.7	2426	22	AAH86948	Human P710P Invent
C	14	1154	56.7	2426	24	AAH95269	Human P710P CDNA s
C	15	1154	56.7	2426	25	ACA59706	Prostate cancer th
C	16	1154	56.7	2426	25	ACA59706	Prostate cancer th
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C	19	1154	56.7	3112	22	AAH93803	Human prostate-spe
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C	22	1154	56.7	3112	22	AAH86946	Human P710P Invent
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C	43	475	23.3	658	23	ABV42450	Human prostate exp
C	44	475	23.3	671	23	ABV41330	Human prostate exp
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ALIGNMENTS

RESULT 1	AAV62427	standard: CDNA; 2037 BP.
ID	AAV62427	
AC	AAV62427;	
XX		
XX	30-DEC-1998	(first entry)
DT		
XX		
DE		Prostate cancer antigen (PCA3) cDNA splice variant 1.
XX		
XX		Prostate cancer antigen cDNA splice variant 1; PCA3; prostatic cancer;
KW		PC; ds.
KW		
OS		Homo sapiens.
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PD	15-OCT-1998.	
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PF	09-APR-1998;	98WO-CA00346.
XX		
PR	10-APR-1997;	97US-0041836.
XX		
PA	(DIAG-) DIAGNOCURE INC.	

XX Bussemakers MJG;
PI
XX MPI: 1998-568347/48.
DR P-SDB; AAM79736.
XX
PT New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
PT prevention and treatment of prostatic cancer
PS
PS Claim 3; Fig 2b-2j; 11pp; English.
XX
XX The present sequence represents the prostate cancer antigen (PCA3)
CC cDNA splice variant 1 sequence comprising of exons 1, 2, 3, 4a and
CC 4b of the PCA3 gene. The PCA3 cDNA splice variant 1 sequence,
CC isolated from a human primary prostatic tumour tissue cDNA library,
CC was found in approximately 5% of the cDNA clones isolated. The
CC invention claims for PCA3 cDNA variants and the proteins they encode.
CC The invention also claims for antibodies against PCA3 protein. The
CC antibodies are claimed to be useful for detecting PCA3 protein in
CC immunoassay tests, for diagnosing, assessing and prognosing of
CC prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed
CC to be useful for treating PC, while determining elevated levels of
CC PCA3 (as RNA or protein) is useful for detecting a predisposition
CC to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
CC allows differentiation between malignant and benign prostatic disease,
CC and the level of PCA3 expression allows correlation with the grade of
CC tumour. PCA3 protein and its fragments are also claimed to be useful
CC in vaccines for preventing PC; in drug screens for identifying
CC specific (ant)agonists (potentially useful therapeutically) and for
CC studying protein-DNA interactions.
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SQ Sequence 2037 BP; 622 A; 426 C; 406 G; 575 T; 8 other;
Query Match 100.0%; Score 2037; DB 19; Length 2037;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2037; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

AAV62428 ID AAV62428 standard; cDNA: 1872 BP.

AAV62428:

30-DEC-1998 (first entry)

Prostate cancer antigen (PCA3) cDNA splice variant 2.

Prostate cancer antigen cDNA splice variant 2; PCA3; prostatic cancer;

PC; ds.

Homo sapiens.

MO9845420-A1.

15-OCT-1998.

09-APR-1998; 98WO-CA00346.

10-APR-1997; 97US-0041836.

(DIAG-) DIAGNOCURE INC.

Bussemakers MDG;

WPI, 1998-568347/48.

New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,

prevention and treatment of prostatic cancer

Claim 4; Pages 76-77; 11lp; English.

The present sequence represents the prostate cancer antigen (PCA3)

cDNA splice variant 2 sequence comprising of exons 1, 3, 4a and

4b of the PCA3 gene. The PCA3 cDNA splice variant 2 sequence,

isolated from a human primary prostatic tumor tissue cDNA library,

was found in approximately 65% of the cDNA clones isolated. The

invention claims for PCA3 cDNA variants and the proteins they encode.

The invention also claims for antibodies against PCA3 protein. The

antibodies are claimed to be useful for detecting PCA3 protein in

immunossay tests, for diagnosing, assessing and prognosing of

prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin

or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed to be useful for treating PC, while determining elevated levels of PCA3 (as RNA or protein) is useful for detecting a predisposition to development of PC, e.g. in prenatal tests. Detecting PCA3 protein allows differentialiation between malignant and benign prostatic disease, and the level of PCA3 expression allows correlation with the grade of tumor. PCA3 protein and its fragments are also claimed to be useful in vaccines for preventing PC; in drug screens for identifying specific (ant)agonists (potentially useful therapeutically) and for studying protein-DNA interactions.

SQ Sequence 1872 BP; 567 A; 389 C; 369 G; 539 T; 8 other;

Query Match 87.1%; Score 1775; DB 19; Length 1872;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;

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DB 1058 TTCCATTAAATACAGAGATTAACTTTTTTTTTTAACCTGGAGAAATTCATGTTACATG 1117
QY 1283 CACGATGGAATTAATTAATCATATTTTGTTCAGTCAAGATGACTAGTCTTTA 1342
DB 1118 CACGATGGAATTAATTAATCATATTTTGTTCAGTCAAGATGACTAGTCTTTA 1177
QY 1343 TTCCCTCCCTTTGTTGATTTTTCAGATTAATTAAGTCTTACCTGTACTG 1402
DB 1178 TTCCCTCCCTTTGTTGATTTTTCAGATTAATTAAGTCTTACCTGTACTG 1237
QY 1403 AGGCTGTATACAGACAGCTCTCCCATCCCTCAGCCTTATCTGCATCACCATCAAC 1462
DB 1238 AGGCTGTATACAGACAGCTCTCCCATCCCTCAGCCTTATCTGCATCACCATCAAC 1297
QY 1463 CCCTCCCATCTTACCTTAACAAATCTAATCTGTAATCTCTGGAATGTCAGGNCATAC 1522
DB 1298 CCCTCCCATCTTACCTTAACAAATCTAATCTGTAATCTCTGGAATGTCAGGNCATAC 1357
QY 1523 ATTCTTCCTCTGCTGAGAGAGCTCTGCTGCTCTTAAATGTCAGAAATGTAAGTT 1592
DB 1358 ATTCTTCCTCTGCTGAGAGAGCTCTGCTGCTCTTAAATGTCAGAAATGTAAGTT 1417
QY 1583 TTGAATTAAGTGAATCTTACTTATCATGCAAGAGGACATATGATTCATCTCA 1642
DB 1418 TTGAATTAAGTGAATCTTACTTATCATGCAAGAGGACATATGATTCATCTCA 1477
QY 1643 CATGAGACAGCAATCTAATTAAGTGAATTAATTAAGAGTTTGAATTAATTAAGAA 1702
DB 1478 CATGAGACAGCAATCTAATTAAGTGAATTAATTAAGAGTTTGAATTAATTAAGAA 1537
QY 1703 ATGCAAGAKCCACAGAGAGGAAATGTTATGCGGACGTTTGAAGCCTGGAGTGAAGMA 1762
DB 1538 ATGCAAGAKCCACAGAGGAAATGTTATGCGGACGTTTGAAGCCTGGAGTGAAGMA 1597
QY 1763 AAGGCAAGGAACTCATAGTATCTTAATTAATTAATCTCAATTTCTATCTATCAAA 1822
DB 1598 AAGGCAAGGAACTCATAGTATCTTAATTAATTAATCTCAATTTCTATCTATCAAA 1657
QY 1823 TATCCAAAGAGCTTTTCAAGAAATTCATGAGTGAAGAAATCCCAAGAGTAACCTTATCC 1882
DB 1658 TATCCAAAGAGCTTTTCAAGAAATTCATGAGTGAAGAAATCCCAAGAGTAACCTTATCC 1717
QY 1883 ATTTCAATGATGATGCGCTTTAGAAATTTTGGCAATCATCTGTCATTAATCTCAACTT 1942
DB 1718 ATTTCAATGATGATGCGCTTTAGAAATTTTGGCAATCATCTGTCATTAATCTCAACTT 1777
QY 1943 TGAAGATGTTTGTCTTGTAGTTAATGAAGAAATAGGGCACTGTTGAGCCACTTT 2002
DB 1778 TGAAGATGTTTGTCTTGTAGTTAATGAAGAAATAGGGCACTGTTGAGCCACTTT 1837
QY 2003 AGGCTCACCTCCGCGCAATTAAGAAATTTACAAAGA 2037
DB 1838 AGGCTCACCTCCGCGCAATTAAGAAATTTACAAAGA 1872
```

```
RESULT 3
AAS64026
ID AAS64026 standard; cdna: 3923 bp.
```

```
XX AAS64026;
AC
XX
DT 29-JAN-2002 (first entry)
XX
```

```
DE Human cDNA encoding DB3.
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN W0200173032-A2.
XX
PD 04-OCT-2001.
XX
PE 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MM, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI: 2001-639232/73.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 473-474; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 3923 bp; 1157 A; 840 C; 740 G; 1186 T; 0 other;
XX
Query Match 80.0%; Score 1629; DB 22; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 AGAAGCTGCGATCAGAAAAACAGAGGGAGATTGTGTGCTCAGCCGAGGAGACCAAG 60
DB 23 AGAAGCTGCGATCAGAAAAACAGAGGGAGATTGTGTGCTCAGCCGAGGAGACCAAG 82
QY 61 GAAGATCTGATGCTGGGAGAGCACTGATATACAGAGAAATTAACAACATATCTTAG 120
DB 83 GAAGATCTGATGCTGGGAGAGCACTGATATACAGAGAAATTAACAACATATCTTAG 142
QY 121 TGTTCATTAACACCAAGATTAATTAAGTAAGAGCTAGTCCGCTGAGTCTCTCAGT 180
DB 143 TGTTCATTAACACCAAGATTAATTAAGTAAGAGCTAGTCCGCTGAGTCTCTCAGT 202
QY 181 GACACAGGCTGATACCATGACGCGACCTTTCTGAGTACTGACGACCAAGAAAGA 240
DB 203 GACACAGGCTGATACCATGACGCGACCTTTCTGAGTACTGACGACCAAGAAAGA 262
QY 241 CTACAGACATCTCAATGCGCAGGGGTGAGAAATTAAGAAAGGCTCTGACTTACCATCTGA 300
```

|||||
Db 263 CTAGAGACATCTCAATGCGAGGGGTGAGAAATAGAAAGCGCTGACTTACCATCTGA 322
Qy 301 GGGCCACNCATCTGCTGAAATGAGATATTAACATCACTAGAAACAGCAATGACATA 360
Db 323 GGGCCACNCATCTGCTGAAATGAGATATTAACATCACTAGAAACAGCAATGACATA 382
Qy 361 TAATGTCTAAGTAGTGCATGTTTGGACATTTCCAGCCCTTAAATATCCACACA 420
Db 383 TAATGTCTAAGTAGTGCATGTTTGGACATTTCCAGCCCTTAAATATCCACACA 442
Qy 421 CAGAGACACAAAAGGAAGACACAGATCCCTGGAGAAATGCCGGCCTCATCTTGG 480
Db 443 CAGAGACACAAAAGGAAGACACAGATCCCTGGAGAAATGCCGGCCTCATCTTGG 502
Qy 481 TCATCATGAGCCCTGCGCTGGCTGGCTGGCTGGAGGAAAGCATTAGAAATG 540
Db 503 TCATCATGAGCCCTGCGCTGGCTGGCTGGCTGGAGGAAAGCATTAGAAATG 562
Qy 541 AATGATGTGTCTCTTAAAGATGGCGAGAAACAGATCCCTGTTGATATTATTTG 600
Db 563 AATGATGTGTCTCTTAAAGATGGCGAGAAACAGATCCCTGTTGATATTATTTG 622
Qy 601 AACGGATTACAGATTGAAATGAGTCACAAAGTGAGCATTACCAATGAGAGAAACA 660
Db 623 AACGGATTACAGATTGAAATGAGTCACAAAGTGAGCATTACCAATGAGAGAAACA 682
Qy 661 GAGGAGAAATCTGATGGCTTCACAGACATGCAACAAACAAATGGAATACGTGTG 720
Db 683 GAGGAGAAATCTGATGGCTTCACAGACATGCAACAAACAAATGGAATACGTGTG 742
Qy 721 ACATGAGGACCCAGCTGGGGAGAGATTAACACAGGGGCGAGGGTCAGGATTCGGC 780
Db 743 ACATGAGGACCCAGCTGGGGAGAGATTAACACAGGGGCGAGGGTCAGGATTCGGC 802
Qy 781 CTGCTGCCCTAACTGCGCTTCATACCAAAATCAATTTCTAACTCTCAAAACA 840
Db 803 CTGCTGCCCTAACTGCGCTTCATACCAAAATCAATTTCTAACTCTCAAAACA 862
Qy 841 AGCTGTGTATATCTGATCTCTACGGTTCCTTGGGCGCCACATTCCTCATATATCA 900
Db 863 AGCTGTGTATATCTGATCTCTACGGTTCCTTGGGCGCCACATTCCTCATATATCA 922
Qy 901 GCCACACTATTTTAAATATTAGTCCAGATCTGTACTGTGACCTTTCACACTGAG 960
Db 923 GCCACACTATTTTAAATATTAGTCCAGATCTGTACTGTGACCTTTCACACTGAG 982
Qy 961 AATACATCTCAATTTTGTCAAGACCTTCTGTTGCTGCTCATATATGACTGACT 1020
Db 983 AATACATCTCAATTTTGTCAAGACCTTCTGTTGCTGCTCATATATGACTGACT 1042
Qy 1021 GTTTTCTTAAGGAGTGTCTGGCCAGGGGATCTGCAACAGGCTGGGAGCATCTCA 1080
Db 1043 GTTTTCTTAAGGAGTGTCTGGCCAGGGGATCTGCAACAGGCTGGGAGCATCTCA 1102
Qy 1081 GATCTTCCAGGTTATCTACTAGCACAGCATGATCTTACGAGTGAATATCTA 1140
Db 1103 GATCTTCCAGGTTATCTACTAGCACAGCATGATCTTACGAGTGAATATCTA 1162
Qy 1141 ATCAACATCTCTCAGTGTCTTGGCCATCTGAATATCTTCCACTTTGTGCCA 1200
Db 1163 ATCAACATCTCTCAGTGTCTTGGCCATCTGAATATCTTCCACTTTGTGCCA 1222
Qy 1201 TTCTCAGACCTCAAAATGTCATTCATATATCAAGGATTAACCTTTTAAACC 1260
Db 1223 TTCTCAGACCTCAAAATGTCATTCATATATCAAGGATTAACCTTTTAAACC 1282
Qy 1261 TGAAGAATTCATATGATGACAGTATGGGAATTTAATACATATTTGTTCCAGT 1320
Db 1283 TGAAGAATTCATATGATGACAGTATGGGAATTTAATACATATTTGTTCCAGT 1342
Qy 1321 GCAAGATGACTAAGTCCCTTATCCCTCCCTTGTGATTTTTCACAGTAAAGT 1380
|||||

Db 1343 GCAAGATGACTAAGTCCCTTATCCCTCCCTTGTGATTTTTTTCAGTATAAAGT 1402
Qy 1381 TAAATGCTTACCTGTACAGAGCTGTATACGACAGGCTCCCATCCCTCCAGC 1440
Db 1403 TAAATGCTTACCTGTACAGAGCTGTATACGACAGGCTCCCATCCCTCCAGC 1462
Qy 1441 CTATCTGTATCATCAATCAACCCCTCCCATNYNSACCTAAACAAATCTACTTGAAT 1500
Db 1463 CTATCTGTATCATCAATCAACCCCTCCCATNYNSACCTAAACAAATCTACTTGAAT 1522
Qy 1501 CCTTGACATGTCAAGNCATACATTTTCTTCTGCTGAGAGCTCTTCTGTCTT 1560
Db 1523 CCTTGACATGTCAAGNCATACATTTTCTTCTGCTGAGAGCTCTTCTGTCTT 1582
Qy 1561 AANTCTAGATGATTAAGTTTGAATTAAGTCTTCTTACTCTCATGCAAGAAAGG 1620
Db 1583 AANTCTAGATGATTAAGTTTGAATTAAGTCTTCTTACTCTCATGCAAGAAAGG 1642
Qy 1621 ACACATATGAGATTCATCATGACATGAGACAGCAAAATCTAAAGTGAATTTGATTA 1680
Db 1643 ACACATATGAGATTCATCATGACATGAGACAGCAAAATCTAAAGTGAATTTGATTA 1702
Qy 1681 AGAGTTTGAATTAATATGTAATGCAAGACACAGAGGAGATTTATGGGCGACTT 1740
Db 1703 AGAGTTTGAATTAATATGTAATGCAAGAGACACAGAGGAGATTTATGGGCGACTT 1762
Qy 1741 TGTAAAGCTGGAGTGAAGAAAGGCGAGGAGCTCTAGATCTTATATATATCTT 1800
Db 1763 TGTAAAGCTGGAGTGAAGAAAGGCGAGGAGCTCTAGATCTTATATATATATCTT 1822
Qy 1801 CATTTCTATCTATCATCAATATCAACAAAGCTTTTACAGAAATTCATGCAAGTCAAA 1860
Db 1823 CATTTCTATCTATCATCAATATCAACAAAGCTTTTACAGAAATTCATGCAAGTCAAA 1882
Qy 1861 TCCCAAGGTAACCTTTATCATTTTCAATGCTGTGAGTGGCTTTTGAATTTGGCAATCA 1920
Db 1883 TCCCAAGGTAACCTTTATCATTTTCAATGCTGTGAGTGGCTTTTGAATTTGGCAATCA 1942
Qy 1921 TACTGTGACTTATCTCAACTTTTGAAGTGTGTTTCTCTTGTAGTAAATGAAGATA 1980
Db 1943 TACTGTGACTTATCTCAACTTTTGAAGTGTGTTTCTCTTGTAGTAAATGAAGATA 2002
Qy 1981 GGGCAGCTTGTGAGCCACTTTAGGGTTCACCTCTGCAATTAAGAAATTTACAAGA 2037
Db 2003 GGGCAGCTTGTGAGCCACTTTAGGGTTCACCTCTGCAATTAAGAAATTTACAAGA 2059

RESULT 4
AAH93861
ID AAH93861 standard; cDNA; 3923 BP.
XX
AC AAH93861;
XX
DT 04-OCT-2001 (first entry)
XX
DE Gene DD3 cDNA sequence.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosolic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN W0200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIYA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kelos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MD;
XX
XX WPL; 2001-425873/45.
DR
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
XX
PS Claim 1; Page 452-453; 543pp; English.
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to
CC AAM01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
CC
XX
SQ Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;

Query Match 80.0%; Score 1629; DB 22; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 202; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCAGAAAAACAGAGGGAGATTGTGTGCTGACGCGGAGAGACAG 60
DB 23 AGAAGCTGGCAGAAAAACAGAGGGAGATTGTGTGCTGACGCGGAGAGACAG 82
QY 61 GAAGATCTGATGGTGGAGGACCTGATATACAGAGGAATTACACATATATTAG 120
DB 83 GAAGATCTGATGGTGGAGGACCTGATATACAGAGGAATTACACATATATTAG 142
QY 121 TGTTCATGACACCAAGATTAATAGTAGAGCTAGTCCGCTGAGTCTCTCAGT 180
DB 143 TGTTCATGACACCAAGATTAATAGTAGAGCTAGTCCGCTGAGTCTCTCAGT 202
QY 181 GACACAGGGCTGATACCATGACGGCATTCTGTGATCTGACAGCAAAAGAGA 240
DB 203 GACACAGGGCTGATACCATGACGGCATTCTGTGATCTGACAGCAAAAGAGA 262
QY 241 CTACAGCATCTCAATGCGAGGGGTGAGAAATAGAAAGGCTGCTACTTACCATCTGA 300
DB 263 CTACAGCATCTCAATGCGAGGGGTGAGAAATAGAAAGGCTGCTACTTACCATCTGA 322
QY 301 GGCCACACATCTGCTGAATGAGATTAATTACATCACTAGAAACAGCAGATGACAATA 360
DB 323 GGCCACACATCTGCTGAATGAGATTAATTACATCACTAGAAACAGCAGATGACAATA 382
QY 361 TAATGCTAAGTAGTACATGTTTTTGACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 383 TAATGCTAAGTAGTACATGTTTTTGACATTTCCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAGGCAAAAGAGACAGAGATCCCTGGGAAATGCCCGGCGCCCATCTTGGG 480
DB 443 CAGGAGGCAAAAGAGACAGAGATCCCTGGGAAATGCCCGGCGCCCATCTTGGG 502
QY 481 TCATCATGAGCTCGCCCTGTGCTGTCCTGCTGTGAGGAGACATTTGAAGAATG 540
DB 503 TCATCATGAGCTCGCCCTGTGCTGTCCTGCTGTGAGGAGACATTTGAAGAATG 562
QY 541 AATTGATGTTCTTAAAGAGTGGCAGAGAAAACAGATCTTGTGATATTTATTTG 600
DB 563 AATTGATGTTCTTAAAGAGTGGCAGAGAAAACAGATCTTGTGATATTTATTTG 622
QY 601 AACGGATTACAGATTGAATGAAGTCAACAAAGTAGATTCCAAATGAGAGAAACA 660

DB 623 AACGGATTACAGATTGAATGAAGTCAACAAAGTAGATTCCAAATGAGAGAAACA 682
QY 661 GACGAGAAATCTGATGSCCTTCACAGACATGCAACAAACAAATGATATCTGATG 720
DB 683 GACGAGAAATCTGATGSCCTTCACAGACATGCAACAAACAAATGATATCTGATG 742
QY 721 ACATGAGGACCCAGAGCTGGGAGAGATTAACCCAGGGGAGAGGCTGAGATTGGCC 780
DB 743 ACATGAGGACCCAGAGCTGGGAGAGATTAACCCAGGGGAGAGGCTGAGATTGGCC 802
QY 781 CTGCTGCTTAACCTGCTGCTCATACCAAAATCATTTATTTCTAACCTCAAAACA 840
DB 803 CTGCTGCTTAACCTGCTGCTCATACCAAAATCATTTATTTCTAACCTCAAAACA 862
QY 841 AGCTGTGTAAATTCATGCTGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 863 AGCTGTGTAAATTCATGCTGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 922
QY 901 GCCACACTATTTTAAATATTTAGTCCAGATCTGATGCTGATACCTTTCTACACTGTAG 960
DB 923 GCCACACTATTTTAAATATTTAGTCCAGATCTGATGCTGATACCTTTCTACACTGTAG 982
QY 961 AATTAACATTAATCTATTTTGTCAAGACCTTGTGTGCTGCTGCTTAAATGATGCTGACT 1020
DB 983 AATTAACATTAATCTATTTTGTCAAGACCTTGTGTGCTGCTGCTTAAATGATGCTGACT 1042
QY 1021 GTTTTTCCTAAGAGTGTCTGCGCCAGAGGATCTGTGAACAGCGGGAGACATCTGCA 1080
DB 1043 GTTTTTCCTAAGAGTGTCTGCGCCAGAGGATCTGTGAACAGCGGGAGACATCTGCA 1102
QY 1081 GATCTTCCAGGGTTATCTTACTTACTAGCACACACATGATCATTTACGAGATTAATCTA 1140
DB 1103 GATCTTCCAGGGTTATCTTACTTACTAGCACACACATGATCATTTACGAGATTAATCTA 1162
QY 1141 ATCAACATTAATCTTCTGAGTGTCTTGGCCATACGAAATTCATTTCCACTTTGTGCCCA 1200
DB 1163 ATCAACATTAATCTTCTGAGTGTCTTGGCCATACGAAATTCATTTCCACTTTGTGCCCA 1222
QY 1201 TTCTCAAGACCTCAAAATGTCATTCATTAATATACAGAGTAACTTTTATTTTAAAC 1260
DB 1223 TTCTCAAGACCTCAAAATGTCATTCATTAATATACAGAGTAACTTTTATTTTAAAC 1282
QY 1261 TGGAGAAATTAATGTTACATGTCAGAGCTATGGAATTAATTACATATTTGTTTCCAGT 1320
DB 1283 TGGAGAAATTAATGTTACATGTCAGAGCTATGGAATTAATTACATATTTGTTTCCAGT 1342
QY 1321 GCAAGATGACTAAGTCCCTTATCCCTCCCTGTTGATTTTTCACGATTAAGT 1380
DB 1343 GCAAGATGACTAAGTCCCTTATCCCTCCCTGTTGATTTTTCACGATTAAGT 1402
QY 1381 TAAATGCTTAACTTACTGAGGCTGTATACAGACAGGCTTCCCATCCCTCCAGC 1440
DB 1403 TAAATGCTTAACTTACTGAGGCTGTATACAGACAGGCTTCCCATCCCTCCAGC 1462
QY 1441 CTTATCTGTCATACATCAACCCCTCCCATCTTAACTTAATTTGTTGATTT 1500
DB 1463 CTTATCTGTCATACATCAACCCCTCCCATCTTAACTTAATTTGTTGATTT 1522
QY 1501 CCTTGAACATGTCAGAGCATTAATTTCTGCTGCTGAGAGGCTTCCCTGCTGCT 1560
DB 1523 CCTTGAACATGTCAGAGCATTAATTTCTGCTGCTGAGAGGCTTCCCTGCTGCT 1582
QY 1561 AANTCTAGATGATTAAGTTTGAATTAAGTTGATCTATCTTATCATGCAAAAGAGG 1620
DB 1583 AANTCTAGATGATTAAGTTTGAATTAAGTTGATCTATCTTATCATGCAAAAGAGG 1642
QY 1621 ACACATATGAGATTCATCATCATGACAGACAGCAAAATCTAAAGTATTTGATTA 1680
DB 1643 ACACATATGAGATTCATCATCATGACAGACAGCAAAATCTAAAGTATTTGATTA 1702
QY 1681 AGAGTTAGTAAATTAATGAAGTGAAGKCCACAGAGGGAATGTTTAAAGGGGCGCT 1740

Db 1703 AGAGTTAGATTAATATATGAAGATGCAGAGCCACAGAGGAATGTTTATGGGACGTT 1762
OY 1741 TGTAAAGCTGGATGTAAGAAAGGACGGAACCTCATGATCTTATATATATCTT 1800
Db 1763 TGTAAAGCTGGATGTAAGAAAGGACGGAACCTCATGATCTTATATATATCTT 1822
OY 1801 CATTTCTGATCTATCATCAATATCCAAAGCTTTTACAGAAATTCATGACAGTCAAA 1860
Db 1823 CATTTCTGATCTATCATCAATATCCAAAGCTTTTACAGAAATTCATGACAGTCAAA 1882
OY 1861 TCCCAAGAGTAACCTTATCCATTTTCATGAGTGGCCTTACAAATTTGGCAATCA 1920
Db 1883 TCCCAAGAGTAACCTTATCCATTTTCATGAGTGGCCTTACAAATTTGGCAATCA 1942
OY 1921 TACTGTGCTATGTCACACTTGTGAGATGTTTGTCTGTAGTTAATTGAAGAAATA 1980
Db 1943 TACTGTGCTATGTCACACTTGTGAGATGTTTGTCTGTAGTTAATTGAAGAAATA 2002
OY 1981 GGGACACTGTTGACGACCACTTTAGGGTTCACCTCGGCAATTAAGAAATTTACAAAGA 2037
Db 2003 GGGACACTGTTGACGACCACTTTAGGGTTCACCTCGGCAATTAAGAAATTTACAAAGA 2059

RESULT 5

ABK92196
ID ABK92196 standard; DNA; 3923 BP.

XX
AC ABK92196;

DT 15-AUG-2002 (first entry)

XX
DE Prostate cancer-associated DNA sequence #82.

XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.

XX
OS Mammalia.

PN W0200230268-A2.

XX
PD 18-APR-2002.

XX
PF 12-OCT-2001; 2001WO-US32045.

XX
PR 13-OCT-2000; 2000US-0687576.

XX
PR 08-DEC-2000; 2000US-0733288.

XX
PR 08-DEC-2000; 2000US-0733288.

XX
PR 24-JAN-2001; 2001US-263957P.

XX
PR 16-MAR-2001; 2001US-276791P.

XX
PR 16-MAR-2001; 2001US-276888P.

XX
PR 06-APR-2001; 2001US-281922P.

XX
PR 24-APR-2001; 2001US-286214P.

XX
PR 30-APR-2001; 2001US-0847046.

XX
PR 04-MAY-2001; 2001US-288589P.

XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX
PI Gish KC, Mack DH, Wilson KE, Afar D, Heyezi P;

XX
DR WPI; 2002-471335/50.

XX
PT Detecting a prostate cancer-associated transcript in a cell in a
PT patient, useful for diagnosing prostate cancer (PC) or screening
PT modulators of PC, by determining if prostate cancer-associated genes
PT are expressed in a prostate tissue
PS Claim 22; Page 365-366; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridise to a sequence that is at least 80% identical

CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC prostate cancer and are derived from the tissues of various
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences.

SO Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;

Query Match 80.0%; Score 1629; DB 24; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 AGAAGCTGATCAGAAAAACAGAGGAGATTTGTGCTGACGCCGAGGACAG 60
Db 23 AGAAGCTGATCAGAAAAACAGAGGAGATTTGTGCTGACGCCGAGGACAG 82
OY 61 GAAGATCTGCATGTTGGGAAGACCTGATGATACAGAGGAATTACACATATCTTAG 120
Db 83 GAAGATCTGCATGTTGGGAAGACCTGATGATACAGAGGAATTACACATATCTTAG 142
OY 121 TGTTCATTAAGAACACCAATATTAATTAAGTGAAGAGCTACTCCGCTGTGCTCTCACT 180
Db 143 TGTTCATTAAGAACACCAATATTAATTAAGTGAAGAGCTACTCCGCTGTGCTCTCACT 202
OY 181 GACACAGGCTGATGATCAGGAGGCTTTGTGAGTACAGTGCAGCAAGAAAGA 240
Db 203 GACACAGGCTGATGATCAGGAGGCTTTGTGAGTACAGTGCAGCAAGAAAGA 262
OY 241 CTACAGACATCTCAATGCGCAGGAGGTGAAGAAATGAAGAGCTGACTTTACATCTGA 300
Db 263 CTACAGACATCTCAATGCGCAGGAGGTGAAGAAATGAAGAGCTGACTTTACATCTGA 322
OY 301 GGCACACATCTGCTGCAAAATGCAATTAATTAATCACTACAGAAACGCAAGTACATA 360
Db 323 GGCACACATCTGCTGCAAAATGCAATTAATTAATCACTACAGAAACGCAAGTACATA 382
OY 361 TATGCTAAGTAGACATGTTTGTGCAATTTCCAGCCCTTTAATATCCACACA 420
Db 383 TATGCTAAGTAGACATGTTTGTGCAATTTCCAGCCCTTTAATATCCACACA 442
OY 421 CAGGAAGCAAAAGGAACACAGAGATCCCTGGGAAGATCCCGGCCCATCTTGGG 480
Db 443 CAGGAAGCAAAAGGAACACAGAGATCCCTGGGAAGATCCCGGCCCATCTTGGG 502
OY 481 TCATGATGAGCCTGCGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 503 TCATGATGAGCCTGCGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 562
OY 541 AATTGATGCTCTTAAGGATGGGACAGAAACAGATCCGTTGTGATATTATTG 600
Db 563 AATTGATGCTCTTAAGGATGGGACAGAAACAGATCCGTTGTGATATTATTG 622
OY 601 AACGGATTACAGATTTGAATGAATGACAAAGTGAGCATTAACCAATGAGGAAACA 660
Db 623 AACGGATTACAGATTTGAATGAATGACAAAGTGAGCATTAACCAATGAGGAAACA 682
OY 661 GACGAGAAATTTGATGCTTACAGACATGCAACAAACAAATGATGATGATG 720
Db 683 GACGAGAAATTTGATGCTTACAGACATGCAACAAACAAATGATGATGATG 742
OY 721 ACATGAGGACCAAGCTGGGAGGAGATTAACACAGGCGCAGAGGTCAGATTCTGGCC 780
Db 743 ACATGAGGACCAAGCTGGGAGGAGATTAACACAGGCGCAGAGGTCAGATTCTGGCC 802
OY 781 CTGCTGCTTAACCTGTGCTTACCAAAATCATTTCTATTTCTTAACCTCAAAACA 840

Db 803 CTGCTGCTTAAAGTGGCTTCATACCAATCATTTCTAATTTCTAACCCCTCAAAACAA 862
Qy 841 AGCTGTGTATATATCTGATCTCTACGGTCTCTTGCGGCCCAACATTTCTCATATATCA 900
Db 863 AGCGTGTATATATCTGATCTCTACGGTCTCTTGCGGCCCAACATTTCTCATATATCA 922
Qy 901 GCCACACTATATTTTAAATTTAGTCCAGATCTGATCTGACCTTTCTACACTGTAG 960
Db 923 GCCACACTATATTTTAAATTTAGTCCAGATCTGATCTGACCTTTCTACACTGTAG 982
Qy 961 AATAACTTCTCATTTTGTTCAAAGACCCCTGCTGTGCTGCTAATATGATCTGACT 1020
Db 983 AATPACTTCTCATTTTGTTCAAAGACCCCTGCTGTGCTGCTAATATGATCTGACT 1042
Qy 1021 GTTTTCTTAAGAGATCTTGCGCCAGGGGATCTGTAACAGGCTGGGAAGCATCTCA 1080
Db 1043 GTTTTCTTAAGAGATCTTGCGCCAGGGGATCTGTAACAGGCTGGGAAGCATCTCA 1102
Qy 1081 GATCTTCCAGGGTATATCTTACTAGACACAGCATATCATTTACGAGTGAATTAATCTA 1140
Db 1103 GATCTTCCAGGGTATATCTTACTAGACACAGCATATCATTTACGAGTGAATTAATCTA 1162
Qy 1141 ATCAACATCATCTCAGTGTCTTGGCCATCTGAATTCATTTCCACTTTTGTGCCCA 1200
Db 1163 ATCAACATCATCTCAGTGTCTTGGCCATCTGAATTCATTTCCACTTTTGTGCCCA 1222
Qy 1201 TTCTCAAGACCTCAAAATGTCAATTCATTAATACAGAGATTAATCTTTTAAACC 1260
Db 1223 TTCTCAAGACCTCAAAATGTCAATTCATTAATACAGAGATTAATCTTTTAAACC 1282
Qy 1261 TGGAGAATTCATATGTCATGACATGAGCATGGAATTAATTAATTTTGTTCAGT 1320
Db 1283 TGGAGAATTCATATGTCATGACATGAGCATGGAATTAATTAATTTTGTTCAGT 1342
Qy 1321 GCAAGATGACTAAGTCTTATCCCTCCCTTTGTTGATTTTTCAGATTAAGT 1380
Db 1343 GCAAGATGACTAAGTCTTATCCCTCCCTTTGTTGATTTTTCAGATTAAGT 1402
Qy 1381 TAAATGCTTACGCTTGTACTGAGGCTGTATACAGACAGCTCTCCCATCCCTCAGC 1440
Db 1403 TAAATGCTTACGCTTGTACTGAGGCTGTATACAGACAGCTCTCCCATCCCTCAGC 1462
Qy 1441 CTATCTGTATACCATCAACCCCTCCCATNTSACCTAACAATAATCTAATCTGATAT 1500
Db 1463 CTATCTGTATACCATCAACCCCTCCCATNTSACCTAACAATAATCTAATCTGATAT 1522
Qy 1501 CCTTGAACATGTAGGNCATATATTTCTCTGCTGAGAGCTTTCTTGTCTCT 1560
Db 1523 CCTTGAACATGTAGGNCATATATTTCTCTGCTGAGAGCTTTCTTGTCTCT 1582
Qy 1561 AATTCATGATGATGTAAATTTTGAATTAAGTGTACTATCTTATCTCAAGAAGAGG 1620
Db 1583 AATTCATGATGATGTAAATTTTGAATTAAGTGTACTATCTTATCTCAAGAAGAGG 1642
Qy 1621 ACACATATGATGATTCATCATCATGAGACGAATAATCTAAGTATTTGATATATA 1680
Db 1643 ACACATATGATGATTCATCATCATGAGACGAATAATCTAAGTATTTGATATATA 1702
Qy 1681 AGAGTTAGATTAATATATGAAATGCAAGKCCACAGAGGGAATGTTATGGGCACTT 1740
Db 1703 AGAGTTAGATTAATATATGAAATGCAAGKCCACAGAGGGAATGTTATGGGCACTT 1762
Qy 1741 TGTAACTCTGGGATGTGAAGMAAAGGAGGAACCTCATAGTATCTTAAATATATCTT 1800
Db 1763 TGTAACTCTGGGATGTGAAGMAAAGGAGGAACCTCATAGTATCTTAAATATATCTT 1822
Qy 1801 CATTTCTATCTCTTCAACAAATATCCAAACACTTTTCCAGAAATTCATGCACTGAAA 1860
Db 1823 CATTTCTATCTCTTCAACAAATATCCAAACACTTTTCCAGAAATTCATGCACTGAAA 1882
Qy 1861 TCCCAAAAGTAACTTTTATCATTTTATGATGAGTGGCTTTAGAAATTTTGGCAATCA 1920
Db 1883 TCCCAAAAGTAACTTTTATCATTTTATGATGAGTGGCTTTAGAAATTTTGGCAATCA 1942

Qy 1921 TACTGTCATCTTATCTCAACTTTGAGATGTTGCTCTGTAGTATTAATGAAGAATA 1980
Db 1943 TACTGTCATCTTATCTCAACTTTGAGATGTTGCTCTGTAGTATTAATGAAGAATA 2002
Qy 1981 GGGCAGCTCTTGTGAGCCACTTTAGGTTCACTCTGSCAATAAAGAAATTTACAAGA 2037
Db 2003 GGGCAGCTCTTGTGAGCCACTTTAGGTTCACTCTGSCAATAAAGAAATTTACAAGA 2059
RESULT 6
ABL95397
ID ABL95397 standard; cDNA: 3923 BP.
XX
AC ABL95397;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human DD3 cDNA sequence SEQ ID NO 690.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KM gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US202022248-A1.
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIANG/) JIANG Y.
PA (KALOS/) KALOS M D.
PA (FRANG/) FRANGER G R.
PA (REIT/) REITER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISK/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Mang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX MPI: 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
XX Claim 1: SEQ ID NO 690; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;

Query Match 80.0%; Score 1629; DB 24; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCAGAAAAACAGAGGAGATTTGTGTGCTGCAGCCGAGGAGACCCAG 60
DB 23 AGAAGCTGGCATCAGAAAAACAGAGGAGATTTGTGTGCTGCAGCCGAGGAGACCCAG 82
QY 61 GAAGATCTGCATGCTGGGAGAGACCTGATGATACAGAGAAATTAAACACATATCTTAG 120
DB 83 GAAGATCTGCATGCTGGGAGAGACCTGATGATACAGAGAAATTAAACACATATCTTAG 142
QY 121 TGTTCATATGAACACCAAGATTAATTAAGTGAAGACTAGTCCGTGTGAGTCTCCTCAGT 180
DB 143 TGTTCATATGAACACCAAGATTAATTAAGTGAAGACTAGTCCGTGTGAGTCTCCTCAGT 202
QY 181 GACACAGGCTGGATGACCATGACGCGCATTTCTGACTACTGACGCAAGAAAGA 240
DB 203 GACACAGGCTGGATGACCATGACGCGCATTTCTGACTACTGACGCAAGAAAGA 262
QY 241 CTACGACATCTCATATGCGAGGGGTGAGAAATTAAGAGGCTGACCTTAACTCCATCGA 300
DB 263 CTACGACATCTCATATGCGAGGGGTGAGAAATTAAGAGGCTGACCTTAACTCCATCGA 322
QY 301 GGCCACACATCTGCTGAATGAGATTAATTAACATCAGTAGAAGACGAAATGACAATA 360
DB 323 GGCCACACATCTGCTGAATGAGATTAATTAACATCAGTAGAAGACGAAATGACAATA 382
QY 361 TAATGCTTAAGTGAAGATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 383 TAATGCTTAAGTGAAGATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAAGCAAAAAGGAAGACACAGATCCCTGGGAGAAATGCCGGCCGCCATCTGGG 480
DB 443 CAGGAAGCAAAAAGGAAGACACAGATCCCTGGGAGAAATGCCGGCCGCCATCTGGG 502
QY 481 TCATGATGAGCCTGCGCTGTGCTGCTCCCGCTTGTGAGGGAAGGACATTAGAAAATG 540
DB 503 TCATGATGAGCCTGCGCTGTGCTGCTCCCGCTTGTGAGGGAAGGACATTAGAAAATG 562
QY 541 AATGATGCTGTTCTTAAAGATGGGCAAGAAACAGATCCTGTTGGATATTATTTTG 600
DB 563 AATGATGCTGTTCTTAAAGATGGGCAAGAAACAGATCCTGTTGGATATTATTTTG 622
QY 601 AACGGATTACAGATTTGAATGAAGTACAAAGAGACATTACCAATGAGAGGAAAACA 660
DB 623 AACGGATTACAGATTTGAATGAAGTACAAAGAGACATTACCAATGAGAGGAAAACA 682
QY 661 GACGAGAAATCTTGATGCTTACACAGACATGCAACAAACAAATGGAATCTGTATG 720
DB 683 GACGAGAAATCTTGATGCTTACACAGACATGCAACAAACAAATGGAATCTGTATG 742
QY 721 ACATGAGGAGCCAAAGCTGGGAGAGATTAACACAGGGGACAGGGTCAAGATTTTGCC 780
DB 743 ACATGAGGAGCCAAAGCTGGGAGAGATTAACACAGGGGACAGGGTCAAGATTTTGCC 802

QY 761 CTGTCGCTAAACGTGGCTTCATTAACCAAAATCATTTGATATTTCTAAACCCGCAAAACA 840
DB 803 CTGTCGCTAAACGTGGCTTCATTAACCAAAATCATTTGATATTTCTAAACCCGCAAAACA 862
QY 841 AGCTGTGAATATATCTGATCTCTAGGCTTCTTGGGCGCCAACTTCATATATATCA 900
DB 863 AGCTGTGAATATATCTGATCTCTAGGCTTCTTGGGCGCCAACTTCATATATCA 922
QY 901 GCCACAGCATTTTAAATATTTAGTTCCAGATCTGTACTGTGACCTTTCTACACTGAG 960
DB 923 GCCACAGCATTTTAAATATTTAGTTCCAGATCTGTACTGTGACCTTTCTACACTGAG 982
QY 961 AATACATTTACTGATTTGTTTAAAGACCTTCGCTGCTGCTCCCAATATGAGTGGCT 1020
DB 983 AATACATTTACTGATTTGTTTAAAGACCTTCGCTGCTGCTCCCAATATGAGTGGCT 1042
QY 1021 GTTTTCCCTAAGAGATGTTCTGGCCAGGAGATCTGTAAACAGGCTGGGAACATCTCA 1080
DB 1043 GTTTTCCCTAAGAGATGTTCTGGCCAGGAGATCTGTAAACAGGCTGGGAACATCTCA 1102
QY 1081 GATCTTCCAGGCTTAATCTTAAGTACACACAGATGATCATTTACGAGTCAATATCTA 1140
DB 1103 GATCTTCCAGGCTTAATCTTAAGTACACACAGATGATCATTTACGAGTCAATATCTA 1162
QY 1141 ATCAACATATCTCAGTGTCTTGGCCATCTGAAATTCATTTCCCACTTTTGGCCCA 1200
DB 1163 ATCAACATATCTCAGTGTCTTGGCCATCTGAAATTCATTTCCCACTTTTGGCCCA 1222
QY 1201 TTCTCAAGACCTCAAAATATGCTATTCATTAATATACAGAGATTAACTTTTAAAC 1260
DB 1223 TTCTCAAGACCTCAAAATATGCTATTCATTAATATACAGAGATTAACTTTTAAAC 1282
QY 1261 TGGAAATTTCAATGTTACATGACAGCTATGGAAATTAATTAATATTTTGTTCAGT 1320
DB 1283 TGGAAATTTCAATGTTACATGACAGCTATGGAAATTAATTAATATTTTGTTCAGT 1342
QY 1321 GCAAGATGACATGATCTTATATCCCTCCCTTTGTTGATTTTTCGAGTAAAGT 1380
DB 1343 GCAAGATGACATGATCTTATATCCCTCCCTTTGTTGATTTTTCGAGTAAAGT 1402
QY 1381 TAAATGCTTACCTGTAGTGAAGCTGTATACAGACAGCCCTCCCATCCCTCAGC 1440
DB 1403 TAAATGCTTACCTGTAGTGAAGCTGTATACAGACAGCCCTCCCATCCCTCAGC 1462
QY 1441 CTTATCTGATCACCATCAACCCCTCCCATATGACCTTAACAAATGTAATCTGTAT 1500
DB 1463 CTTATCTGATCACCATCAACCCCTCCCATACACCTTAACAAATGTAATCTGTAT 1522
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DB 1523 CTTGACATGTCAGGATATACATTTTCTCTGCTGAGAAAGCTCTGCTCTCTCT 1582
QY 1561 AANTCTAGATGATTAAGTTTGAATTAAGTGAATTAAGTGAATTAAGTGAATTAAGT 1620
DB 1583 AANTCTAGATGATTAAGTTTGAATTAAGTGAATTAAGTGAATTAAGTGAATTAAGT 1642
QY 1621 ACACATATGAGATTTATCATCATGAGACAGCAAAATTAATTAATTTGATTTA 1680
DB 1643 ACACATATGAGATTTATCATCATGAGACAGCAAAATTAATTAATTTGATTTA 1702
QY 1681 AGAGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
DB 1703 AGAGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1762
QY 1741 TGTAACTGGGATGAGAAAGGAGGAACTCATATCTTATTAATTAATTAAT 1800
DB 1763 TGTAACTGGGATGAGAAAGGAGGAACTCATATCTTATTAATTAATTAAT 1822
QY 1801 CATTTCTATCTATCATCAATATCCAAAGCTTTTACAGAAATTTATGACATGCA 1860
DB 1823 CATTTCTATCTATCATCAATATCCAAAGCTTTTACAGAAATTTATGACATGCA 1882


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Db      743 ACATAGAGGAGCAAGCTGGGGAGAGATTAACACAGGGGACAGAGGCTGAGGTTGTGGCC 802
Qy      741 CTGTGCTCTAAACCTGCGCTTCATTAACCAATCATTTCTTAACCTCTCAACAA 840
Db      803 CTGCGCTCTAAACCTGCGCTTCATTAACCAATCATTTCTTAACCTCTCAACAA 862
Qy      841 AGCGTTGTAAATCTGATCTGAGGTTCCCTTCGGGGCCCAACCTCCCTCAATATCA 900
Db      863 AGCGTTGTAAATCTGATCTGAGGTTCCCTTCGGGGCCCAACCTCCCTCAATATCA 922
Qy      901 GCCACACTCATTTTAAATATTTAGTTCACAGATCTGACTGACCTTTCTCACTAG 960
Db      923 GCCACACTCATTTTAAATATTTAGTTCACAGATCTGACTGACCTTTCTCACTAG 982
Qy      961 AATAACATTTACTCATTTTGTTCAAAGACCTTCGTGTGCTCCCTAATATGAGTGA 1020
Db      983 AATAACATTTACTCATTTTGTTCAAAGACCTTCGTGTGCTCCCTAATATGAGTGA 1042
Qy      1021 GTTTTTCCTAAGGAGTCTTCGGCCGAGGATCTGTAACAGGCTGGGAACATCTCA 1080
Db      1043 GTTTTTCCTAAGGAGTCTTCGGCCGAGGATCTGTAACAGGCTGGGAACATCTCA 1102
Qy      1081 GATCTTTCAGGGTATCTTACTAGCACACAGATGATCATTTAGGAGTGAATATCTA 1140
Db      1103 GATCTTTCAGGGTATCTTACTAGCACACAGATGATCATTTAGGAGTGAATATCTA 1162
Qy      1141 ATCAACATCTCTCAGTGTCTTGTCCCATCTGAATTCATTTCCCATTTTGTGCCA 1200
Db      1163 ATCAACATCTCTCAGTGTCTTGTCCCATCTGAATTCATTTCCCATTTTGTGCCA 1222
Qy      1201 TTTCGAAGACCTCAAAATGTCAATTCATTAATACAGGATTAATTTTCTTAACC 1260
Db      1223 TTTCGAAGACCTCAAAATGTCAATTCATTAATACAGGATTAATTTTCTTAACC 1282
Qy      1261 TGGGAATTCATTAATGTACATGACAGCTATGGAATTAATTCATTTTGTTCACGT 1320
Db      1283 TGGGAATTCATTAATGTACATGACAGCTATGGAATTAATTCATTTTGTTCACGT 1342
Qy      1321 GCAAAAGATGACTAGTCTTATCCCTCCCTCTTGTGATTTTTCACATTAAGT 1380
Db      1343 GCAAAAGATGACTAGTCTTATCCCTCCCTCTTGTGATTTTTCACATTAAGT 1402
Qy      1381 TAAATGCTTACGCTGTAGTGAAGGCTGATACACACAGCCTCCCATCCCTCCAGC 1440
Db      1403 TAAATGCTTACGCTGTAGTGAAGGCTGATACACACAGCCTCCCATCCCTCCAGC 1462
Qy      1441 CTTATCTGTCATCACCATCAACCCCTCCCATNYTSACTAAACAATCTAATCTTAAT 1500
Db      1463 CTTATCTGTCATCACCATCAACCCCTCCCATNYTSACTAAACAATCTAATCTTAAT 1522
Qy      1501 CCTTGACATGTGAGGNCATATCTATTTCTTCCTGCTGAGAGGCTCTTCTGCTCTT 1560
Db      1523 CCTTGACATGTGAGGNCATATCTATTTCTTCCTGCTGAGAGGCTCTTCTGCTCTT 1582
Qy      1561 AANTCTAGAAGATTAAGTTTGAATTAAGTGAATGATCTACTCATGCAAAAGAGG 1620
Db      1583 AANTCTAGAAGATTAAGTTTGAATTAAGTGAATGATCTACTCATGCAAAAGAGG 1642
Qy      1621 ACACATATGAGATTCATCATGAGAGCAAGCAATCTAAAGTGAATTTGATTTATA 1680
Db      1643 ACACATATGAGATTCATCATGAGAGCAAGCAATCTAAAGTGAATTTGATTTATA 1702
Qy      1681 AGAGTTTGAATTAATTAATGAATGAATGAAGCAAGAGGAGATTTTATGGGACGTT 1740
Db      1703 AGAGTTTGAATTAATTAATGAATGAATGAAGCAAGAGGAGATTTTATGGGACGTT 1762
Qy      1741 TGTAGCCCTGGGATGTGAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
Db      1763 TGTAGCCCTGGGATGTGAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1822
Qy      1801 CATTTCTATCTATCATCAATATCAACAAAGCTTTTACAGATTCATGAGTGCAGAA 1860

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Db      1823 CATTTCTATCTATCATCAATATCAACAAAGCTTTTACAGATTCATGAGTGCAGAA 1882
Qy      1861 TCCCAAGAGTAACTTTATTCATTTGATGAGTGGGCTTTAACAATTTTGGCAATCA 1920
Db      1883 TCCCAAGAGTAACTTTATTCATTTGATGAGTGGGCTTTAACAATTTTGGCAATCA 1942
Qy      1921 TACTGTCATCTATCTATCAACTTTGAGATGTGTTGCTGCTGATGATTAATGAAGAAATA 1980
Db      1943 TACTGTCATCTATCTATCAACTTTGAGATGTGTTGCTGCTGATGATTAATGAAGAAATA 2002
Qy      1981 GGGCAGCTCTGTGAGCCACTTTAGGTTCTACTCTGCGAATTAAGATTTTACAAAGA 2037
Db      2003 GGGCAGCTCTGTGAGCCACTTTAGGTTCTACTCTGCGAATTAAGATTTTACAAAGA 2059

RESULT 8
AAV62430
ID AAV62430 standard; cDNA; 3582 BP.
XX
AC AAV62430;
XX
DT 30-DEC-1998 (first entry)
XX
DE Prostate cancer antigen (PCA3) wild-type cDNA.
XX
KW Prostate cancer antigen cDNA; PCA3; prostatic cancer;
KW PC; ds.
XX
OS Homo sapiens.
XX
FH Key
FH CDS location/Qualifiers
FT /*tag= a
FT /*product= "PCA3 protein"
FT polyA_signal
FT /*tag= b
FT polyA_signal
FT /*tag= c
FT /*tag= d
FT polyA_signal
FT /*tag= e
XX
PN W09845420-A1.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98WO-CA00346.
XX
PR 10-APR-1997; 97US-0041836.
XX
DIAG- ) DIAGNOCURE INC.
XX
BUSSEMAKERS MJG;
XX
WPI: 1998-568347/48.
XX
P-PSDB: AAM79738.
XX
PT New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
PT prevention and treatment of prostatic cancer
XX
PS Claim 3; Fig 5B-5F; 11pp; English.
XX
CC The present sequence represents the prostate cancer antigen (PCA3)
CC wild-type cDNA sequence comprising of exons 1, 2, 3, 4a-4d of the
CC PCA3 gene. The invention claims for PCA3 cDNA variants and the
CC proteins they encode. The invention also claims for antibodies
CC against PCA3 protein. The antibodies are claimed to be useful for
CC detecting PCA3 protein in immunoassay tests, for diagnosing, assessing
CC and prognosing of prostatic cancer (PC). Antibodies, optionally
CC coupled to a cytotoxin or radioisotope, and nucleic acids antisense
CC to PCA3 cDNA are claimed to be useful for treating PC, while determining
CC elevated levels of PCA3 (as RNA or protein) is useful for detecting a

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CC predisposition to development of PC, e.g. in prenatal tests. Detecting
CC PCa3 protein allows differentiation between malignant and benign
CC prostatic disease, and the level of PCa3 expression allows correlation
CC with the grade of tumour. PCa3 protein and its fragments are also
CC claimed to be useful in vaccines for preventing PC; in drug screens
CC for identifying specific (ant)agonists (potentially useful
CC therapeutically) and for studying protein-DNA interactions.

XX Sequence 3582 BP; 1052 A; 788 C; 679 G; 1063 T; 0 other;

Query Match 77.5%; Score 1578; DB 19; Length 3582;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2028; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 AGAAGCTGCAATCAGAAAAACAGAGGGAATTTGTGTGCTGCAGCCGAGGAGACAG 60
DB 23 AGAAGCTGCGATCAGAAAAACAGAGGGAATTTGTGTGCTGCAGCCGAGGAGACAG 82
QY 61 GAAGATTCGATGTTGGGAAGGACCTGATATACAGAGGAATTAACAACATATCTTAG 120
DB 83 GAAGATTCGATGTTGGGAAGGACCTGATATACAGAGGAATTAACAACATATCTTAG 142
QY 121 TGTTCATTAACACCAAGATTAATAGTGAAGAGCTAGTCCGCTGAGTCTCCAGT 180
DB 143 TGTTCATTAACACCAAGATTAATAGTGAAGAGCTAGTCCGCTGAGTCTCCAGT 202
QY 181 GACACAGGCTGATCACCATCGACGCGACTTCTGATCTAGTCTAGTCCAGCAAGAAAGA 240
DB 203 GACACAGGCTGATCACCATCGACGCGACTTCTGATCTAGTCTAGTCCAGCAAGAAAGA 262
QY 241 CTACAGACATCTCAATGGGAGGGGTGAGAAATGAAGAGCTGTGACTTTACATCTGA 300
DB 263 CTACAGACATCTCAATGGGAGGGGTGAGAAATGAAGAGCTGTGACTTTACATCTGA 322
QY 301 GGCCACACATCTCTGTAATAGAGATTAATTAACATCTAGTAAACAGACAGATGACATA 360
DB 323 GGCCACACATCTCTGTAATAGAGATTAATTAACATCTAGTAAACAGACAGATGACATA 382
QY 361 TAATGTCTAAGTAGTGAATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 383 TAATGTCTAAGTAGTGAATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAAGCACAAAAGGAGACAGAGATCCCTGGGAGAAATGCCCGGCGCCCACTTGGG 480
DB 443 CAGGAAGCACAAAAGGAGACAGAGATCCCTGGGAGAAATGCCCGGCGCCCACTTGGG 502
QY 481 TCATCGATGAGCTCGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 503 TCATCGATGAGCTCGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 562
QY 541 AATTGATGTCTCTTAAGAGATGGCAGAGAAAACAGATCTGTGTGTGATATTTATTTG 600
DB 563 AATTGATGTCTCTTAAGAGATGGCAGAGAAAACAGATCTGTGTGTGATATTTATTTG 622
QY 601 AAGGGATTCAGATTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 660
DB 623 AAGGGATTCAGATTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 682
QY 661 GAGGAGAAAATCTTGTATGCTTCAACAAGATGCAACAACAAATGAATGATCTGATG 720
DB 683 GAGGAGAAAATCTTGTATGCTTCAACAAGATGCAACAACAAATGAATGATCTGATG 742
QY 721 ACATGAGGAGCCAGCTGGGAGAGATTAACACGCGGAGAGAGGTGAGATTTCTGGCC 780
DB 743 ACATGAGGAGCCAGCTGGGAGAGATTAACACGCGGAGAGAGGTGAGATTTCTGGCC 802
QY 781 CTGCTGCTTAATCTGCTGCTTCAATACCAATCATTTTCATTTCTTAACCTCAAAACA 840
DB 803 CTGCTGCTTAATCTGCTGCTTCAATACCAATCATTTTCATTTCTTAACCTCAAAACA 862
QY 841 AGCTGTGTAAATCTGATCTACGTTCTCTGCGGCCACACATTTCTCATATATCCA 900
DB 863 AGCTGTGTAAATCTGATCTACGTTCTCTGCGGCCACACATTTCTCATATATCCA 922

QY 901 GCCACACTATTTTAAATATTAATAGTCCAGATCTGATCTGACCTTTCTACACTGTAG 960
DB 923 GCCACACTATTTTAAATATTAATAGTCCAGATCTGATCTGACCTTTCTACACTGTAG 982
QY 961 AATTAACATTAATCTATTTTGTTCAAAGACCTTGTGTGCTGCTTAATATGATGCTACT 1020
DB 983 AATTAACATTAATCTATTTTGTTCAAAGACCTTGTGTGCTGCTTAATATGATGCTACT 1042
QY 1021 GTTTTCTTAAGGAGTGTTCGCGCCAGGGAGATCTGTAACAGCTGGAGAGATCTCAA 1080
DB 1043 GTTTTCTTAAGGAGTGTTCGCGCCAGGGAGATCTGTAACAGCTGGAGAGATCTCAA 1102
QY 1081 GATCTTTCAGGGTATTAATCTTACTAGCACACAGATGATCATTAACGAGTGAATATCTA 1140
DB 1103 GATCTTTCAGGGTATTAATCTTACTAGCACACAGATGATCATTAACGAGTGAATATCTA 1162
QY 1141 ATCAACATCAATCTCACTGATGCTTTGCCCATATCTGAAATTTATTTCCACTTTGTGCCA 1200
DB 1163 ATCAACATCAATCTCACTGATGCTTTGCCCATATCTGAAATTTATTTCCACTTTGTGCCA 1222
QY 1201 TTCTCAAGACCTCAAAATGATTCATTCATTAATATACAGAGATTAACCTTTTATTAAC 1260
DB 1223 TTCTCAAGACCTCAAAATGATTCATTCATTAATATACAGAGATTAACCTTTTATTAAC 1282
QY 1261 TGGAAATTAATCAATGTTTACATGACAGCTATGGAATTAATTAATATTTTGTTCAGT 1320
DB 1283 TGGAAATTAATCAATGTTTACATGACAGCTATGGAATTAATTAATATTTTGTTCAGT 1342
QY 1321 GCAAAAGTGAATGCTTATTCCTTTATCCCTCCCTTTGTTGATTTTTCAGATATAAGT 1380
DB 1343 GCAAAAGTGAATGCTTATTCCTTTATCCCTCCCTTTGTTGATTTTTCAGATATAAGT 1402
QY 1381 TAAATAGCTTACGCTTGTACTGAGGCTGTATACAGACACGCTTCGCCCTCCAGC 1440
DB 1403 TAAATAGCTTATGCTTGTACTGAGGCTGTATACAGACACGCTTCGCCCTCCAGC 1462
QY 1441 CTTATCTGATCAATCAATCAACCTTCCATYNY SACCTAAACAATAATCTAATCTGTAAT 1500
DB 1463 CTTATCTGATCAATCAATCAACCTTCCATYNY SACCTAAACAATAATCTAATCTGTAAT 1522
QY 1501 CTTGAAACATGTCAGGACATCAATTTTCTGCTGCTGAGAGCTTCTGCTGCTGCT 1560
DB 1523 CTTGAAACATGTCAGGACATCAATTTTCTGCTGCTGAGAGCTTCTGCTGCTGCT 1582
QY 1561 AANTCTAGATGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1620
DB 1583 AANTCTAGATGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1642
QY 1621 ACACATATGAGATTCATCATCATGAGACAGCAAAATCTAATAAGTATTAATTTGATTTA 1680
DB 1643 ACACATATGAGATTCATCATCATGAGACAGCAAAATCTAATAAGTATTAATTTGATTTA 1702
QY 1681 AGAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1740
DB 1703 AGAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1762
QY 1741 TGTAAAGCTGAGATGTAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
DB 1763 TGTAAAGCTGAGATGTAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1822
QY 1801 CATTTCTATCTATCTATCATCAATATCAACAGCTTTTCAACAGATTCATGACAGTCAAA 1860
DB 1823 CATTTCTATCTATCTATCATCAATATCAACAGCTTTTCAACAGATTCATGACAGTCAAA 1882
QY 1861 TCCCAAGGTAACCTTTTATCAATTCATGAGTGAAGGCTTTAGAAATTTGGCAATTA 1920
DB 1883 TCCCAAGGTAACCTTTTATCAATTCATGAGTGAAGGCTTTAGAAATTTGGCAATTA 1942
QY 1921 TACTGTGATTAATCTCAACTTTGAGATGATGTTGCTGTGATTAATTTGAAGAATAA 1980
DB 1943 TACTGTGATTAATCTCAACTTTGAGATGATGTTGCTGTGATTAATTTGAAGAATAA 2002

Qy 1981 GGGCAGCTCTGTGAGCCACTTTAGGGTTCCTGCAATTAAGATTACAAAGA 2037
|||||
Db 2003 GGGCAGCTCTGTGAGCCACTTTAGGGTTCCTGCAATTAAGATTACAAAGA 2059

RESULT 9
AAA06689/c
ID AAA06689 standard; cDNA; 2426 BP.
XX
XX AAA06689;

DT 13-JUN-2000 (first entry)

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:470.

KM Human; prostate cancer; diagnosis; tumour; gene therapy; detection;

XX Immunogenic; cytosolic; vaccine; ss.

OS Homo sapiens.

PN MO200004149-A2.

PD 27-JAN-2000.

PF 14-JUL-1999; 99WO-US15838.

PR 14-JUL-1998; 98US-0115453.

PR 14-JUL-1998; 98US-0116134.

PR 23-SEP-1998; 98US-0159812.

PR 15-JAN-1999; 98US-0159822.

PR 15-JAN-1999; 99US-0232149.

PR 09-APR-1999; 99US-0232880.

PA (CORI-) CORIXA CORP.

PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;

XX WPI: 2000-171268/15.

XX New polypeptide useful for treating and diagnosing prostate cancer

PT comprises an immunogenic portion of prostate tumor protein -

PS Claim 1; Page 261-262; 263pp; English.

XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06689 to AAA06691 and
CC AA182000 to AA182020 represent sequences used in the exemplification of
CC the present invention.

XX Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;

Qy Query Match 56.7%; Score 1154; DB 21; Length 2426;

Db Best Local Similarity 100.0%; Pred. No. 0;

Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 263 GGTGAATAAAGAGGCTGCTGACTTACCATGTAGGCCACATCTGCTGAATGG 322

Db 1769 GGTGAATAAAGAGGCTGCTGACTTACCATGTAGGCCACATCTGCTGAATGG 1710

Qy 323 AGATAATTACATCTAGAAAACAGCAAGATGACATAATATGTCTAAGTAGTGCATGT 382

Db 1709 AGATAATTACATCTAGAAAACAGCAAGATGACATAATATGTCTAAGTAGTGCATGT 1650

Qy 383 TTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGAGCAC 442
|||||
Db 1649 TTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGAGCAC 1590

Qy 443 AGAGATCCCTGGGAGAAATGCCCGCCGCATCTTGGGTATCATCATGAGCCCTGGCTGT 502

Db 1589 AGAGATCCCTGGGAGAAATGCCCGCCGCATCTTGGGTATCATCATGAGCCCTGGCTGT 1530

Qy 503 GCCTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTAAAGA 562

Db 1529 GCCTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTAAAGA 1470

Qy 563 TGGCAGGAGAAACAGATCCTGTGTGATATTTATTTAAGCGGATTCAGATTTGAAT 622

Db 1469 TGGCAGGAGAAACAGATCCTGTGTGATATTTATTTAAGCGGATTCAGATTTGAAT 1410

Qy 623 GAAGTCACAAAGTGAATTTACCAATGAGAGAGAAACAGACAGAAATCTTGATGGCT 682

Db 1409 GAAGTCACAAAGTGAATTTACCAATGAGAGAGAAACAGACAGAAATCTTGATGGCT 1350

Qy 683 CACAAGACATGCAACAAACAAATGGAATGATGATGATGATGATGATGATGATGATG 742

Db 1349 CACAAGACATGCAACAAACAAATGGAATGATGATGATGATGATGATGATGATGATG 1290

Qy 743 AGGAGATFACACAGGGGAGAGGAGGATTCGGCCCTGCTGAACGTGCGTTC 802

Db 1289 AGGAGATFACACAGGGGAGAGGAGGATTCGGCCCTGCTGAACGTGCGTTC 1230

Qy 803 ATACCAATCATTTTCATATTTTCATACCCCTGCAACAAAGGCTGTGTAATATGATGTC 862

Db 1229 ATACCAATCATTTTCATATTTTCATACCCCTGCAACAAAGGCTGTGTAATATGATGTC 1170

Qy 863 TACGTTCTCTTGGGCCCCACATTCCTCATATATCCAGCCACTCTTTTAAATTT 922

Db 1169 TACGTTCTCTTGGGCCCCACATTCCTCATATATCCAGCCACTCTTTTAAATTT 1110

Qy 923 AGTCCAGATCTGACTGTGACCTTTACACCTGTAATATACATTCATTTGTC 982

Db 1109 AGTCCAGATCTGACTGTGACCTTTACACCTGTAATATACATTCATTTGTC 1050

Qy 983 AAAGACCTTCTGTTGCTGCTTAATATATGACTGATCTTTTCTTAAGAGTGTCTG 1042

Db 1049 AAAGACCTTCTGTTGCTGCTTAATATATGACTGATCTTTTCTTAAGAGTGTCTG 990

Qy 1043 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATCTTA 1102

Db 989 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATCTTA 930

Qy 1103 CTAGCAGACAGATGATCATTAAGAGATTAATCAATCAATCCATGATGCT 1162

Db 929 CTAGCAGACAGATGATCATTAAGAGATTAATCAATCAATCCATGATGCT 870

Qy 1163 TTGCCATACAGAAATTAATTTCCACTTTTGGCCATTTCCAGAGCTCAAAATGTCA 1222

Db 869 TTGCCATACAGAAATTAATTTCCACTTTTGGCCATTTCCAGAGCTCAAAATGTCA 810

Qy 1223 TTCCATTAATATACAGAAATTAATTTTAACTCGAAGATTCATATGTTACATG 1282

Db 809 TTCCATTAATATACAGAAATTAATTTTAACTCGAAGATTCATATGTTACATG 750

Qy 1283 CAGCATATGGAATTAATTTATTTTGTTCAGTGCAGAAAGTACTAAGTCTTTA 1342

Db 749 CAGCATATGGAATTAATTTATTTTGTTCAGTGCAGAAAGTACTAAGTCTTTA 690

Qy 1343 TCCCTCCCTTGTGATTTTTCAGAGTTAAAGTTAAATCTTACGCTTACTG 1402

Db 689 TCCCTCCCTTGTGATTTTTCAGAGTTAAAGTTAAATCTTACGCTTACTG 630

Qy 1403 AGGCTGATACAGC 1416

Db 629 AGGCTGATACAGC 616

RESULT 10
AAS63898/c
ID AAS63898 standard: cDNA; 2426 BP.
XX
XX AAS63898:
XX
XX 29-JAN-2002 (first entry)
XX
XX Human prostate cDNA sequence #432.
XX
XX Human; prostate cancer; ss; cytosstatic; immunostimulant; tumour.
XX
XX Homo sapiens.
XX
XX WO200173032-A2.
XX
XX 04-OCT-2001.
XX
XX 27-MAR-2001; 2001MO-US09919.
XX
XX 27-MAR-2000; 2000US-0536857.
XX
XX 09-MAY-2000; 2000US-0568100.
XX
XX 12-MAY-2000; 2000US-0570737.
XX
XX 13-JUN-2000; 2000US-0593793.
XX
XX 27-JUN-2000; 2000US-0605783.
XX
XX 10-AUG-2000; 2000US-0636215.
XX
XX 29-AUG-2000; 2000US-0651236.
XX
XX 06-SEP-2000; 2000US-0657279.
XX
XX 02-OCT-2000; 2000US-0679426.
XX
XX 10-OCT-2000; 2000US-0685166.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI Fanger GF, Retter MW, Stolk JA, Day CH, Vedicik TS, Carter D;
PI Li SX, Wang A, Skelky YAM, Hepler WT, Henderson RA;
XX
XX WPI; 2001-639232/73.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX Claim 1; Page 386; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
XX Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;
SQ
Query Match 56.7%; Score 1154; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1649 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGGAAGCAAAAGGAAGCAC 1590
Qy 443 AGAGATCCCTGGGAGAAATGCCGGCGGCATCTGGGTCATGATGAGCTGCCCTGT 502
Db 1589 AGAGATCCCTGGGAGAAATGCCGGCGGCATCTGGGTCATGATGAGCTGCCCTGT 1530
Qy 503 GCCTGTGCCCTGTGGAGGAAGACATTAGAAAATGAATGTATGTCTCTTAAGGA 562
Db 1529 GCCTGTGCCCTGTGGAGGAAGACATTAGAAAATGAATGTATGTCTCTTAAGGA 1470
Qy 563 TGGGACAGAAACAGATCCCTGTGTGATATTTGAACGGGATTTACGATTTGAAT 622
Db 1469 TGGGACAGAAACAGATCCCTGTGTGATATTTGAACGGGATTTACGATTTGAAT 1410
Qy 623 GAAGTCACAAAGTGACATTTACCAATGAGAGAAAACAGACGAAAAATCTTGATGCTT 682
Db 1409 GAAGTCACAAAGTGACATTTACCAATGAGAGAAAACAGACGAAAAATCTTGATGCTT 1350
Qy 683 CACAAGACATGACAAACAAATGGAATACCTGTGATGACATGAGCAGCAAGCTGGGG 742
Db 1349 CACAAGACATGACAAACAAATGGAATACCTGTGATGACATGAGCAGCAAGCTGGGG 1290
Qy 743 AGAGATTAACCAAGGGGACAGAGGTGAGATTTGCGCCCTGCTAAACGTGGCTTC 802
Db 1289 AGAGATTAACCAAGGGGACAGAGGTGAGATTTGCGCCCTGCTAAACGTGGCTTC 1230
Qy 803 ATAAACCAATCATTTATATTTCTAACCCCAAAACAAAGCTTTGTAATATGATCTC 862
Db 1229 ATAAACCAATCATTTATATTTCTAACCCCAAAACAAAGCTTTGTAATATGATCTC 1170
Qy 863 TACGGTTCCTTGTGGGCCCAACATTCCTCAATATCCAGCCACATCATTTTAATTTT 922
Db 1169 TACGGTTCCTTGTGGGCCCAACATTCCTCAATATCCAGCCACATCATTTTAATTTT 1110
Qy 923 AGTTCCAGATCTGTCTGTGACCTTTCTACCTGATAGAAATACATTTACATTTGTC 982
Db 1109 AGTTCCAGATCTGTCTGTGACCTTTCTACCTGATAGAAATACATTTACATTTGTC 1050
Qy 983 AAAGACCTTCGTGTGTGCTGCTCAATATATGATGACTGTTTCTTAAGGAGTGTCTG 1042
Db 1049 AAAGACCTTCGTGTGTGCTGCTCAATATATGATGACTGTTTCTTAAGGAGTGTCTG 990
Qy 1043 GCCCAGGGATCTGTGTAACAGGCTGGGAACATCTCAAGTCTTCCAGGTTATACTTA 1102
Db 989 GCCCAGGGATCTGTGTAACAGGCTGGGAACATCTCAAGTCTTCCAGGTTATACTTA 930
Qy 1103 CTAGCACACAGATGATCATTTACGAGTGAATATCTAATCAACATCATCTCAGTGTCT 1162
Db 929 CTAGCACACAGATGATCATTTACGAGTGAATATCTAATCAACATCATCTCAGTGTCT 870
Qy 1163 TTGCCCATCTGAAATTCATTTCCCACTTTGTGCCCATCTCAGACCTCAAAATGTCA 1222
Db 869 TTGCCCATCTGAAATTCATTTCCCACTTTGTGCCCATCTCAGACCTCAAAATGTCA 810
Qy 1223 TTCCATTAATATACAGGATTAATCTTTTAACTGGAAGTAATCAAGTTGTCATG 1282
Db 809 TTCCATTAATATACAGGATTAATCTTTTAACTGGAAGTAATCAAGTTGTCATG 750
Qy 1283 CAGCTATGGAATTAATTAATCATATTTGTTTCCAGTGAAGATGACTTAAGTCTTTA 1342
Db 749 CAGCTATGGAATTAATTAATCATATTTGTTTCCAGTGAAGATGACTTAAGTCTTTA 690
Qy 1343 TCCCTCCCTCTTGTGTGATTTTTCACATTAAGTTAAAGTCTTACCTGTGACTG 1402
Db 689 TCCCTCCCTCTTGTGTGATTTTTCACATTAAGTTAAAGTCTTACCTGTGACTG 630
Qy 1403 AGGCTGTAATCAGC 1416
Db 629 AGGCTGTAATCAGC 616

RESULT 11

AAH93805/c
ID AAH93805 standard; cDNA; 2426 BP.
XX
AC AAH93805;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence p710P #3.
XX
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KM cytosolic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PM WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001MO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAM;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
PS
XX
XX Claim 1: Page 384-385; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytosolic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
XX
SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;

Query Match 56.7%; Score 1154; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGTGGAATAAGAAAGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 322
DB 1769 GGTGGAATAAGAAAGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 1710

QY 323 AGATTATTACATCTCTGAAAGACAGATGACATAATATAGTAGTGACATGT 382
DB 1709 AGATTATTACATCTCTGAAACACAGATGACATAATATAGTAGTGACATGT 1650

QY 383 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAACACAAAAGAACAC 442
DB 1649 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAACACAAAAGAACAC 1590

QY 443 AGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTCAATGATGAGCCTGCCCTGT 502
DB 1589 AGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTCAATGATGAGCCTGCCCTGT 1530

QY 503 GCCTGTCCCGCTTGTGAGGAGACATTAAGAAATGATGTGCTCTTAAGCA 562
DB 1529 GCCTGTCCCGCTTGTGAGGAGACATTAAGAAATGATGTGCTCTTAAGCA 1470

QY 563 TGGGAGAGAAAACAGATCCTGTGTGATATTATTTAGGAGATTAAGATTGAAT 622
DB 1469 TGGGAGAGAAAACAGATCCTGTGTGATATTATTTAGGAGATTAAGATTGAAT 1410

QY 623 GAGTCACAAAGTGAAGCATTTACCAATGAGAGAAAACAGAGCAAAATCTTGATGCTT 682
DB 1409 GAGTCACAAAGTGAAGCATTTACCAATGAGAGAAAACAGAGCAAAATCTTGATGCTT 1350

QY 683 CACAAGACATGCAACAAACAAATGAGTACGTGATGATGACATGAGCGCAAGCTGGGG 742
DB 1349 CACAAGACATGCAACAAACAAATGAGTACGTGATGATGACATGAGCGCAAGCTGGGG 1290

QY 743 AGAGATTAACACAGGGGAGAGGGTCAGAGATTCCTGGCCCTGCTTAACCTGCTTC 802
DB 1289 AGAGATTAACACAGGGGAGAGGGTCAGAGATTCCTGGCCCTGCTTAACCTGCTTC 1230

QY 803 ATACCAAAATCATTTCAATTTCTAACCCTCAAAACAAAGCTGTGTAATCTGATCTC 862
DB 1229 ATACCAAAATCATTTCAATTTCTAACCCTCAAAACAAAGCTGTGTAATCTGATCTC 1170

QY 863 TACGGTCTCTTGGGGCCCAACATCTGCTATATCCAGCCACACTCAATTTTATATT 922
DB 1169 TACGGTCTCTTGGGGCCCAACATCTGCTATATCCAGCCACACTCAATTTTATATT 1110

QY 923 AGTTCCAGATCTGACTGTGACCTTCTACACTTAATAATATCTCATATTTTGTTC 982
DB 1109 AGTTCCAGATCTGACTGTGACCTTCTACACTTAATAATATCTCATATTTTGTTC 1050

QY 983 AAAGACCTTGCTGTGCTGCTTAATATAGTACGAGCTGTTTTCTTAAGAGTGTCTG 1042
DB 1049 AAAGACCTTGCTGTGCTGCTTAATATAGTACGAGCTGTTTTCTTAAGAGTGTCTG 990

QY 1043 GCCCGAGGATCTGAGACAGCTGAGCAATCAAGATCTTCCAGGGTTAACTTA 1102
DB 989 GCCCGAGGATCTGAGACAGCTGAGCAATCAAGATCTTCCAGGGTTAACTTA 930

QY 1103 CTAGCAGACAGATGATCATTAAGGAGTAATATCTAATCAATCATCTCAAGTCT 1162
DB 929 CTAGCAGACAGATGATCATTAAGGAGTAATATCTAATCAATCATCTCAAGTCT 870

QY 1163 TTGCCCACTAGTAATTAATTTCCACTTTTGTGCCCATTCTCAAGACCTCAAAATGCA 1222
DB 869 TTGCCCACTAGTAATTAATTTCCACTTTTGTGCCCATTCTCAAGACCTCAAAATGCA 810

QY 1223 TTCCATTAAATACAGAGATTAATCTTTTAACTGGAAGAAATTCATGTATACAG 1282
DB 809 TTCCATTAAATACAGAGATTAATCTTTTAACTGGAAGAAATTCATGTATACAG 750

QY 1283 CAGCTATGGAATTAATTAATTAATTTTCCAGTGCAAAAGATGATAGTCTTTA 1342
DB 749 CAGCTATGGAATTAATTAATTAATTTTCCAGTGCAAAAGATGATAGTCTTTA 690

QY 1343 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATCTTAAGCTTACTG 1402
DB 689 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATCTTAAGCTTACTG 630

QY 1403 AGGCTGTATACAGC 1416
DB 629 AGGCTGTATACAGC 616

RESULT 12
AAH85119/c
ID AAH85119 standard; cDNA; 2426 BP.
XX
AC AAH85119;
XX
DT 25-SEP-2001 (first entry)
XX

DE Human prostate-specific cDNA sequence P710P #3.
XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KM chromosome 22q11.2; prostate-specific protein; chromosome 1;
KM prostate specific antigen; PSN; ss.
XX Homo sapiens.
OS
PN W0200134802-A2.
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000MO-US30904.
XX
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX
PA (CORI-) CORIXA CORP.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Reltter MW, Stolk JA, Day CH, Skeiky YAM, Wang A;
DR WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer -
XX
PS Claim 5; Page 284; 325p; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;

Query Match 56.7%; Score 1154; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 623 GAAGTCACAAAGTGACGATTACCAATGAGAGAGAAAACAGACGAGAAAATCTGATGGCTT 682
DB 1409 GAAGTCACAAAGTGAGGATTTACCAATGAGAGAGAAAACAGACGAGAAAATCTGATGGCTT 1350
QY 683 CACAAGCATGCAACAAACAAATGGAATCTGTGATGACATAGGACGACGAAAGCTGGGG 742
DB 1349 CACAAGCATGCAACAAACAAATGGAATCTGTGATGACATAGGACGACGAAAGCTGGGG 1290
QY 743 AGGAGATTAACGAGGGGACAGAGGTCAGATTTGGCCCTGCTGCTTAACTGGCTTC 802
DB 1289 AGGAGATTAACGAGGGGACAGAGGTCAGATTTGGCCCTGCTGCTTAACTGGCTTC 1230
QY 803 ATTAACCAATCAATTCATATTTCTAAACCTCAAAACAAAGCTGTGTAATATCTGATC 862
DB 1229 ATTAACCAATCAATTCATATTTCTAAACCTCAAAACAAAGCTGTGTAATATCTGATC 1170
QY 863 TAGGGTTCCTTCGGGCGCCCAACATCTCCATATATCCAGCCACACATTTTAAATATT 922
DB 1169 TAGGGTTCCTTCGGGCGCCCAACATCTCCATATATCCAGCCACACATTTTAAATATT 1110
QY 923 AGTTCCAGATCTGTACTGTGACCTTCTACACTGATGATTAACATTAATCTATTTGTT 982
DB 1109 AGTTCCAGATCTGTACTGTGACCTTCTACACTGATGATTAACATTAATCTATTTGTT 1050
QY 983 AAAGACCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1042
DB 1049 AAAGACCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 990
QY 1043 GCCAGGGGATCTGTGTAACAGGCTGGGAGGATCTCAAGATCTTTCAGGGTATCTTA 1102
DB 989 GCCAGGGGATCTGTGTAACAGGCTGGGAGGATCTCAAGATCTTTCAGGGTATCTTA 930
QY 1103 CTAGCACACAGCATGATCATTTAGGAGTGAATTAATCAACATCATCTCAGTGTCT 1162
DB 929 CTAGCACACAGCATGATCATTTAGGAGTGAATTAATCAACATCATCTCAGTGTCT 870
QY 1163 TTCCCTCATCTGTAATTTATTTCCCACTTTTGCCCATTTCTCAACACCTCAAAATGTA 1222
DB 869 TTCCCTCATCTGTAATTTATTTCCCACTTTTGCCCATTTCTCAACACCTCAAAATGTA 810
QY 1223 TTCCATTAATATACAGGATTAATTTTTCATCTGGAAGATTAATGATGATG 1282
DB 809 TTCCATTAATATACAGGATTAATTTTTCATCTGGAAGATTAATGATGATG 750
QY 1283 CAGCTATGGGAATTAATTAATATTTTTCAGTGCAGCAAGATGACTAGTCCCTTA 1342
DB 749 CAGCTATGGGAATTAATTAATATTTTTCAGTGCAGCAAGATGACTAGTCCCTTA 690
QY 1343 TCCCTCCCTTTGTTGATTTTTCAGTGCAGTAAAGTTAAAGTTAGCTTACCTTGACTG 1402
DB 689 TCCCTCCCTTTGTTGATTTTTCAGTGCAGTAAAGTTAAAGTTAGCTTACCTTGACTG 630
QY 1403 AGGCTGTATACAGC 1416
DB 629 AGGCTGTATACAGC 616

RESULT 13
AAH02870/c
ID AAH02870 standard; cDNA; 2426 BP.
XX
XX AAH02870;
DT 14-JUN-2001 (first entry)
XX
DE Prostate tumour antigen cDNA sequence for P710P #3.
XX
KM Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
KM prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN W0200125272-A2.

XX 12-APR-2001.
XX 04-OCT-2000; 2000MO-US27464.
XX 04-OCT-1999; 99US-0157455.
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Skeiky YAM, Reed SG, Cheever MA:
XX WPI: 2001-245062/25.
XX
XX Prostate specific protein and its encoding polynucleotide, useful for
XX the treatment and diagnosis of prostate cancer -
XX
XX Claim 4: Page 266-267; 276pp; English.
XX
XX The present invention describes an isolated polypeptide (I) comprising
XX at least an immunogenic portion of a prostate tumour antigen protein or
XX its variant. (I) have cytostatic activity and can be used in vaccine
XX production. (I) prostate tumour antigen polynucleotides, an antigen
XX presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
XX pharmaceutical composition containing (I) are useful for inhibiting the
XX development of cancer in a patient. Antibodies specific for prostate
XX specific proteins and oligonucleotides that hybridise to a
XX polynucleotide that encodes a prostate specific protein are useful
XX for detecting the presence or absence of a cancer or monitoring the
XX progression the progression of a cancer, especially prostate cancer.
XX AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
XX used in the exemplification of the present invention.
XX
XX Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;

Query Match 56.7%; Score 1154; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGTGAATTAAGAAAGGCTGCTGACCTTACCACCTGAGGCACACATCGTGAAATGG 322
DB 1769 GGTGAATTAAGAAAGGCTGCTGACCTTACCACCTGAGGCACACATCGTGAAATGG 1710
QY 323 AGATTAATTACATCCTAGAAACAGCAAGATGACATTAATTAATGTTCTAAGTAGTACATGT 382
DB 1709 AGATTAATTACATCCTAGAAACAGCAAGATGACATTAATTAATGTTCTAAGTAGTACATGT 1650
QY 383 TTTTGACATTTCCAGCCCCCTTTAAATATCCACACACACAGAGACACAAAAGAGACAC 442
DB 1649 TTTTGACATTTCCAGCCCCCTTTAAATATCCACACACAGAGACACAAAAGAGACAC 1590
QY 443 AGAGATCCCTGGGGAATGCGCGCGCCCATCTGGTCATGATGAGCCCTCGCCCTGT 502
DB 1589 AGAGATCCCTGGGGAATGCGCGCGCCCATCTGGTCATGATGAGCCCTCGCCCTGT 1530
QY 503 GCTGGTCCCGCTTGAGGAGAGACATTTAGAAAATGAATGATGTCTTCTTAAAGA 562
DB 1529 GCTGGTCCCGCTTGAGGAGAGACATTTAGAAAATGAATGATGTCTTCTTAAAGA 1470
QY 563 TGGGACGAAAAACAGATCCTGTGTGATATTATTATTAACGGGATACAGATTTGAAT 622
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QY 623 GAAGTCACAAAGTGAAGTATCCCAATGAGGAAACAGAGAGAAATCTTGAAGGCTT 682
DB 1409 GAAGTCACAAAGTGAAGTATCCCAATGAGGAAACAGAGAGAAATCTTGAAGGCTT 1350
QY 683 CACAAGACATGCACAAACAAATGGAATGATGTGATGACATGAGGACGCAAGCTGGGG 742
DB 1349 CACAAGACATGCACAAACAAATGGAATGATGTGATGACATGAGGACGCAAGCTGGGG 1290
QY 743 AGGAGATACCAAGGGGAGAGGATTCGAGATTTCGCGCTGCTCTAAACTGTGCGTTC 802
DB 1289 AGGAGATACCAAGGGGAGAGGATTCGAGATTTCGCGCTGCTCTAAACTGTGCGTTC 1230

QY 803 ATAACCAATCATTTATTTCTTAACCTCAAAACAAAGCTGTGTAATATCTGATCTC 862
DB 1229 ATAACCAATCATTTATTTCTTAACCTCAAAACAAAGCTGTGTAATATCTGATCTC 1170
QY 863 TACGGTTCCTCTGGGGCCCAACATCTCCATATATCCAGCACACTCATTTTAAATATT 922
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DB 809 TTCCATTAATATCACAGGATTAATCTTTTAAACCTGGAAGATTCATTTGTTACATG 750
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DB 749 CAGCTATGGAATTAATTAATATTTGTTTTCAGTGCAAAAGTACTAAGTCTTTA 690
QY 1343 TCCCTCCCTCTGTTGATTTTTCAGTATTAAGTTAAATAGCTTACGCTTACTG 1402
DB 689 TCCCTCCCTCTGTTGATTTTTCAGTATTAAGTTAAATAGCTTACGCTTACTG 630
QY 1403 AGGCTGTATACAGC 1416
DB 629 AGGCTGTATACAGC 616

RESULT 14
AAF86948/C
ID AAF86948 standard; cDNA; 2426 BP.
XX
XX AAF86948;
XX
XX 06-JUL-2001 (first entry)
XX
XX Human P710P Inventive antigen coding sequence SEQ ID NO: 344.
XX
XX Human; mouse; immunotherapy; cancer; leukaemia; Wt1; Wilm's tumour gene;
XX chromosome 11p13; zinc finger transcription factor; ss.
XX
XX Homo sapiens.
XX
XX W0200125273-A2.
XX
XX 12-APR-2001.
XX
XX 04-OCT-2000; 2000MO-US27465.
XX
XX 04-OCT-1999; 99US-0157455.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAM, Xu J, Cheever MA, Reed SG;
PI

DR WPI: 2001-328324/34.
XX Polypeptide comprising part of the Wilm's Tumour gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with WT1
XX
PS Disclosure: Page 219-220; 228pp; English.
XX
CC The present invention describes compositions comprising peptides derived
CC from the Wilm's tumour protein WT1 and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WT1
CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukemia. The present sequence is
CC a coding sequence used in the exemplification of the invention.
XX
SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;
Query Match 56.7%; Score 1154; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 263 GGTGAGAAATAGAAAGGCTGTGACTTACATCTGAGGCCACACATCTGCTGAATG 322
DB 1769 GGTGAGAAATAGAAAGGCTGTGACTTACATCTGAGGCCACACATCTGCTGAATG 1710
QY 323 AGATTAATTAACATCAGTAGAAGACAGATGACATTAATATGTCATAGTAGACATGT 382
DB 1709 AGATTAATTAACATCAGTAGAAGACAGATGACATTAATATGTCATAGTAGACATGT 1650
QY 383 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGAGAC 442
DB 1649 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGAGAC 1590
QY 443 AGAGATCCCTGGGAGAAATGCCGCCCATCTGGGTATGATGAGCTGCCCTGT 502
DB 1589 AGAGATCCCTGGGAGAAATGCCGCCCATCTGGGTATGATGAGCTGCCCTGT 1530
QY 503 GCCTGTCCCGCTGTGAGGAGAGACATTAGAAATGAATGATGTTCTCTTAAAGA 562
DB 1529 GCCTGTCCCGCTGTGAGGAGAGACATTAGAAATGAATGATGTTCTCTTAAAGA 1470
QY 563 TGGGCAAGAAAGACATCTGTTGTGATATTTATTTGAACGGGATTTACGATTTGAAT 622
DB 1469 TGGGCAAGAAAGACATCTGTTGTGATATTTATTTGAACGGGATTTACGATTTGAAT 1410
QY 623 GAAGTACAAAGTGAGCATTAACCATGAGAGAAACAGACGAGAAATCTTGATGGCTT 682
DB 1409 GAAGTACAAAGTGAGCATTAACCATGAGAGAAACAGACGAGAAATCTTGATGGCTT 1350
QY 683 CACAGACATGCAACAAACAAATGAATTAAGTGTGATGACATGAGCAGCAGCTGGG 742
DB 1349 CACAGACATGCAACAAACAAATGAATTAAGTGTGATGACATGAGCAGCAGCTGGG 1290
QY 743 AGAGATTAACAGAGGGGAGAGGTCAGATTTCTGGCCCTGCTCTAACTGCGCTT 802
DB 1289 AGAGATTAACAGAGGGGAGAGGTCAGATTTCTGGCCCTGCTCTAACTGCGCTT 1230
QY 803 ATACCAAAATCATTTATATATTTCTAACCCCTCAAAACAAAGCTTTGTAATATGATCTC 862
DB 1229 ATACCAAAATCATTTATATATTTCTAACCCCTCAAAACAAAGCTTTGTAATATGATCTC 1170
QY 863 TACGGTCTCTTGGGCCCAACATTCCTCATATATCCAGCAGACATCATTTTAAATTT 922
DB 1169 TACGGTCTCTTGGGCCCAACATTCCTCATATATCCAGCAGACATCATTTTAAATTT 1110
QY 923 AGTTCACATCTGTACTGTGACCTTTCTACATGTAGAAATTAACATTTACTTTGCTC 962
DB 1109 AGTTCACATCTGTACTGTGACCTTTCTACATGTAGAAATTAACATTTACTTTGCTC 1050
QY 983 AAAGACCTTGTGCTGTGCTGAATATGATGATGCTGTTTCTTAAGGATGTTCTG 1042

DB 1049 AAAGACCTTGTGCTGTGCTGAATATGATGATGCTGTTTCTTAAGGATGTTCTG 990
QY 1043 GCCCAGGGATCTGTGAACAGAGCTGGAGACATCTCAAGATCTTCCAGGTTATCTTA 1102
DB 989 GCCCAGGGATCTGTGAACAGAGCTGGAGACATCTCAAGATCTTCCAGGTTATCTTA 930
QY 1103 CTAGCAGACAGCATGATCATTTACGAGAGTGAATTAATCAACATCATCTGATGCTT 1162
DB 929 CTAGCAGACAGCATGATCATTTACGAGAGTGAATTAATCAACATCATCTGATGCTT 870
QY 1163 TTGGCCCTACTGAATTCATTTCCACTTTTGGCCCATCTCAAGACCTCAAAATGTCA 1222
DB 869 TTGGCCCTACTGAATTCATTTCCACTTTTGGCCCATCTCAAGACCTCAAAATGTCA 810
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QY 1283 CAGCTATGGAATTTAATTCATATTTTGTTCACAGTGCAGAAAGATGACTAATCTTTA 1342
DB 749 CAGCTATGGAATTTAATTCATATTTTGTTCACAGTGCAGAAAGATGACTAATCTTTA 690
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DB 689 TCCCTCCCTTTGTTGATTTTTCACAGTGCAGTAAAGTTAAATGCTTGTACTG 630
QY 1403 AGGCTGTATACAGC 1416
DB 629 AGGCTGTATACAGC 616
RESULT 15
ABL95269/c
ID ABL95269 standard; cDNA; 2426 BP.
XX
AC ABL95269;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P710P cDNA sequence SEQ ID NO 470.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US200202248-A1.
XX
PD 21-FEB-2002.
XX
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PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
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PR 12-NOV-1999; 99US-0439213.
PR 18-NOV-1999; 99US-0443686.
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PR 27-MAR-2000; 2000US-0536857.
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PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-SEP-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.

PR 10-OCT-2000; 2000US-0685166.
 XX
 (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIANG/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISK/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEL/) SKELLY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skelly YAW, Hepler WT, Henderson RA;
 DR WPI: 2002-255649/30.
 XX
 PT New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer -
 XX
 PS Claim 1: SEQ ID NO 470; 87PP; English.
 CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention.
 XX
 SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other:
 Query Match 56.7%; Score 1154; DB 24; Length 2426;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 263 GGTGAATAATGAAGGCTGCTGACTTACCATCTGAGGCCACATCTGCTGAATGG 322
 DB 1769 GGTGAATAATGAAGGCTGCTGACTTACCATCTGAGGCCACATCTGCTGAATGG 1710
 OY 323 AGATAATTACATCTAGAAAACAGCAAGATGACATATATATCTAAGTAGTACATGT 382
 DB 1709 AGATAATTACATCTAGAAAACAGCAAGATGACATATATATCTAAGTAGTACATGT 1650
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 DB 1649 TTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGACACAAAAGAGACAC 1590
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 DB 629 AGGCTGATACAGC 616

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1629	80.0	3923	9	US-09-822-827-690
4	1629	80.0	3923	10	US-09-895-793-690
5	1629	80.0	3923	10	US-09-895-814-690
6	1629	80.0	3923	12	US-10-144-678A-690
7	1629	80.0	3923	13	US-10-012-896-690
8	1629	80.0	3923	14	US-10-205-823-316
9	1629	80.0	3923	14	US-09-759-143-470
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c 11	1154	56.7	2426	9	US-09-822-827-470
c 12	1154	56.7	2426	10	US-09-895-793-470
c 13	1154	56.7	2426	10	US-09-895-814-470
c 14	1154	56.7	2426	12	US-10-144-678A-470
c 15	1154	56.7	2426	13	US-10-012-896-470
c 16	1154	56.7	2426	14	US-10-010-940-470

c 17	1154	56.7	2426	14	US-10-205-823-448	Sequence 448, App
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c 29	1033	50.7	2229	10	US-09-895-793-469	Sequence 469, App
c 30	1033	50.7	2229	10	US-09-895-814-469	Sequence 469, App
c 31	1033	50.7	2229	12	US-10-144-678A-469	Sequence 469, App
c 32	1033	50.7	2229	13	US-10-012-896-469	Sequence 469, App
c 33	1033	50.7	2229	14	US-10-010-940-469	Sequence 469, App
c 34	738	36.2	826	11	US-09-957-708-3	Sequence 3, Appl1
c 35	720	35.3	812	9	US-09-759-143-471	Sequence 471, App
c 36	720	35.3	812	9	US-09-780-669-471	Sequence 471, App
c 37	720	35.3	812	9	US-09-822-827-471	Sequence 471, App
c 38	720	35.3	812	10	US-09-895-793-471	Sequence 471, App
c 39	720	35.3	812	10	US-09-895-814-471	Sequence 471, App
c 40	720	35.3	812	12	US-10-144-678A-471	Sequence 471, App
c 41	720	35.3	812	13	US-10-012-896-471	Sequence 471, App
c 42	720	35.3	812	14	US-10-010-940-471	Sequence 471, App
c 43	473	23.2	597	12	US-10-195-730-46	Sequence 46, Appl
c 44	467	22.9	1102	14	US-10-198-846-11000	Sequence 11000, A
c 45	465	22.8	1036	14	US-10-198-846-13213	Sequence 13213, A

ALIGNMENTS

RESULT 1
US-09-759-143-690
Sequence 690, Application US/09759143
Patent No. US200202248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kallou, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Veddyck, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-690
Query Match 80.0%; Score 1629; DB 9; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGAAGCTGCATGAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACAG 60
DB 23 AGAAGCTGCATGAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACAG 82
QY 61 GAAGATCGATGCTGGGAGGACCTGATGATACAGAGGAATTAACAACATATAGTAG 120
DB 83 GAAGATCGATGCTGGGAGGACCTGATGATACAGAGGAATTAACAACATATAGTAG 142
QY 121 TGTTCATGACACCAAGATTAATAGTAAAGAGTAGTCCGCTGTGATCTCTAGT 180
DB 143 TGTTCATGACACCAAGATTAATAGTAAAGAGTAGTCCGCTGTGATCTCTAGT 202
QY 181 GACACAGGCTGATACCATTCACAGGCACTTTCTGATCTACAGTACAGCAAGAAAGA 240
DB 203 GACACAGGCTGATACCATTCACAGGCACTTTCTGATCTACAGTACAGCAAGAAAGA 262
QY 241 CTACAGACATCTCAATGCGAGGGGTGGAATTAAGAAAGGCTGTGCTTACCATCTGA 300
DB 263 CTACAGACATCTCAATGCGAGGGGTGGAATTAAGAAAGGCTGTGCTTACCATCTGA 322
QY 301 GGCACACATCTCTGAAATGGAATTAATTAACATCACTAGAAACAGCAAGATGACATA 360
DB 323 GGCACACATCTCTGAAATGGAATTAATTAACATCACTAGAAACAGCAAGATGACATA 382
QY 361 TAATGCTAGTAGTACATGTTTTCGACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 383 TAATGCTAGTAGTACATGTTTTCGACATTTCCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAAGCACAAAGAGACACAGAGATCCCTGGGAGAAATGCGCGGCCCATCTTGGG 480
DB 443 CAGGAAGCACAAAGAGACACAGAGATCCCTGGGAGAAATGCGCGGCCCATCTTGGG 502
QY 481 TCATCATGAGCTCGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 503 TCATCATGAGCTCGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 562
QY 541 AATTGATGCTGCTTAAAGAGAGGAGAGAAACAGATCTGTGAGATATTTATTTG 600
DB 563 AATTGATGCTGCTTAAAGAGAGGAGAGAAACAGATCTGTGAGATATTTATTTG 622
QY 601 AACGGGATTACAGATTTGAATGAATGATCAACAAAGTAGCATTTACATGAGAGAAACA 660
DB 623 AACGGGATTACAGATTTGAATGAATGATCAACAAAGTAGCATTTACATGAGAGAAACA 682
QY 661 GACGAGAAAATCTTGATGCTTCACAAAGCATGCAACAAACAAATGGAATGATGATG 720
DB 683 GACGAGAAAATCTTGATGCTTCACAAAGCATGCAACAAACAAATGGAATGATGATG 742
QY 721 ACATGAGGCGACGAGCTGGGAGAGATTAACACGCGGAGAGAGGATTCGAGCC 780
DB 743 ACATGAGGCGACGAGCTGGGAGAGATTAACACGCGGAGAGAGGATTCGAGCC 802
QY 781 CTGCTGCTTAACATGCTGCTTCATTAACCAATCATTTCAATTTTCAACCTCAAAACA 840
DB 803 CTGCTGCTTAACATGCTGCTTCATTAACCAATCATTTTCAATTTTCAACCTCAAAACA 862
QY 841 AGCTGTTGTAATCTGATCTCAAGGCTTCCTTCTGGGCCCAACATTTCCATATATCCA 900
DB 863 AGCTGTTGTAATCTGATCTCAAGGCTTCCTTCTGGGCCCAACATTTCCATATATCCA 922
QY 901 GCGACACGATTTTAAATATTTAGTTCACAGATCTGTACATCTTCTTACACTGTAG 960
DB 923 GCGACACGATTTTAAATATTTAGTTCACAGATCTGTACATCTTCTTACACTGTAG 982
QY 961 AATAACATTAATCTATTTGTTCAAGACCTTGTGTGCTGCTAATATGATGCTGACT 1020
DB 983 AATAACATTAATCTATTTGTTCAAGACCTTGTGTGCTGCTAATATGATGCTGACT 1042
QY 1021 GTTTTTCCTAAGAGTGTCTGCGCCAGGGGATCTGTGAACAGCTGCGGAAGCATCTCAA 1080
DB 1043 GTTTTTCCTAAGAGTGTCTGCGCCAGGGGATCTGTGAACAGCTGCGGAAGCATCTCAA 1102
QY 1081 GATCTTTCAGGGGTATCTTACTAGCACACAGCATGATCATTTACGAGAGTGAATTTATCTA 1140

DB 1103 GATCTTTCAGGGGTATCTTACTAGCACACAGCATGATCATTCGAGAGTGAATTTATCTA 1162
QY 1141 ATCAACATCATCTCCAGCTGTCTTGGCCATACAGAAATTCATTTCCACTTTGTGCCCA 1200
DB 1163 ATCAACATCATCTCCAGCTGTCTTGGCCATACAGAAATTCATTTCCACTTTGTGCCCA 1222
QY 1201 TTCTCAAGACCTCAAAATGTCAATTCATTAATATTCACAGAGATTAACCTTTTATTAAC 1260
DB 1223 TTCTCAAGACCTCAAAATGTCAATTCATTAATATTCACAGAGATTAACCTTTTATTAAC 1282
QY 1261 TGAAGAAATTCATTTTACATGCAAGCTATGGAATTAATTAATATTTTGTTCAGT 1320
DB 1283 TGAAGAAATTCATTTTACATGCAAGCTATGGAATTAATTAATATTTTGTTCAGT 1342
QY 1321 GCAAGATGACTAAGCTTATTCCTCCCTTGTGTTGATTTTTCAGATATAAGT 1380
DB 1343 GCAAGATGACTAAGCTTATTCCTCCCTTGTGTTGATTTTTCAGATATAAGT 1402
QY 1381 TAAATGCTTAAAGCTTGTACTGAGGCTGTATACAGACAGCCCTCCCATCCCTCAGC 1440
DB 1403 TAAATGCTTAAAGCTTGTACTGAGGCTGTATACAGACAGCCCTCCCATCCCTCAGC 1462
QY 1441 CTATATCTGATCATCATCAACCCCTCCCATTTTSACTTAACAAATCTTACTTGTAAAT 1500
DB 1463 CTATATCTGATCATCATCAACCCCTCCCATTTTSACTTAACAAATCTTACTTGTAAAT 1522
QY 1501 CCTTGAACATGTAGAGCATCATATTTCTTCTGCTGAGAGCTTCTGCTGCTT 1560
DB 1523 CCTTGAACATGTAGAGCATCATATTTCTTCTGCTGAGAGCTTCTGCTGCTT 1582
QY 1561 AANTCTAGAAATGATGAAGTTTGAATTAAGTTGACTATCTTACTCATGCAAGAGG 1620
DB 1583 AANTCTAGAAATGATGAAGTTTGAATTAAGTTGACTATCTTACTCATGCAAGAGG 1642
QY 1621 ACACATATGATGATTCATCATCATATGAGACAGCAAGTAATTAAGTATGATTA 1680
DB 1643 ACACATATGATGATTCATCATCATATGAGACAGCAAGTAATTAAGTATGATTA 1702
QY 1681 AGAGTTTGAATTAATTAATGAATTAAGCAAGCAAGAGGAAATGTTTATGGGCACTT 1740
DB 1703 AGAGTTTGAATTAATTAATGAATTAAGCAAGCAAGAGGAAATGTTTATGGGCACTT 1762
QY 1741 TGTAAAGCTGGGATGTGAAGMAAGGACAGGAACTCATATGATCTTATTAATATGACT 1800
DB 1763 TGTAAAGCTGGGATGTGAAGMAAGGACAGGAACTCATATGATCTTATTAATATGACT 1822
QY 1801 CATTTCTCATATCTTATCAAAATATTCACAAAGCTTTTCAAGAAATTCATGAGTGCAAA 1860
DB 1823 CATTTCTCATATCTTATCAAAATATTCACAAAGCTTTTCAAGAAATTCATGAGTGCAAA 1882
QY 1861 TCCCAAGGTAACCTTTATTCATTTTATGATGAGTGGCTTTAGAAATTTGGCAATCA 1920
DB 1883 TCCCAAGGTAACCTTTATTCATTTTATGATGAGTGGCTTTAGAAATTTGGCAATCA 1942
QY 1921 TACTGTCTATATCTTCAACTTTGAGATGTGTTTGTCTGTGATTAATTTGAAGAAATA 1980
DB 1943 TACTGTCTATATCTTCAACTTTGAGATGTGTTTGTCTGTGATTAATTTGAAGAAATA 2002
QY 1981 GGGCACTCTTGTGAGGCACTTTAGGTTTACATCTGCGCAATTAAGAAATTTAACAAGA 2037
DB 2003 GGGCACTCTTGTGAGGCACTTTAGGTTTACATCTGCGCAATTAAGAAATTTAACAAGA 2059

RESULT 2

US-09-780-669-690
; Sequence 690, Application US/09780669
; Patent No. US2002051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuyui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-690

Query Match 80.0%; Score 1629; DB 9; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

1 AGAAGCTGGCATCAAAAAACAGAGGGAGATTGTGTGCTGCGACGGAGGAGACAG 60
23 AGAAGCTGGCATCAAAAAACAGAGGGAGATTGTGTGCTGCGACGGAGGAGACAG 82
61 GAAAGTTCGATGGTGGGAGGAGCCTGATGATACAGAGGATTTAAACATATCTTGG 120
83 GAAAGTTCGATGGTGGGAGGAGCCTGATGATACAGAGGATTTAAACATATCTTGG 142
121 TGTTCATGAACACCAAGATTAATAGTGAAGAGCTAGTCCGTGTGAGTCTCTCACT 180
143 TGTTCATGAACACCAAGATTAATAGTGAAGAGCTAGTCCGTGTGAGTCTCTCACT 202
161 GACACAGGGCTGATCACCATGACGAGCCTTTCGAGTACTCACTGACGACAAAGAGA 240
203 GACACAGGGCTGATCACCATGACGAGCCTTTCGAGTACTCACTGACGACAAAGAGA 262
241 CTACAGACATCTCAATGGGAGGGGTGAGAAATGAAGAGGCTGTGACTTTTACCATCTGA 300
263 CTACAGACATCTCAATGGGAGGGGTGAGAAATGAAGAGGCTGTGACTTTTACCATCTGA 322
301 GGCACACATCTGTGAAATGAGATTAATTAACATCACTAGAAACAGCAAGATGACATA 360
323 GGCACACATCTGTGAAATGAGATTAATTAACATCACTAGAAACAGCAAGATGACATA 382
361 TAAATCTTAAGTAGAGCATGTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACA 420
383 TAAATCTTAAGTAGAGCATGTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACA 442
421 CAGGAGACCAAAAGAGACAGAGATCCCTGGGAGAAATGCCGGCCGCCATCTTGGG 480
443 CAGGAGACCAAAAGAGACAGAGATCCCTGGGAGAAATGCCGGCCGCCATCTTGGG 502
481 TCATGATGAGCCTGCGCTGTGCTGTCCCGCTTGTGAGGAGGAGGACATTAGAAATG 540
503 TCATGATGAGCCTGCGCTGTGCTGTCCCGCTTGTGAGGAGGAGGACATTAGAAATG 562
541 AATTGATGTTCTTTAAAGATGGGAGGAGAAACAGATCCCTGTTGTGATATTTATTTG 600
563 AATTGATGTTCTTTAAAGATGGGAGGAGAAACAGATCCCTGTTGTGATATTTATTTG 622

601 AACGGATTACAGATTTGAATGAATGACACAAAGTGAGCATTTACCAATGAGAGAAACA 660
623 AACGGATTACAGATTTGAATGAATGACACAAAGTGAGCATTTACCAATGAGAGAAACA 682
661 GACGAGAAATCTTGATGGCTTACAGACATGACAAACAAATGAAATGATCTGTATG 720
683 GACGAGAAATCTTGATGGCTTACAGACATGACAAACAAATGAAATGATCTGTATG 742
721 ACATGAGCAGCCAAAGCTGGGAGAGATTAACACAGGGGACAGAGGTCTGAGTTCTGGCC 780
743 ACATGAGCAGCCAAAGCTGGGAGAGATTAACACAGGGGACAGAGGTCTGAGTTCTGGCC 802
781 CTGCTGCCCTAAAGCTGGCTGTATACCAATCATTTTCTATTTCTAAACCTCAAAACA 840
803 CTGCTGCCCTAAAGCTGGCTGTATACCAATCATTTTCTATTTCTAAACCTCAAAACA 862
841 ACCTGTTGTAATCTGATCTCTAGCGTTCTTGTGGGCCAACAATCTCATATATCA 900
863 ACCTGTTGTAATCTGATCTCTAGCGTTCTTGTGGGCCAACAATCTCATATATCA 922
901 GCCACATCATTTTAAATATTTAGTTCCAGATCTGTACTGTGACCTTCTACCTGTAG 960
923 GCCACATCATTTTAAATATTTAGTTCCAGATCTGTACTGTGACCTTCTACCTGTAG 982
961 AATAACATCTCATTTTGTTCGAAAGACCTTCGTTGCTGCTGCTAATATGAGTGACT 1020
983 AATAACATCTCATTTTGTTCGAAAGACCTTCGTTGCTGCTGCTAATATGAGTGACT 1042
1021 GTTTTCTTAAGAGAGTTCTGCGCCAGGGGATCTGTGAACAGGCTGGGAGACATCTCA 1080
1043 GTTTTCTTAAGAGAGTTCTGCGCCAGGGGATCTGTGAACAGGCTGGGAGACATCTCA 1102
1081 GATCTTTCAGAGGTTATCTTCTAGACACAGCATGATCATTTAGGAGTGAATATCTA 1140
1103 GATCTTTCAGAGGTTATCTTCTAGACACAGCATGATCATTTAGGAGTGAATATCTA 1162
1141 ATCAACATCTCATTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
1163 ATCAACATCTCATTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1222
1201 TTCTCAAGACCTCAAAATGTCATTTCCATTAATATACAGATTAACCTTTTTTTTAAAC 1260
1223 TTCTCAAGACCTCAAAATGTCATTTCCATTAATATACAGATTAACCTTTTTTTTAAAC 1282
1261 TGGAGAAATCAATGTTATATGACAGCTATGAGGAAATTAATATATTTGTTTCCACT 1320
1283 TGGAGAAATCAATGTTATATGACAGCTATGAGGAAATTAATATATTTGTTTCCACT 1342
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1343 GCAAGATGACTAAGTCTTATCCCTCCCTGTTGTTGATTTTTCACATATAAGT 1402
1381 TAAATCTTAAAGCTTTGACTAGAGCTGTATACAGACAGCTCTCCCATCCCTCACAC 1440
1403 TAAATCTTAAAGCTTTGACTAGAGCTGTATACAGACAGCTCTCCCATCCCTCACAC 1462
1441 CTATCTGTCATCACCACCAACCCCTCCCATTTTAAATATCAATGTTTAAAT 1500
1463 CTATCTGTCATCACCACCAACCCCTCCCATTTTAAATATCAATGTTTAAAT 1522
1501 CCTTGAACATGTCAGAGNCATATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1523 CCTTGAACATGTCAGAGNCATATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1582
1561 AANTCTAGATGATTAAGGTTTGAATATGACTATCTTATCTTATGCAAGAGGG 1620
1583 AANTCTAGATGATTAAGGTTTGAATATGACTATCTTATCTTATGCAAGAGGG 1642
1621 ACACATATGAGATTCATCTACATGAGACACCAAAATATCAAGGTTATTTATTA 1680
1643 ACACATATGAGATTCATCTACATGAGACACCAAAATATCAAGGTTATTTATTA 1702
1681 AGAGTTAGATTAATATATGAATGCAAGACACAGAGGAGATGTTATGCGGACGTT 1740

Db 1703 AGAGTTAGATTAATATATATAAATGACAGACCAAGGAAATGTTATGGGCGACGTT 1762
QY 1741 TGTAAAGCTGGATGTGAAGAAAAGCAGGAAACCTCATAGTATCTATATATATCTT 1800
Db 1763 TGTAAAGCTGGATGTGAAGAAAAGCAGGAAACCTCATAGTATCTATATATATCTT 1822
QY 1801 CATTTCTATCTCTATACAAATATCCACAAAGCTTTTTCACAGAAATTCATGCAATG 1860
Db 1823 CATTTCTATCTCTATACAAATATCCACAAAGCTTTTTCACAGAAATTCATGCAATG 1882
QY 1861 TCCCAAGGTAACCTTTATCATCTTTCATGCTGAGTGCCTTTAGATTTTGGCAATCA 1920
Db 1883 TCCCAAGGTAACCTTTATCATCTTTCATGCTGAGTGCCTTTAGATTTTGGCAATCA 1942
QY 1921 TACTGTCACTTATCTCAACCTTTGAGATGTGTGTCTCTGTAGTATTTGAAGAAATA 1980
Db 1943 TACTGTCACTTATCTCAACCTTTGAGATGTGTGTCTCTGTAGTATTTGAAGAAATA 2002
QY 1981 GGGCACTCTTGTGAGCCACTTTAGGGTTCACTCTCGCAATTAAGAAATTTACAAGA 2037
Db 2003 GGGCACTCTTGTGAGCCACTTTAGGGTTCACTCTCGCAATTAAGAAATTTACAAGA 2059

RESULT 3

US-09-822-827-690
; Sequence 690, Application us/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: us/09/822, 827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ. ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ. ID NO: 690
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-690

Query Match 80.08; Score 1629; DB 9; Length 3923;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCAGAAAACAGAGGGGAGATTTGTGGCTGCAGCCGAGGAGACAG 60
Db 23 AGAAGCTGGCATCAGAAAACAGAGGGGAGATTTGTGGCTGCAGCCGAGGAGACAG 82
QY 61 GAAGATCTGCATGGTGGAGAGACCTGATGATACAGAGGAATTACACACATATCTTAG 120
Db 83 GAAGATCTGCATGGTGGAGAGACCTGATGATACAGAGGAATTACACACATATCTTAG 142
QY 121 TGTTCATATGACACCAAGATTAATAATGTAAGAGCTAGTCCGCTGTGATCTTCCAGT 180
Db 143 TGTTCATATGACACCAAGATTAATAATGTAAGAGCTAGTCCGCTGTGATCTTCCAGT 202
QY 181 GACACAGGGCTGATACCAATGACGAGGCACTTCTGATCTACAGTGCAGCAAGAAAGA 240
Db 203 GACACAGGGCTGATACCAATGACGAGGCACTTCTGATCTACAGTGCAGCAAGAAAGA 262
QY 241 CTACAGACATCTCAATGSCAGGGGTGAGAAATGAAGAAAGCTGCTACTTTACCATCTGA 300
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QY 301 GGGCACAACATCTGCTGAATGAGATTAATTAACATCTAAGAAACAGCAAGATGACATA 360
Db 323 GGGCACAACATCTGCTGAATGAGATTAATTAACATCTAAGAAACAGCAAGATGACATA 382
QY 361 TAATGCTAGTAGTACATGTTTTCACATTTCCAGCCCTTTAAATTCACACACA 420
|||||

Db 383 TAATGCTAGTAGTACATGTTTTCACATTTCCAGCCCTTTAAATTCACACACA 442
QY 421 CAGGAAGCAGAAAAAGAAAGCAGAGATCCCTGGAGAAATGGCCGGCCCATCTTGGG 480
Db 443 CAGGAAGCAGAAAAAGAAAGCAGAGATCCCTGGAGAAATGGCCGGCCCATCTTGGG 502
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QY 541 AATGATGTTGCTCTTAAGAGATGGGAGAAAAACAGATCCTGTGGATTTATTTT 600
Db 563 AATGATGTTGCTCTTAAGAGATGGGAGAAAAACAGATCCTGTGGATTTATTTT 622
QY 601 AAGGGAATTCAGATTTGAATGAATGACACAAAGTAGCATTTACATGAGAGAAACA 660
Db 623 AAGGGAATTCAGATTTGAATGAATGACACAAAGTAGCATTTACATGAGAGAAACA 682
QY 661 GACGAGAAATCTTGATGCTTCCACAAAGATGCAACAAACAAATGAATACGTGATG 720
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QY 721 ACATGAGCAGCCAGCTGGGAGAGATTAACCAAGGAGGAGAGGTCAGATTTGCGCC 780
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QY 781 CTGCTGCTTAACCTGCTGCTTCAATTAACCAATGATTTCAATTTCTAACCTCAAAACA 840
Db 803 CTGCTGCTTAACCTGCTGCTTCAATTAACCAATGATTTCAATTTCTAACCTCAAAACA 862
QY 841 AGCTGTGTAATATCTGATCTTACAGGTCCTTCTGCGCCCAACATTTCTCAATATCCA 900
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QY 901 GCCACACTATTTTATATTTAGTTCGCCAGATCTGATGATGACCTTTTACACGTAG 960
Db 923 GCCACACTATTTTATATTTAGTTCGCCAGATCTGATGATGACCTTTTACACGTAG 982
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Db 1103 GATCTTCCAGGGTTATCTTACTATGACACACATGATATTAACGAGATTAATCA 1162
QY 1141 ATCAACATCAATCCCTAGTGTCTTGGCCATAGTGAATTCATTTCCACTTTGTGCCCA 1200
Db 1163 ATCAACATCAATCCCTAGTGTCTTGGCCATAGTGAATTCATTTCCACTTTGTGCCCA 1222
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Db 1283 TGGAGAAATTCATATGTTACTATGACAGCTATGGGAATTAATTAACATTTTGTTCAGT 1342
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Db 1343 GCAAGATGACTAAGTCTTATCCCTCCCTTGTGTTGATTTTTCAGTATAAAGT 1402
QY 1381 TAAATGCTTAAGCTTGTACTGAGGCTGTATACAGACAGCCTCTCCCATCTCCAGC 1440
Db 1403 TAAATGCTTAAGCTTGTACTGAGGCTGTATACAGACAGCCTCTCCCATCTCCAGC 1462
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Db 1463 CTATATGCTATACACATCAACCCCTCCCATTAACCTTAACCTTAACCTTAACCT 1522

1501 CTTGACATGTCAGNCATACATTTCTCTGCTGAGAGGCTTCCCTGCTCTT 1560
1523 CTTGACATGTCAGNCATACATTTCTCTGCTGAGAGGCTTCCCTGCTCTT 1582
1561 AANTCTAGATGATGTAAGTTTGCATTAAGTGAATGCTTCTTACTTCAAGCAAGAGG 1620
1583 AATCTAGATGATGTAAGTTTGCATTAAGTGAATGCTTCTTACTTCAAGCAAGAGG 1642
1621 ACACATATGATATCATCATCATGAGACGCAATATCTTAAAGTGTAAATTTGATATA 1680
1643 ACACATATGATATCATCATCATGAGACGCAATATCTTAAAGTGTAAATTTGATATA 1702
1681 AGAGTTTGAATTAATATATGAATGCAACACACAGAGGGAATTTGAGGAGCTT 1740
1703 AGAGTTTGAATTAATATATGAATGCAACACACAGAGGGAATTTGAGGAGCTT 1762
1741 TGTAAAGCTGGAGTGTGAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
1763 TGTAAAGCTGGAGTGTGAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1822
1801 CATTTCTATCTCTATATACAAATATCCAAAGCTTTTACAGAAATTTATGACAGTGA 1860
1823 CATTTCTATCTCTATATACAAATATCCAAAGCTTTTACAGAAATTTATGACAGTGA 1882
1861 TCCCAAGAGTAACTTATATCATCTTATGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1920
1883 TCCCAAGAGTAACTTATATCATCTTATGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1942
1921 TACTGTCTATCTATATCTCAAGCTTTGAGATGTGTGTCTTGTAGTTAAATGAAGATA 1980
1943 TACTGTCTATCTATATCTCAAGCTTTGAGATGTGTGTCTTGTAGTTAAATGAAGATA 2002
1981 GGGACATCTTGTGAGCCACTTTAGGCTTCACTCCCGGCAATTAAGAAATTTACAAAGA 2037
2003 GGGACATCTTGTGAGCCACTTTAGGCTTCACTCCCGGCAATTAAGAAATTTACAAAGA 2059

RESULT 4
US-09-895-793-690
; Sequence 690, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
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; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 690

LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-690

Query Match
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

80.0%; Score 1629; DB 10; Length 3923;

1 AGAAGCTGGCATCAGAAAAACAGAGGAGATTTGTGTGCTGACGCGGAGGAGACAG 60
23 AGAAGCTGGCATCAGAAAAACAGAGGAGATTTGTGTGCTGACGCGGAGGAGACAG 82
61 GAAAGTCTGCATGTGGGAAAGAGCTGATGATACAGAGGATTTACAAACATATCTTAG 120
83 GAAAGTCTGCATGTGGGAAAGAGCTGATGATACAGAGGATTTACAAACATATCTTAG 142
121 TGTTCATATGAACCAAGATTAATTAAGTGAAGAGCTAGTCCGCTGATGATCTCTCAGT 180
143 TGTTCATATGAACCAAGATTAATTAAGTGAAGAGCTAGTCCGCTGATGATCTCTCAGT 202
181 GACACAGGCTGATCACCATGACGACGCTTCTGAGTACTCACTGACGCAAGAAAGA 240
203 GACACAGGCTGATCACCATGACGACGCTTCTGAGTACTCACTGACGCAAGAAAGA 262
241 CTACAGACATGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
263 CTACAGACATGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 322
301 GGGCACACATCTGCTGAATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
323 GGGCACACATCTGCTGAATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 382
361 TAAATGCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
383 TAAATGCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 442
421 CAGGAGGACAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
443 CAGGAGGACAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 502
481 TCATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
503 TCATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 562
541 AATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
563 AATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 622
601 AACGGATTACAGATTTGAATGAAGTACAAAGGAGCATTTACCAATGAGAGGAAACA 660
623 AACGGATTACAGATTTGAATGAAGTACAAAGGAGCATTTACCAATGAGAGGAAACA 682
661 GACGAGAAATCTTGATGCTTACAAAGCATGCAACAAACAAATGGAATACTGTGATG 720
683 GACGAGAAATCTTGATGCTTACAAAGCATGCAACAAACAAATGGAATACTGTGATG 742
721 ACATGAGGACCCAAAGCTGGGAGAGATTAACACAGGAGGAGGAGGAGGAGGAGGAGG 780
743 ACATGAGGACCCAAAGCTGGGAGAGATTAACACAGGAGGAGGAGGAGGAGGAGGAGG 802
781 CTGCTGCTTAAAGTGGCTTCAATACCAATATCTATATTTCTAACCTCAAAACAA 840
803 CTGCTGCTTAAAGTGGCTTCAATACCAATATCTATATTTCTAACCTCAAAACAA 862
841 AGCTGTTGATATCTGATCTCTACAGTCTCTTGTGGGCCCAATCTCCATATATCA 900
863 AGCTGTTGATATCTGATCTCTACAGTCTCTTGTGGGCCCAATCTCCATATATCA 922
901 GCCACACTATTTTAAATATTAATTTAGTCCAGATCTGATGACCTTTCTACACTGTAG 960
923 GCCACACTATTTTAAATATTAATTTAGTCCAGATCTGATGACCTTTCTACACTGTAG 982

OY	961	AATAACATTAACCAATTTGGTCAAGAACCCCTCGTGGTGGCCCAATATATCTACTACT	1020
Db	963	AATAACATTAACCAATTTGGTCAAGAACCCCTCGTGGTGGCCCAATATATCTACTACT	1042
OY	1021	GTTTTTCCTAAGGAGTGTTCGGCCACAGGGGATCTGTGCAAGAGCCTGGGAACATCCAA	1080
Db	1043	GTTTTTCCTAAGGAGTGTTCGGCCACAGGGGATCTGTGCAAGAGCCTGGGAACATCCAA	1102
OY	1081	GATCTTTCACAGGGTTATATCTTACTAGCAGACAGCATGATCATATACGAGTGAATATCTA	1140
Db	1103	GATCTTTCACAGGGTTATATCTTACTAGCAGACAGCATGATCATATACGAGTGAATATCTA	1162
OY	1141	ATCAACATCATCCACAGTGTCTTGGCCATCTGAAATTCATTTCCACTTTGTGGCCA	1200
Db	1163	ATCAACATCATCCACAGTGTCTTGGCCATCTGAAATTCATTTCCACTTTGTGGCCA	1222
OY	1201	TTCTCAAGACCTCAAAATGTCATTCATCAATTAATACAGATTAATCACTTTTATTAAC	1260
Db	1223	TTCTCAAGACCTCAAAATGTCATTCATTAATACAGATTAATCACTTTTATTAAC	1282
OY	1261	TGGAAGAATTAATGTTATCATGACAGCCTATGGGAATTAATACATATTTTGTCCAGT	1320
Db	1283	TGGAAGAATTAATGTTATCATGACAGCCTATGGGAATTAATACATATTTTGTCCAGT	1342
OY	1321	GCAAGAATGATCAAGTCTTATCCCTCCCTCTTGTGATTTTTCAGATTAAGT	1380
Db	1343	GCAAGAATGATCAAGTCTTATCCCTCCCTCTTGTGATTTTTCAGATTAAGT	1402
OY	1381	TAAATATGCTTAGCTTGTACTGAGGCTGTATACGACAGCCTCTCCCATCCCTCAGC	1440
Db	1403	TAAATATGCTTAGCTTGTACTGAGGCTGTATACGACAGCCTCTCCCATCCCTCAGC	1462
OY	1441	CTATATCTGTATCACCACATCAACCCCTCCCATATYACCTAAACAAATCTAATCTGTATT	1500
Db	1463	CTATATCTGTATCACCACATCAACCCCTCCCATATYACCTAAACAAATCTAATCTGTATT	1522
OY	1501	CCTTGAACATGTCAAGMCATATATTTCTTCTGCTGAGAACTCTCTCTGTCTT	1560
Db	1523	CCTTGAACATGTCAAGMCATATATTTCTTCTGCTGAGAACTCTCTCTGTCTT	1582
OY	1561	AANTCTGAATGATGTAAAGTTTGGATTAAGTTGACATATCTTACTTATCAAAAGAGG	1620
Db	1583	AANTCTGAATGATGTAAAGTTTGGATTAAGTTGACATATCTTACTTATCAAAAGAGG	1642
OY	1621	ACACATATGAGATTTCATCATCATCATGAGACAGCAAAATCACTAAAGTAAATTTGATTATA	1680
Db	1643	ACACATATGAGATTTCATCATCATCATGAGACAGCAAAATCACTAAAGTAAATTTGATTATA	1702
OY	1681	AGACTTTATGATTAATATATGAAATGCAAGAKCCACAGAGGAATGTTATGGGACAGTT	1740
Db	1703	AGACTTTATGATTAATATATGAAATGCAAGAKCCACAGAGGAATGTTATGGGACAGTT	1762
OY	1741	TGTAAAGCTGAGGATGTGAAGAAAAGGACAGGAACCTATAGTATCTAATATATCTT	1800
Db	1763	TGTAAAGCTGAGGATGTGAAGAAAAGGACAGGAACCTATAGTATCTAATATATCTT	1822
OY	1801	CATTTCCTATCTCTATACAAATATCCACAAGCTTTTCAACAGAAATTCATGACAGTCAAA	1860
Db	1823	CATTTCCTATCTCTATACAAATATCCACAAGCTTTTCAACAGAAATTCATGACAGTCAAA	1882
OY	1861	TCCCAAAAGGAACCTTATATCAATTTATGAGTGAGTGCGTTTATGAAATTTTGGCAATCA	1920
Db	1883	TCCCAAAAGGAACCTTATATCAATTTATGAGTGAGTGCGTTTATGAAATTTTGGCAATCA	1942
OY	1921	TACTGTGTCACTTATCTCAACTTTGAGATGTGTTTGTCTTGTATGTAAATGAAGAATAA	1980
Db	1943	TACTGTGTCACTTATCTCAACTTTGAGATGTGTTTGTCTTGTATGTAAATGAAGAATAA	2002
OY	1981	GGGACACTTGTGTAGGCCACTTTAGGGTTCACCTCTGGCAATTAAGAAATTTACAAAGA	2037
Db	2003	GGGACACTTGTGTAGGCCACTTTAGGGTTCACCTCTGGCAATTAAGAAATTTACAAAGA	2059

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RESULT 5
US-09-895-814-690
; Sequence 690, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yastir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 690
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-690

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Query Match	80.0%	Score 1629	DB 10	Length 3923
Best Local Similarity	99.6%	Pred. No. 0		
Matches 2023	Conservative 0	Mismatches 8	Indels 0	Gaps 0
QY 1 AGAAGCTGCATCAGAAAAACAGAGGGGACATTTCGTGGCTGCACCGAGGAGACAG 60				
Db 23 AGAAGCTGCATCAGAAAAACAGAGGGGAGATTTCGTGGCTGCACCGAGGAGACAG 82				
QY 61 GAAGATCTGCATGGTGGGAAGGACCTGATGATTCAGAGCAATTACAAACATTAATTAG 120				
Db 83 GAAGATCTGCATGGTGGGAAGGACCTGATGATTCAGAGCAATTACAAACATTAATTAG 142				
QY 121 TGTTCATTAACACCAAGATAAATAAGTGAAGAGTAGTCGCTGTGATGCTCCCAT 180				
Db 143 TGTTCATTAACACCAAGATAAATAAGTGAAGAGTAGTCGCTGTGATGCTCCCAT 202				
QY 181 GACACAGGGCTGCATCCATCGACGGCATTCTCAAGTACTGACGACAAAGAAAGA 240				
Db 203 GACACAGGGCTGCATCCATCGACGGCATTCTCAAGTACTGACGACAAAGAAAGA 262				
QY 241 CTACAGACATCTCAATGGCAGGGGTGAGAAATTAAGAAAGGCTGCTACTTACCATCTGA 300				
Db 263 CTACAGACATCTCAATGGCAGGGGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGA 322				
QY 301 GGCACACATCTGCTGAATGAGATTAATTACATCATAGAAACGCAAGATGACATA 360				
Db 323 GGCACACATCTGCTGAATGAGATTAATTACATCATAGAAACGCAAGATGACATA 382				
QY 361 TAATGCTAAGTGTGACATGTTTTGGCACAATTCGAGCCCTTTAATATATCACACACA 420				
Db 383 TAATGCTAAGTGTGACATGTTTTGGCACAATTCGAGCCCTTTAATATATCACACACA 442				
QY 421 CAGGAAGCAAAAAGGAGACACAGAAATCCCTGGGAGAAATGCCGGCCCATCTTGGG 480				

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Db 443 CAGAGACACAAAAGAAAGCAGAGATCCCTGGAGAAATGCCCGCCGACATCTGGG 502
Qy 481 TCATCATGATGACCCCGCCCTGTGCTGGTCCCGCTGTGAGAGGAAGACATTAAAGATG 540
Db 503 TCATCATGATGACCCCGCCCTGTGCTGGTCCCGCTGTGAGAGGAAGACATTAAAGATG 562
Qy 541 AATGATGATGTTCTTAAAGATGGCGAGAAACAGATCCTGTGTGATATTTATTTG 600
Db 563 AATGATGATGTTCTTAAAGATGGCGAGAAACAGATCCTGTGTGATATTTATTTG 622
Qy 601 AACGGGATTACAGATTTGAAATGAATGCACAAAGTGAGCATTACCAATGAGAGAAAAACA 660
Db 623 AACGGGATTACAGATTTGAAATGAATGCACAAAGTGAGCATTACCAATGAGAGAAAAACA 682
Qy 661 GACGAGAAAATCTGATGAGGCTTCACAAAGACATGCAACAAACAAATGGAATACGTGATG 720
Db 683 GACGAGAAAATCTGATGAGGCTTCACAAAGACATGCAACAAACAAATGGAATACGTGATG 742
Qy 721 ACATGAGGACAGCCAGGCTGGGGAGAGATTAACACAGGGGACAGAGGTCAGGATTCGGCC 780
Db 743 ACATGAGGACAGCCAGGCTGGGGAGAGATTAACACAGGGGACAGAGGTCAGGATTCGGCC 802
Qy 781 CTGCTGCCATTAAGCTGTGCGTTCAATACCAAAATCAATTCATATTTCTAAACCTCAAAACA 840
Db 803 CTGCTGCCATTAAGCTGTGCGTTCAATACCAAAATCAATTCATATTTCTAAACCTCAAAACA 862
Qy 841 AGCGTGTATATCTGATCTACGAGTCTCTGCGGCCACAAATCTCCATATATATATATATAT 900
Db 863 AGCGTGTATATCTGATCTACGAGTCTCTGCGGCCACAAATCTCCATATATATATATATAT 922
Qy 901 GCCACACATATTTTAAAT 960
Db 923 GCCACACATATTTTAAAT 982
Qy 961 AATAACATTAATCTATTTTGTCAAAAGACCTTGTGTGTGCTGCTAATATATATATATATAT 1020
Db 983 AATAACATTAATCTATTTTGTCAAAAGACCTTGTGTGTGCTGCTAATATATATATATATAT 1042
Qy 1021 GTTTTTCCTAAGAGAGTGTCTGGGCCAGGGATCTGTGAACAGGCTGGGAGACATCTCA 1080
Db 1043 GTTTTTCCTAAGAGAGTGTCTGGGCCAGGGATCTGTGAACAGGCTGGGAGACATCTCA 1102
Qy 1081 GATCTTTCAGAGGTTATATCTACTAGCACACAGCATGATCTATTCAGAGTGAATATATCTA 1140
Db 1103 GATCTTTCAGAGGTTATATCTACTAGCACACAGCATGATCTATTCAGAGTGAATATATCTA 1162
Qy 1141 ATCAACATCATCTCAGTGTCTTGGCCATCTGAAATTCATTTCCACATTTGTGCCCA 1200
Db 1163 ATCAACATCATCTCAGTGTCTTGGCCATCTGAAATTCATTTCCACATTTGTGCCCA 1222
Qy 1201 TTTTCAAGACCTCAAAATGTCATTCATTAATATACAGGATTAATCTTTTAAAAAC 1260
Db 1223 TTTTCAAGACCTCAAAATGTCATTCATTAATATACAGGATTAATCTTTTAAAAAC 1282
Qy 1261 TGAAGAATTCATATGATGACAGCATGATGGGAATTAATATACATTTTGTCCAGT 1320
Db 1283 TGAAGAATTCATATGATGACAGCATGATGGGAATTAATATACATTTTGTCCAGT 1342
Qy 1321 GCAAGAATGACTAAGTCTTATTCCTTCCCTTTGTTGATTTTTCAGATTAAGT 1380
Db 1343 GCAAGAATGACTAAGTCTTATTCCTTCCCTTTGTTGATTTTTCAGATTAAGT 1402
Qy 1381 TAAATGCTTAGCTGTGATGAGGCTGTATACAGACAGGCTCTCCCATCCCTCCAGC 1440
Db 1403 TAAATGCTTAGCTGTGATGAGGCTGTATACAGACAGGCTCTCCCATCCCTCCAGC 1462
Qy 1441 CTATCTGTATCATCATCAACCCCTCCCATNYSACCAAAACAAATATCTATCTGATAT 1500
Db 1463 CTATCTGTATCATCATCAACCCCTCCCATNYSACCAAAACAAATATCTATCTGATAT 1522
Qy 1501 CTTGAACATGTCAGGACAT 1560
|||||

Db 1523 CTTGAACATGTCAGGACAT 1582
Qy 1561 AANTCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1583 AANTCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1642
Qy 1621 ACACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1643 ACACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1702
Qy 1681 AGAGTTAGATTAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Db 1703 AGAGTTAGATTAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1762
Qy 1741 TGTAGGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
Db 1763 TGTAGGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1822
Qy 1801 CATTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 1860
Db 1823 CATTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 1882
Qy 1861 TCCCAAGGATTAACCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 1920
Db 1883 TCCCAAGGATTAACCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 1942
Qy 1921 TACTGTGATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 1980
Db 1943 TACTGTGATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 2002
Qy 1981 GGGACATCTTGTGAGCCACTTTAGGCTTCACTCTGCAATTAAGAAATTTCAAGA 2037
Db 2003 GGGACATCTTGTGAGCCACTTTAGGCTTCACTCTGCAATTAAGAAATTTCAAGA 2059
|||||

RESULT 6
US-10-144-678A-690
; Sequence 690, Application US/10144678A
; Publication No. US20030157089A1
GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Vasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ya
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144.678A
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 690
; LENGTH: 3923

TYPE: DNA
ORGANISM: Homo sapiens
US-10-144-678A-690

Query Match 80.0%; Score 1629; DB 12; Length 3923;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCGAAGAAACAGAGGAGGATTTGTGGCTGCGAGCGAGGAGACAG 60
DB 23 AGAAGCTGGCATCGAAGAAACAGAGGAGGATTTGTGGCTGCGAGCGAGGAGACAG 82
QY 61 GAAGATCTGATGGTGGGAAAGACCTGATGATACAGAGGATTAACAACATATATCTAG 120
DB 83 GAAGATCTGATGGTGGGAAAGACCTGATGATACAGAGGATTAACAACATATATCTAG 142
QY 121 TGTATCAATGAACACCAAGATTAATAGTGAAGAGCTAAGTCCGTGAGATCTCTAGT 180
DB 143 TGTATCAATGAACACCAAGATTAATAGTGAAGAGCTAAGTCCGTGAGATCTCTAGT 202
QY 181 GACACAGGCTGGATCCATCGACGCGACTTTCTGATCTAGTCTAGTCTAGCAAGAGA 240
DB 203 GACACAGGCTGGATCCATCGACGCGACTTTCTGATCTAGTCTAGTCTAGCAAGAGA 262
QY 241 CTACAGCATCTCAATGGCAGGGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGA 300
DB 263 CTACAGCATCTCAATGGCAGGGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGA 322
QY 301 GGGCACACATCTGCTGAATGAGATTAATTAACATCTAGTGAAGACCAAGATGACATA 360
DB 323 GGGCACACATCTGCTGAATGAGATTAATTAACATCTAGTGAAGACCAAGATGACATA 382
QY 361 TAATGCTAAGTAGTGAATGATTTTGGACATTTCCAGCCCTTTAAATATCCACACACA 420
DB 383 TAATGCTAAGTAGTGAATGATTTTGGACATTTCCAGCCCTTTAAATATCCACACACA 442
QY 421 CAGGAAGCAAAAAGAGACAGACAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGG 480
DB 443 CAGGAAGCAAAAAGAGACAGACAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGG 502
QY 481 TCATCGATGAGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 503 TCATCGATGAGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 562
QY 541 AATGATGCTGCTTAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 563 AATGATGCTGCTTAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 622
QY 601 AACGGATTACGATTTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 660
DB 623 AACGGATTACGATTTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 682
QY 661 GAGGAGAAATCTTGATGGCTTCAACAAGATGCAACAACAACAACAACAACAACAACA 720
DB 683 GAGGAGAAATCTTGATGGCTTCAACAAGATGCAACAACAACAACAACAACAACAACA 742
QY 721 ACATGAGGACGCAAGCTGGGAGAGATTAACACGCGGACAGAGGTCAGATTTGGCC 780
DB 743 ACATGAGGACGCAAGCTGGGAGAGATTAACACGCGGACAGAGGTCAGATTTGGCC 802
QY 781 CTGCTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 803 CTGCTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 862
QY 841 AGCTGTTGAATATCTGATCTACGTTCTCTGCGGCCACACATTTCCATATATATCA 900
DB 863 AGCTGTTGAATATCTGATCTACGTTCTCTGCGGCCACACATTTCCATATATATCA 922
QY 901 GCCACACTATTTTAAATATTTAGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAG 960
DB 923 GCCACACTATTTTAAATATTTAGTTCCAGATCTGTACTGTGACCTTTCTACACTGTAG 982
QY 961 AATAACATTAATCTATTTGTTCAAAAGACCTTGTGTTGCTGCTAATATGATGCTGACT 1020

DB 983 AATAACATTAATCTATTTGTTCAAAAGACCTTGTGTTGCTGCTAATATGATGCTGACT 1042
QY 1021 GTTTTTCCTAAGGAGTCTTGGCCAGGGGATCTGTGAACACAGCTGGGAGCATCTCAA 1080
DB 1043 GTTTTTCCTAAGGAGTCTTGGCCAGGGGATCTGTGAACACAGCTGGGAGCATCTCAA 1102
QY 1081 GATCTTCCAGGGTATATCTTACTAGCACACACATGATATATTCGAGAGGATTAATCTA 1140
DB 1103 GATCTTCCAGGGTATATCTTACTAGCACACACATGATATATTCGAGAGGATTAATCTA 1162
QY 1141 ATCAACATCAATCTCAATGCTGCTTGGCCATATGAAATTCATTTCCACTTTTGTGCCA 1200
DB 1163 ATCAACATCAATCTCAATGCTGCTTGGCCATATGAAATTCATTTCCACTTTTGTGCCA 1222
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DB 1223 TTCTCAAGACCTCAAAATGTCATTCATTAATATCAACAGATTAATCTTTTCTTAAC 1282
QY 1261 TGGAGAAATCAATGTTACATGACAGTATGGAATTAATTAATATTTTGTTCAGT 1320
DB 1283 TGGAGAAATCAATGTTACATGACAGTATGGAATTAATTAATATTTTGTTCAGT 1342
QY 1321 GCAAGATGACTAATGCTTTATTCCTCCCTTTGTTGATTTTTCAGTATAAGT 1380
DB 1343 GCAAGATGACTAATGCTTTATTCCTCCCTTTGTTGATTTTTCAGTATAAGT 1402
QY 1381 TAAATGCTTAGCTTGTACTGAGGCTGATTAACAGACAGGCTTCGCCATCCCTGACG 1440
DB 1403 TAAATGCTTAGCTTGTACTGAGGCTGATTAACAGACAGGCTTCGCCATCCCTGACG 1462
QY 1441 CTATGCTGATCAGCATCAACCCCTCCCATATTAACCTTAACCTTAATTT 1500
DB 1463 CTATGCTGATCAGCATCAACCCCTCCCATATTAACCTTAACCTTAATTT 1522
QY 1501 CCTTGAACATGTAGGNCATTAATTTCTGCTTGGCTGAGAGCTTCTCTGCTCTT 1560
DB 1523 CCTTGAACATGTAGGNCATTAATTTCTGCTTGGCTGAGAGCTTCTCTGCTCTT 1582
QY 1561 AANTCTAGATGATGTAAGTTTGAATTAAGTGAATGATCTTACTCATGCAAGAGAGG 1620
DB 1583 AANTCTAGATGATGTAAGTTTGAATTAAGTGAATGATCTTACTCATGCAAGAGAGG 1642
QY 1621 ACACATATGATGATTCATCATCATGACAGACAGCAATTAATAATGATATATA 1680
DB 1643 ACACATATGATGATTCATCATCATGACAGACAGCAATTAATAATGATATATA 1702
QY 1681 AGAGTTAGATTAATATGAAATGCAAGACCCAGAGGAGGATGTTATGAGGACGCTT 1740
DB 1703 AGAGTTAGATTAATATGAAATGCAAGACCCAGAGGAGGATGTTATGAGGACGCTT 1762
QY 1741 TGTAAAGCTGGGATGTGAAGMAAGGACAGGAACTCATAGTATCTTATATATATCTT 1800
DB 1763 TGTAAAGCTGGGATGTGAAGMAAGGACAGGAACTCATAGTATCTTATATATATCTT 1822
QY 1801 CATTTCTATCTCTATCAACATATCAACAAGCTTTTCAAGAAATTCATGACATGCA 1860
DB 1823 CATTTCTATCTCTATCAACATATCAACAAGCTTTTCAAGAAATTCATGACATGCA 1882
QY 1861 TCCCAAGGTAACCTTATATCAATTCATGAGGAGGCTTTAGAAATTTGGCAATTA 1920
DB 1883 TCCCAAGGTAACCTTATATCAATTCATGAGGAGGCTTTAGAAATTTGGCAATTA 1942
QY 1921 TACTGTCACTATATCAACATTTGAGATGTTGTTGCTTGTAGTAAATTTGAAGAATA 1980
DB 1943 TACTGTCACTATATCAACATTTGAGATGTTGTTGCTTGTAGTAAATTTGAAGAATA 2002
QY 1981 GGGCACTCTTGTAGGCACTTAAAGGTTAGGCTCTGCGCAATTAAGAATTTTACAAGA 2037
DB 2003 GGGCACTCTTGTAGGCACTTAAAGGTTAGGCTCTGCGCAATTAAGAATTTTACAAGA 2059

RESULT 7

Db 983 AATAACATTACTATTTTGTTCAAAGACCCTTGCTGCTGCTAATATGTAGTCACT 1042
QY 1021 GTTTTCTTAAGGAGTGTTCGGCCAGGAGATCTGTACACAGCTGGGAACATCTCA 1080
Db 1043 GTTTTCTTAAGGAGTGTTCGGCCAGGAGATCTGTACACAGCTGGGAACATCTCA 1102
QY 1081 GATCTTTCCAGGGTATCTACTAGACACAGCATGTATTCATTAGGAGTGAATATCTA 1140
Db 1103 GATCTTTCCAGGGTATCTACTAGACACAGCATGTATTCATTAGGAGTGAATATCTA 1162
QY 1141 ATCAACATATCTCAGTGTCTTTGGCCAACTGAAATTCATTTCCACTTTTGGCCCA 1200
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QY 1201 TTTCACAGCCTCAAAAATGTGATTTCCATTAAATACAGAGATTAATCTTTTAAAC 1260
Db 1223 TTTCACAGCCTCAAAAATGTGATTTCCATTAAATACAGAGATTAATCTTTTAAAC 1282
QY 1261 TGAAGAAATTCATGTATACATGACAGCTATGGGAATTTAATTCATATTTTCCAGT 1320
Db 1283 TGAAGAAATTCATGTATACATGACAGCTATGGGAATTTAATTCATATTTTCCAGT 1342
QY 1321 GCAAGAGTACATAGCTCTTATCCCTCCCTTTGTTGATTTTTCACAGTAAAGT 1380
Db 1343 GCAAGAGTACATAGCTCTTATCCCTCCCTTTGTTGATTTTTCACAGTAAAGT 1402
QY 1381 TAAATGCTTACCTTGTACAGGCTGTATACAGACAGCTCTCCCATCCCTCCAGC 1440
Db 1403 TAAATGCTTACCTTGTACAGGCTGTATACAGACAGCTCTCCCATCCCTCCAGC 1462
QY 1441 CTATCTGTACATCACATCAACCCCTCCCATNYSACTAAACAAATCAATCTGTAAT 1500
Db 1463 CTATCTGTACATCACATCAACCCCTCCCATNYSACTAAACAAATCAATCTGTAAT 1522
QY 1501 CCTTGACATGTACAGGCTATCATTTTCTCTGCTGAGAGGCTCTTCTGCTCTT 1560
Db 1523 CCTTGACATGTACAGGCTATCATTTTCTCTGCTGAGAGGCTCTTCTGCTCTT 1582
QY 1561 AANTCTAGAAATGTAAGTTTGAATTAAGTGAATCTTACTTCAATGCAAAAGAGG 1620
Db 1583 AANTCTAGAAATGTAAGTTTGAATTAAGTGAATCTTACTTCAATGCAAAAGAGG 1642
QY 1621 ACACATATGAGATTCATCATCATGACAGACAAATCTAAAGTGTATTTGATTATA 1680
Db 1643 ACACATATGAGATTCATCATCATGACAGACAAATCTAAAGTGTATTTGATTATA 1702
QY 1681 AGAGTTAGATTAATATATGAAGATGCAAGACCAAGAGGAGTGTATGAGGACGTT 1740
Db 1703 AGAGTTAGATTAATATATGAAGATGCAAGACCAAGAGGAGTGTATGAGGACGTT 1762
QY 1741 TGTAGCCTGGAGTGTGAAGAAAGGAGGAACTCATAGTATCTTATATATATACTT 1800
Db 1763 TGTAGCCTGGAGTGTGAAGAAAGGAGGAACTCATAGTATCTTATATATATACTT 1822
QY 1801 CATTTCTATCTATCATCAATATCAACAAGCTTTTACAGAAATTCAGAGTCAAA 1860
Db 1823 CATTTCTATCTATCATCAATATCAACAAGCTTTTACAGAAATTCAGAGTCAAA 1882
QY 1861 TCCCCAAAAGTAACTTATCCATTTTCATGTGAGTGGCTTTAAGATTTTGGCAATCA 1920
Db 1883 TCCCCAAAAGTAACTTATCCATTTTCATGTGAGTGGCTTTAAGATTTTGGCAATCA 1942
QY 1921 TACGTGTACATATCAACTGTGAGATGTGTTTCCCTGTAGTAAATGGAAGAAATA 1980
Db 1943 TACGTGTACATATCAACTGTGAGATGTGTTTCCCTGTAGTAAATGGAAGAAATA 2002
QY 1981 GGGGACCTGTTGAGACCACTTTAGGTTTCACTCTGCAATTAAGAAATTTACAAAGA 2037
Db 2003 GGGGACCTGTTGAGACCACTTTAGGTTTCACTCTGCAATTAAGAAATTTACAAAGA 2059

RESULT 9
US-09-759-143-470/c

Sequence 470, Application US/09759143
Patent No. US2002022248A1
GENERAL INFORMATION:
APPLICANT: Xu, JIANGCHUN
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, YUQI
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yashir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 470
LENGTH: 2426
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-470

Query Match 56.7%; Score 1154; DB 9; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGTGAATAATGAAGAGGCTGCTGACTTATTCATCTGAGGCGACATCTGCTGAATG 322
Db 1769 GGTGAATAATGAAGAGGCTGCTGACTTATTCATCTGAGGCGACATCTGCTGAATG 1710
QY 323 AGATATTAATACATCACTAGAAACAGCAAGATGACATATATATATGTCTAAGTAGCATGT 382
Db 1709 AGATATTAATACATCACTAGAAACAGCAAGATGACATATATATATGTCTAAGTAGCATGT 1650
QY 383 TTTTGACATTTTCCAGCCCTTTAATATCCACACACAGAGAGACACAAAAGAACAC 442
Db 1649 TTTTGACATTTTCCAGCCCTTTAATATCCACACACAGAGAGACACAAAAGAACAC 1590
QY 443 AGAGATCCCTGGGAAATATGCCGCGCATCTTGGGTCATGATGAGACCTCGCCCTGT 502
Db 1589 AGAGATCCCTGGGAAATATGCCGCGCATCTTGGGTCATGATGAGACCTCGCCCTGT 1530
QY 503 GCCTGTCCTCCCTTGTGAGGGAAGACATTTAGAAATGAATGATGTCTTCTTAAAGA 562
Db 1529 GCCTGTCCTCCCTTGTGAGGGAAGACATTTAGAAATGAATGATGTCTTCTTAAAGA 1470
QY 563 TGGGCAAGAAAAACAGATCTGTTGTGATATTTTGAACGGGATTTACAGATTTGAAT 622
Db 1469 TGGGCAAGAAAAACAGATCTGTTGTGATATTTTGAACGGGATTTACAGATTTGAAT 1410
QY 623 GAAGTCACAAATGAGCATTTACCAATGAGAGAAAAACAGAGAAAAATCTTGATGCTT 682
Db 1409 GAAGTCACAAATGAGCATTTACCAATGAGAGAAAAACAGAGAAAAATCTTGATGCTT 1350
QY 683 CACAAGACATGCAACAAACAAATGAAATCTGTATGATGATGAGGACCAAGCTGGGG 742
Db 1349 CACAAGACATGCAACAAACAAATGAAATCTGTATGATGATGAGGACCAAGCTGGGG 1290
QY 743 AGAGATTAACCAAGGGGCGAGAGGTCAGGATTTCTGGCCTGTGCTTAACCTGTGCTTC 802
Db 1289 AGAGATTAACCAAGGGGCGAGAGGTCAGGATTTCTGGCCTGTGCTTAACCTGTGCTTC 1230

QY	803	ATATCCAAATATATTTCAATTTTCACCCCTCAAAAACAAGCTGTGGATATTCGATCTC	862
Db	1229	ATATCCAAATATTTTCATATTTTCTTAACCCCTCAAAAACAAGCTGTGGATATTCGATCTC	1170
QY	863	TACGGTTCCTTCTGCGGCCCAACATTTCTCATATATATCCAGCCACATCATATTTTAAATTT	922
Db	1169	TACGGTTCCTTCTGCGGCCCAACATTTCTCATATATATCCAGCCACATCATATTTTAAATTT	1110
QY	923	AGTTCCACAGATCTGTACTGTGACCTTCTTCACCTGTAGAGATTAACATTTACTATTTGTTC	982
Db	1109	AGTTCCACAGATCTGTACTGTGACCTTCTTCACCTGTAGAGATTAACATTTACTATTTGTTC	1050
QY	983	AAATACCCCTGCTGTGCTGGCTAAATATATGTAGCTGACCTGTTTTCCTAAGAGAGTCTG	1042
Db	1049	AAATACCCCTGCTGTGCTGGCTAAATATATGTAGCTGACCTGTTTTCCTAAGAGAGTCTG	990
QY	1043	GCCCAAGGGGATCTGTGAACAAGCTGGGAGAGCATCTCAAGATCTTCCAGGGTATATCTTA	1102
Db	989	GCCCAAGGGGATCTGTGAACAAGCTGGGAGAGCATCTCAAGATCTTCCAGGGTATATCTTA	930
QY	1103	CTACACACAGACATGATCATTTACGAGAGTGAATATCTAATCAGATCATCTCAGTGTCT	1162
Db	929	CTACACACAGACATGATCATTTACGAGAGTGAATATCTAATCAGATCATCTCAGTGTCT	870
QY	1163	TTGGCCCATACAGAAATTCATTTCCCACTTTTGTGCGCCATTTCTCAAGACCTCAAAATGTCA	1222
Db	869	TTGGCCCATACAGAAATTCATTTCCCACTTTTGTGCGCCATTTCTCAAGACCTCAAAATGTCA	810
QY	1223	TTCCATTAAATTCACAGATTAACCTTTTCTTTTAACTGGAGAAATTCATTTTACATG	1282
Db	809	TTCCATTAAATTCACAGATTAACCTTTTCTTTTAACTGGAGAAATTCATTTTACATG	750
QY	1283	CAGCTATGGGAATTTAAATTACATATTTTGTTCACGTCAAAAGATGACTAAGTCTTTTA	1342
Db	749	CAGCTATGGGAATTTAAATTACATATTTTGTTCACGTCAAAAGATGACTAAGTCTTTTA	690
QY	1343	TCCTCTCCCTTGTGTGATTTTTCACGATATAAGTTAAATAGCTTAGCTGTACTG	1402
Db	689	TCCTCTCCCTTGTGTGATTTTTCACGATATAAGTTAAATAGCTTAGCTGTACTG	630
QY	1403	AGCCTGTATACAGC	1416
Db	629	AGCCTGTATACAGC	616

RESULT 10
 US-09-780-669-470/c
 : Sequence 470, Application US/09780669
 : Patent No. US2002005197A1
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Jiangchun
 : APPLICANT: Dillon, Devin C.
 : APPLICANT: Mitcham, Jennifer L.
 : APPLICANT: Harlocker, Susan L.
 : APPLICANT: Jiang, Yugu
 : APPLICANT: Henderson, Robert A.
 : APPLICANT: Kalos, Michael D.
 : APPLICANT: Fanger, Gary R.
 : APPLICANT: Retter, Marc W.
 : APPLICANT: Stolk, John A.
 : APPLICANT: Day, Craig H.
 : APPLICANT: Vedvick, Thomas S.
 : APPLICANT: Carter, Derrick
 : APPLICANT: Li, Samuel
 : APPLICANT: Wang, Aijun
 : APPLICANT: Skeiky, Yasir A.W.
 : APPLICANT: Hepler, William
 : APPLICANT: Hurst, John
 : APPLICANT: McNeill, Patricia D.
 : APPLICANT: Houghton, Raymond L.
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 : FILE REFERENCE: 210121.427C24

CURRENT APPLICATION NUMBER: US-09/780,669									
CURRENT FILING DATE: 2001-02-09									
NUMBER OF SEQ ID NOS: 943									
SOFTWARE: FastSeq for Windows Version 3.0									
SEQ ID NO 470									
LENGTH: 2426									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-09-780-669-470									
Query Match									
Best Local Similarity 56.7%; Score 1154; DB 9; Length 2426;									
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	263	GGTGAGAAATAGAAAGGCTGCTGACATTACCATCTGAGGCCACACATCTGCTGAATAG	322						
DB	1769	GGTGAGAAATAGAAAGGCTGCTGACATTACCATCTGAGGCCACACATCTGCTGAATAG	1710						
QY	323	AGATATATACATCACTAGAAAACGCAAGATGACATATATATGTCTAAGTGTGACATGT	382						
DB	1709	AGATATATACATCACTAGAAAACGCAAGATGACATATATATGTCTAAGTGTGACATGT	1650						
QY	383	TTTTCGACATTTCCAGCCCTTTTAAATATCCACACACACAGAGAACACAAAGAACAC	442						
DB	1649	TTTTCGACATTTCCAGCCCTTTTAAATATCCACACACACAGAGAACACAAAGAACAC	1590						
-QY	443	AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATCGATGAGCCTCGCCCTGT	502						
DB	1589	AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATCGATGAGCCTCGCCCTGT	1530						
QY	503	GCTGTGTCCTGCTGTGTGAGGAGACATTTGAAAATGATATGATGTCTTCTTAAGGA	562						
DB	1529	GCTGTGTCCTGCTGTGTGAGGAGACATTTGAAAATGATATGATGTCTTCTTAAGGA	1470						
QY	563	TGGGAGAGAAACAGATCCTGTGTGATATTTATTTGACGGGATTACAGATTTGAAT	622						
DB	1469	TGGGAGAGAAACAGATCCTGTGTGATATTTATTTGACGGGATTACAGATTTGAAT	1410						
QY	623	GAACTCAACAAAGTGAAGATTTACCAATGAGAGGAAACACAGAGAAATCTTGATGCTT	682						
DB	1409	GAACTCAACAAAGTGAAGATTTACCAATGAGAGGAAACACAGAGAAATCTTGATGCTT	1350						
QY	683	CACAAGACATGCAACAAACAAATGGAATACTGTGATGACATGAGGCGCCAGCTGGGG	742						
DB	1349	CACAAGACATGCAACAAACAAATGGAATACTGTGATGACATGAGGCGCCAGCTGGGG	1290						
QY	743	AGGAGATTAACACAGGGGAGAGGGTACAGATTTGCGCCCTGCTCAACTGTGCGCTC	802						
DB	1289	AGGAGATTAACACAGGGGAGAGGGTACAGATTTGCGCCCTGCTCAACTGTGCGCTC	1230						
QY	803	ATAACCAATCATTTTCAATTTTCAACCCCTAAACAAAGAGCTGTGTATATCGATCTC	862						
DB	1229	ATAACCAATCATTTTCAATTTTCAACCCCTAAACAAAGAGCTGTGTATATCGATCTC	1170						
QY	863	TAGGTTCTCTTCTGGGCCCAACATTTCCATATATCCAGCCACATCTTTTAAATTT	922						
DB	1169	TAGGTTCTCTTCTGGGCCCAACATTTCCATATATCCAGCCACATCTTTTAAATTT	1110						
QY	923	AGTTCCAGATCTGTACTGTACCTTTCTACAGTGTGAATTAACATTAACATTTGCTC	982						
DB	1109	AGTTCCAGATCTGTACTGTACCTTTCTACAGTGTGAATTAACATTAACATTTGCTC	1050						
QY	983	AAAGACCTTGTGTGCTGCTTAATATGTAGCGACGTTTTTCCTAAGAGGTGCTG	1042						
DB	1049	AAAGACCTTGTGTGCTGCTTAATATGTAGCGACGTTTTTCCTAAGAGGTGCTG	990						
QY	1043	GCCCAAGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCCAGGGTTATCTTA	1102						
DB	989	GCCCAAGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCCAGGGTTATCTTA	930						
QY	1103	CTAGCACACAGCATGATCATTTACGAGATGATATCTTAATCAATCATCTCTAGTGTCT	1162						
DB	929	CTAGCACACAGCATGATCATTTACGAGATGATATCTTAATCAATCATCTCTAGTGTCT	870						

QY	1153	TTGCCCATPACTGGAATTCATTCCCACTTTTGTCACATTCCTCAAGACCTCAAAATGCA	12222
Db	869	TTGGCCCAATACGGAATTCATTCTCCACATTTTGTCGCCATTCCTCAAGACCTCAAAATGCA	810
QY	1223	TTCCATTAATATACACAGATTAATACCTTTTTTTTTTAACCTGGAGAAATTCATGTTATACG	1282
Db	809	TTCCATTAATATACACAGATTAATACCTTTTTTTTTTAACCTGGAGAAATTCATGTTATACG	750
QY	1283	CAGCTATGGAATTTAATTAACAATTTTGTTTCCAGTGCAAAGATGACTAATGTCCTTTA	1342
Db	749	CAGCTATGGAATTTAATTAACAATTTTGTTTCCAGTGCAAAGATGACTAATGTCCTTTA	690
QY	1343	TCCCTCCCCCTTGTTGATTTTTTTTTTCCAGATTAAGTTAAATAGCTATGACCTGTACTG	1402
Db	689	TCCCTCCCCCTTGTTGATTTTTTTTTTCCAGATTAAGTTAAATAGCTATGACCTGTACTG	630
QY	1403	AGGCTGTATACAGC	1416
Db	629	AGGCTGTATACAGC	616

RESULT 11
 US-09-822-827-470/c
 Sequence 470, Application US/09822827
 Patent No. US20020081650A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.534C1
 CURRENT FILING DATE: 2001-03-28
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FASTSEQ For Windows Version 3.0
 SEQ ID NO 470
 LENGTH: 2426
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-822-827-470

Query Match	56.7%	Score 1154;	DB 9;	Length 2426;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1154;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	263	GGTGAGAATTAAGAAAGCGCTGCTGACTTTACCATCTTGAGGCCACACATCTGCTGAATGG	322
Dd	1769	GGTGGAAATTAAGAAAGCGCTGCTGACTTTACCATCTTGAGGCCACACATCTGCTGAATGG	1710
OY	323	AGATAATTACATCACTGTAAGAACAGCAAGATGACAATTAATTCGTAACTAGTAGTGACATGT	382
Dd	1709	AGATAATTACATCACTGTAAGAACAGCAAGATGACAATTAATTCGTAACTAGTAGTGACATGT	1656
OY	383	TTTTGCACATTTCCAGCCCCCTTAAATATCCACACACACAGAGAAGCACAAAAGNAGCAGC	442
Dd	1649	TTTTGCACATTTCCAGCCCCCTTAAATATCCACACACACAGAGAAGCACAAAAGNAGCAGC	1590
OY	443	AGAGATCCCTGGGAGAAATGCCCGCGCCCATCTTGGGTCAITCGATGAGCTCGCCCTGT	502
Dd	1589	AGAGATCCCTGGGAGAAATGCCCGCGCCCATCTTGGGTCAITCGATGAGCTCGCCCTGT	1530
OY	503	GCGTGGTCCCGCTGTGAGGGAAGGACATTGAANAATGAATGATGCTTCCTTAAGAGA	562
Dd	1529	GCGTGGTCCCGCTGTGAGGGAAGGACATTGAANAATGAATGATGCTTCCTTAAGAGA	1470
OY	563	TGGCGAGAAAAACAGATCCTGTGTTGGATTATTTAATTAAGGGGATTCAGATTTGAAT	622
Dd	1469	TGGCGAGAAAAACAGATCCTGTGTTGGATTATTTAATTAAGGGGATTCAGATTTGAAT	1410
OY	623	GAAGTCACAAAGTGAGCATTTACCAATGAGAGGAAAAACAGCAGAGAAATCTTGATGCGTT	682
Dd	1409	GAAGTCACAAAGTGAGCATTTACCAATGAGAGGAAAAACAGCAGAGAAATCTTGATGCGTT	1350

OY	683	CACAAAGCATGCAACAAACAAATGGATCTACTGTGATGACACTGAGGCAAGCCAGCTGGG	742
Db	1349	CACAAAGCATGCAACAAACAAATGGAAATCTGTGATGACACTGAGGCAAGCCAGCTGGG	1290
OY	743	AGGAGATPACCAAGGGGAGAGGGGTCAAGGATCTTGGGCCCTGCTCCATAACTGAGCGTTC	802
Db	1289	AGGAGATPACCAAGGGGAGAGGGGTCAAGGATCTTGGGCCCTGCTCCATAACTGAGCGTTC	1230
OY	803	ATAACCAAAATCATTTATTTCTPACCCCTCAAAACAAGCTGTGTAAATCTGATCTC	862
Db	1229	ATAACCAAAATCATTTATTTCTPACCCCTCAAAACAAGCTGTGTAAATCTGATCTC	1170
OY	863	TACGGTTCCTTCTGGGGCCCAACATTTCTCATATATCCAGCCACACTATTTTAAATTT	922
Db	1169	TACGGTTCCTTCTGGGGCCCAACATTTCTCATATATCCAGCCACACTATTTTAAATTT	1110
OY	923	AGTTCCCGAGCTGTGACTGTGACCTTTCACGTGAGAAATPACATTAAGTATTTGTTTC	982
Db	1109	AGTTCCCGAGCTGTGACTGTGACCTTTCACGTGAGAAATPACATTAAGTATTTGTTTC	1050
OY	983	AAAGACCCCTTGCTGTGCTGCCATAATATGATGACTGTTTTTCTPAAAGAGTGTCTG	1042
Db	1049	AAAGACCCCTTGCTGTGCTGCCATAATATGATGACTGTTTTTCTPAAAGAGTGTCTG	990
OY	1043	GCCCAAGGGGATCTGTGAACAGGCTGGGAGAGCATCTCAAGATCTTTCAGGGTTATCTTA	1102
Db	989	GCCCAAGGGGATCTGTGAACAGGCTGGGAGAGCATCTCAAGATCTTTCAGGGTTATCTTA	930
OY	1103	CTACGACACACATGATCATTTAGGAGATTTTCTPAAATACATCATCCTCAGTGCT	1162
Db	929	CTACGACACACATGATCATTTAGGAGATTTTCTPAAATACATCATCCTCAGTGCT	870
OY	1163	TTGGCCATACTGAATTCATTTCCCACTTTTGTCGCCATCTCTCAAGACCTTCAAAATGTCA	1222
Db	869	TTGGCCATACTGAATTCATTTCCCACTTTTGTCGCCATCTCTCAAGACCTTCAAAATGTCA	810
OY	1223	TTCCATTAATATCACAGGATTAACTTTTTTTTTTTAACTGGAAGATTCATGTTACATG	1282
Db	809	TTCCATTAATATCACAGGATTAACTTTTTTTTTTTAACTGGAAGATTCATGTTACATG	750
OY	1283	CAGCATAGGGGAATTAATTAACATTTTGTTCAGAGCAAGAGTGCAATGACCTTTTA	1342
Db	749	CAGCATAGGGGAATTAATTAACATTTTGTTCAGAGCAAGAGTGCAATGACCTTTTA	690
OY	1343	TCCCTCCCCCTTGTGTGATTTTTTTTTTCCAGATPAAAGTTAAATGCTTAAAGCTGTACTG	1402
Db	689	TCCCTCCCCCTTGTGTGATTTTTTTTTTCCAGATPAAAGTTAAATGCTTAAAGCTGTACTG	630
OY	1403	AGGCTGTATACAGC	1416
Db	629	AGGCTGTATACAGC	616

RESULT 12
US-09-895-793-470/c
Sequence 470, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlockner, Susan L.
APPLICANT: Jiang, Yuyu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stoltz, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yssir A.W.
APPLICANT: Hepler, William T.

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: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.534C2
: CURRENT APPLICATION NUMBER: US/09/895,793
: CURRENT FILING DATE: 2001-06-29
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 470
: LENGTH: 2426
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-895-793-470

Query Match      56.7%; Score 1154; DB 10; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGTGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATG 322
DB 1769 GGTGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATG 1710
QY 323 AGATAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTAAGTAGCATGT 382
DB 1709 AGATAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTAAGTAGCATGT 1650
QY 383 TTTTGACATTTTCAGCCCTTTAAATATCCACACAGAGAAAGCAAAAGGAAGCAC 442
DB 1649 TTTTGACATTTTCAGCCCTTTAAATATCCACACAGAGAAAGCAAAAGGAAGCAC 1590
QY 443 AAGAGATCCCTGGAGAAATCCCGCGCCGATCTGGGTATGATGAGCCTGCGCCTGT 502
DB 1589 AAGAGATCCCTGGAGAAATCCCGCGCCGATCTGGGTATGATGAGCCTGCGCCTGT 1530
QY 503 GCCTGCTCCCGCTTGTGAGGAAAGACATTTAGAAATGATGTGTTCTTAAAGGA 562
DB 1529 GCCTGCTCCCGCTTGTGAGGAAAGACATTTAGAAATGATGTGTTCTTAAAGGA 1470
QY 563 TGGGCGAGAAACAGATCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAT 622
DB 1469 TGGGCGAGAAACAGATCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAT 1410
QY 623 GAAGTCACAAAGTGACATTTACCAATGAGAGAAACACAGGAAATCTTGATGGCTT 682
DB 1409 GAAGTCACAAAGTGACATTTACCAATGAGAGAAACACAGGAAATCTTGATGGCTT 1350
QY 683 CACAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACGACCAAGCTGGGG 742
DB 1349 CACAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACGACCAAGCTGGGG 1290
QY 743 AAGAGATTAACCAAGGGGCAAGAGGTCAGATTCCTGCGCTCTAAACTGTGCGTTC 802
DB 1289 AAGAGATTAACCAAGGGGCAAGAGGTCAGATTCCTGCGCTCTAAACTGTGCGTTC 1230
QY 803 AATACCAATTCATTTCTATTTCTAACCTCAAAACAAAGCTGTGTATATCTGATCTC 862
DB 1229 AATACCAATTCATTTCTATTTCTAACCTCAAAACAAAGCTGTGTATATCTGATCTC 1170
QY 863 TAGGTTCTCTTGCGGCCCAACATTCCTCATATATCCAGCCACATCTTTTAATATTT 922
DB 1169 TAGGTTCTCTTGCGGCCCAACATTCCTCATATATCCAGCCACATCTTTTAATATTT 1110
QY 923 AGTTCCAGATCTGTAAGTGTGACCTTTGACACTGTAGAAATAACATTAATCTTTGTTT 982
DB 1109 AGTTCCAGATCTGTAAGTGTGACCTTTGACACTGTAGAAATAACATTAATCTTTGTTT 1050
QY 983 AAGAGCCCTTCTGTTGCTGCTAATATGATGACTGTTCTTCTAAGAGGTCTTCG 1042
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DB 1049 AAGAGCCCTTCTGTTGCTGCTAATATGATGACTGTTCTTCTAAGAGGTCTTCG 990
QY 1043 GCCAGGAGATCTGTGAAACAGGCTGGGAAACATCTCAAGATCTTCCAGGCTTATCTTA 1102
DB 989 GCCAGGAGATCTGTGAAACAGGCTGGGAAACATCTCAAGATCTTCCAGGCTTATCTTA 930
QY 1103 CTAGCACACAGCATGATCATTTAGGAGTGAATATATCAATCAATCATCTCAGTGTCT 1162
DB 929 CTAGCACACAGCATGATCATTTAGGAGTGAATATATCAATCAATCATCTCAGTGTCT 870
QY 1163 TTGCCCCATCTGAAATTTCAATTTCCACATTTTGGCCCATTTCTAAGACCTCAAAATGTCA 1222
DB 869 TTGCCCCATCTGAAATTTCAATTTCCACATTTTGGCCCATTTCTAAGACCTCAAAATGTCA 810
QY 1223 TTCCATTAATATACAGGATTAATCTTTTAAACCTGGAAGATTCATGTTACATG 1282
DB 809 TTCCATTAATATACAGGATTAATCTTTTAAACCTGGAAGATTCATGTTACATG 750
QY 1283 CAGCTATGGGAATTTAATTAATATTTTGTTCAGTGCAGAAAGATGACTAAGTCCCTTA 1342
DB 749 CAGCTATGGGAATTTAATTAATATTTTGTTCAGTGCAGAAAGATGACTAAGTCCCTTA 690
QY 1343 TCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAAGTTAAAGTCTTAGCCTTGACG 1402
DB 689 TCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAAGTTAAAGTCTTAGCCTTGACG 630
QY 1403 AGGCTGTATACAGC 1416
DB 629 AGGCTGTATACAGC 616

RESULT 13
US-09-895-814-470/c
: Sequence 470, Application US/09895814
: Publication No. US20020193296A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuguu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Derrick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C26
: CURRENT APPLICATION NUMBER: US/09/895,814
: CURRENT FILING DATE: 2001-06-29
: NUMBER OF SEQ ID NOS: 990
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 470
: LENGTH: 2426
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-895-814-470

Query Match      56.7%; Score 1154; DB 10; Length 2426;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGTGAGAAATGAGAAAGCTGCTGACTTTTACCATCTGAGGCCACACATCTGCTGAATGG 322
Db 1769 GGTGAGAAATGAGAAAGCTGCTGACTTTTACCATCTGAGGCCACACATCTGCTGAATGG 1710

QY 323 AGATAATTAACATCACTAGAAACGCAAGATGACATATATATAGTCTAGTAGTACATGT 382
Db 1709 AGATAATTAACATCACTAGAAACGCAAGATGACATATATATAGTCTAGTAGTACATGT 1650

QY 383 TTTTGCACATTTCCAGCCCTTTTAAATATCCACACACAGCAAGCAACAAAGAGAACAC 442
Db 1649 TTTTGCACATTTCCAGCCCTTTTAAATATCCACACACAGCAAGCAACAAAGAGAACAC 1590

QY 443 AGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTGATGATGAGCCTGCCTGT 502
Db 1589 AGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTGATGATGAGCCTGCCTGT 1530

QY 503 GCCGTGTCGGCTTGTGAGGGAAGGACATTAGAAATGAATGTGATGCTTAAAGGA 562
Db 1529 GCCGTGTCGGCTTGTGAGGGAAGGACATTAGAAATGAATGTGATGCTTAAAGGA 1470

QY 563 TGGGCAAGAAACAGATCTGTGTGATTTTATTTGAACGSGATTACAGATTTGAAT 622
Db 1469 TGGGCAAGAAACAGATCTGTGTGATTTTATTTGAACGSGATTACAGATTTGAAT 1410

QY 623 GAAGTCAAAAGTGACATTACCAATGAGAGAAACAGACGAGAAATCTTGATGCTT 682
Db 1409 GAAGTCAAAAGTGACATTACCAATGAGAGAAACAGACGAGAAATCTTGATGCTT 1350

QY 683 CACAAGCATGCAACAAACAAATGAAATCTGTGATGACATGAGGAGCCAACTGGGG 742
Db 1349 CACAAGCATGCAACAAACAAATGAAATCTGTGATGACATGAGGAGCCAACTGGGG 1290

QY 743 AGGAGATTAACACAGGGGCGAGAGGCTCAGATTTGCGCCCTGCTCTAACTGCGCTTC 802
Db 1289 AGGAGATTAACACAGGGGCGAGAGGCTCAGATTTGCGCCCTGCTCTAACTGCGCTTC 1230

QY 803 ATAAACCAATCATTTCTATTTCTTACCCCTCAAAAACAAAGCTGTTGTAATATCTGATCTC 862
Db 1229 ATAAACCAATCATTTCTATTTCTTACCCCTCAAAAACAAAGCTGTTGTAATATCTGATCTC 1170

QY 863 TAGCGTCTCTTGGGCGCAACATTCACATATTCAGCCACACCTCATTTTAAATTT 922
Db 1169 TAGCGTCTCTTGGGCGCAACATTCACATATTCAGCCACACCTCATTTTAAATTT 1110

QY 923 AGTTCCAGATCTGTACTGTGACTTCTACACGTGAAATTAACATTACTCATTTTGTTC 982
Db 1109 AGTTCCAGATCTGTACTGTGACTTCTACACGTGAAATTAACATTACTCATTTTGTTC 1050

QY 983 AAAGACCTTTCGTGTTGCTGCTGCTTAATATGATGACTGTTTTCCTAAGAGATGTTCTG 1042
Db 1049 AAAGACCTTTCGTGTTGCTGCTGCTTAATATGATGACTGTTTTCCTAAGAGATGTTCTG 990

QY 1043 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTTACTTA 1102
Db 989 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTTACTTA 930

QY 1103 CTAGACACAGCATGATCTTACGAGTGAATTTCTAATCAACATCATCTCAGTGTCT 1162
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QY 1163 TTGGCCACTGTAATTCATTTCCCATTTTGTGCCATTTCTCAAGACCTCAAAATGTCA 1222
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Db 629 AGCGTATACAGC 616

RESULT 14
US-10-144-678A-470/c
: Sequence 470, Application US/10144678A
: Publication No. US20030157089A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jlangchun
: APPLICANT: Dillon, Devin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A. W.
: APPLICANT: Hepler, William F.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals y de Bassols, Carloia
: APPLICANT: Foy, Teresa M.
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Deng, Ta
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C28
: CURRENT APPLICATION NUMBER: US/10/144,678A
: CURRENT FILING DATE: 2002-08-12
: NUMBER OF SEQ ID NOS: 1033
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 470
: LENGTH: 2426
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-144-678A-470

Query Match 56.7%; Score 1154; DB 12; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGTGAGAAATGAGAAAGCTGCTGACTTTTACCATCTGAGGCCACACATCTGCTGAATGG 322
Db 1769 GGTGAGAAATGAGAAAGCTGCTGACTTTTACCATCTGAGGCCACACATCTGCTGAATGG 1710

QY 323 AGATAATTAACATCACTAGAAACGCAAGATGACATATATATAGTCTAGTAGTACATGT 382
Db 1709 AGATAATTAACATCACTAGAAACGCAAGATGACATATATATAGTCTAGTAGTACATGT 1650

QY 383 TTTTGCACATTTCCAGCCCTTTTAAATATCCACACAGCAAGCAACAAAGAGAACAC 442
Db 1649 TTTTGCACATTTCCAGCCCTTTTAAATATCCACACAGCAAGCAACAAAGAGAACAC 1590

QY 443 AGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTGATGATGAGCCTGCCTGT 502
Db 1589 AGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTGATGATGAGCCTGCCTGT 1530

QY 503 GCCTGCTCCCGCTGTGAGGGAAGACATTAGAAAAATGATGTCTCTTAAGA 562
 Db 1529 GCTGTGCTCCCGCTGTGAGGGAAGACATTAGAAAAATGATGTCTCTTAAGA 1470
 QY 563 TGGGCAAGGAAACAGATCCCTGTGTGATTTATTTGAAACGGGATTACGATTTGAAT 622
 Db 1469 TGGGCAAGGAAACAGATCCCTGTGTGATTTATTTGAAACGGGATTACGATTTGAAT 1410
 QY 623 GAAGTCACAAAGTACATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGGCTT 682
 Db 1409 GAAGTCACAAAGTACATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGGCTT 1350
 QY 683 CACAAGACATGCACACAAACAAATGGAATCTGTATGACATGAGCAGCCAAAGCTGGGG 742
 Db 1349 CACAAGACATGCACACAAACAAATGGAATCTGTATGACATGAGCAGCCAAAGCTGGGG 1290
 QY 743 AGGAGATTAACCAAGGGGCAAGAGGTCAGGATTCCTGGCCCTGCTTAACCTGGCTTC 802
 Db 1289 AGGAGATTAACCAAGGGGCAAGAGGTCAGGATTCCTGGCCCTGCTTAACCTGGCTTC 1230
 QY 803 ATTAACCAATTCATTTCTATTTCTTAACCTCAAAACAAAGCTGTGTATCTGATCTC 862
 Db 1229 ATTAACCAATTCATTTCTATTTCTTAACCTCAAAACAAAGCTGTGTATCTGATCTC 1170
 QY 863 TAGGTTCCCTCTGGGGCCCAACATCTCCATATATCCAGCAGACATCTTTTAATATT 922
 Db 1169 TAGGTTCCCTCTGGGGCCCAACATCTCCATATATCCAGCAGACATCTTTTAATATT 1110
 QY 923 AGTTCCAGATCTGTCTGTGACCTTCTCACTAGATAATACATTTACTTTTGTTC 982
 Db 1109 AGTTCCAGATCTGTCTGTGACCTTCTCACTAGATAATACATTTACTTTTGTTC 1050
 QY 983 AAGACCTTCTGTGTGTCTGCTAATATATGATGATGATCTTTTCTTAAGAGATGTTCTG 1042
 Db 1049 AAGACCTTCTGTGTGTCTGCTAATATATGATGATGATCTTTTCTTAAGAGATGTTCTG 990
 QY 1043 GCCCAGGGATCTGTAAACAGCTGGGAAGCATCTCAAGATCTTCCAGGTTATCTTA 1102
 Db 989 GCCCAGGGATCTGTAAACAGCTGGGAAGCATCTCAAGATCTTCCAGGTTATCTTA 930
 QY 1103 CTAGCACACAGCATGATCTTAACGAGATGAATATATCAACATCATCTCAGTGTCT 1162
 Db 929 CTAGCACACAGCATGATCTTAACGAGATGAATATATCAACATCATCTCAGTGTCT 870
 QY 1163 TTGCCATACCTGAATTCATTTCCCACTTTTGTGCCATTCCTCAAGACCTCAAAATGTCA 1222
 Db 869 TTGCCATACCTGAATTCATTTCCCACTTTTGTGCCATTCCTCAAGACCTCAAAATGTCA 810
 QY 1223 TTCCATTAAATACAGGATTAACCTTTTAACTGGAAGAAATTCGAATCTTCAATG 1282
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 QY 1283 CAGCTATGGGAATTAATTAACATTTTGTTCACAGTGCAGAAAGATGACTAAGCTCTTA 1342
 Db 749 CAGCTATGGGAATTAATTAACATTTTGTTCACAGTGCAGAAAGATGACTAAGCTCTTA 690
 QY 1343 TCCCTCCCTTTGTTGATTTTTCAGATFAAAGTTAAAGTCTTACCTGTACTG 1402
 Db 689 TCCCTCCCTTTGTTGATTTTTCAGATFAAAGTCTTACCTGTACTG 630
 QY 1403 AGGCTGTATACAGC 1416
 Db 629 AGGCTGTATACAGC 616

; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Wang, Samuel X.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Bassols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Mantabe, Yoshihiro
 ; APPLICANT: Meagher, Madeleine Joy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.427C27
 ; CURRENT FILING DATE: 05/10/012, 896
 ; NUMBER OF SEQ ID NOS: 1011
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 470
 ; LENGTH: 2426
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-012-896-470
 Query Match 56.7%; Score 1154; DB 13; Length 2426;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 263 GGTGAGAAATTAAGAAAGCTGTGACTTTCATCTGAGGCAACATCTGTGAATG 322
 Db 1769 GGTGAGAAATTAAGAAAGCTGTGACTTTCATCTGAGGCAACATCTGTGAATG 1710
 QY 323 AGATTAATTAACATCACTAATAACAGCAATGCAATATTAATGTCTAAGTACATGT 382
 Db 1709 AGATTAATTAACATCACTAATAACAGCAATGCAATATTAATGTCTAAGTACATGT 1650
 QY 383 TTTTGACATTTCCAGCCCTTTAATATCCACACACAGAGAACGACAAAGGAAGCAC 442
 Db 1649 TTTTGACATTTCCAGCCCTTTAATATTCACACACAGAGAACGACAAAGGAAGCAC 1590
 QY 443 AGAGATCCCTGGAGAAATGCCCCGCCCATCTTGATCATGATGAGCTCGCCCTGT 502
 Db 1589 AGAGATCCCTGGAGAAATGCCCCGCCCATCTTGATCATGATGAGCTCGCCCTGT 1530
 QY 503 GCCTGTCCCGCTGTGAGAGGAAGACATTAAGAAATGAATGATGTCTCTTAAGGA 562
 Db 1529 GCCTGTCCCGCTGTGAGAGGAAGACATTAAGAAATGAATGATGTCTCTTAAGGA 1470
 QY 563 TGGGCAAGGAAACAGATCCCTGTGTGATTTATTTGAAACGGGATTACGATTTGAAT 622
 Db 1469 TGGGCAAGGAAACAGATCCCTGTGTGATTTATTTGAAACGGGATTACGATTTGAAT 1410
 QY 623 GAAGTCACAAAGTACATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGGCTT 682
 Db 1409 GAAGTCACAAAGTACATTTACCAATGAGAGAAAACAGAGAAAATCTTGATGGCTT 1350
 QY 683 CACAAGACATGCACACAAACAAATGGAATCTGTATGACATGAGCAGCCAAAGCTGGGG 742
 Db 1349 CACAAGACATGCACACAAACAAATGGAATCTGTATGACATGAGCAGCCAAAGCTGGGG 1290
 QY 743 AGGAGATTAACCAAGGGGCAAGAGGTCAGGATTCCTGGCCCTGCTTAACCTGGCTTC 802
 Db 1289 AGGAGATTAACCAAGGGGCAAGAGGTCAGGATTCCTGGCCCTGCTTAACCTGGCTTC 1230

RESULT 15
 US-10-012-896-470/C
 ; Sequence 470, Application US/10012896
 ; Publication No. US2002018351A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiaogchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.

QY 803 ATACCAATCATTTTCATATTTCTAACCCCTCAAAAACAAGCTGTGTATATCTGATCTC 862
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 Db 1229 ATACCAATCATTTTCATATTTCTAACCCCTCAAAAACAAGCTGTGTATATCTGATCTC 1170
 QY 863 TACGGTTCCTCTGGGCCCAACATTCATATATCCAGCCACACTCATTTTTTAATAT 922
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 Db 1169 TACGGTTCCTCTGGGCCCAACATTCATATATCCAGCCACACTCATTTTTTAATAT 1110
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 Db 629 AGGCTGTATACAGC 616

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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OLIGO_NUC
Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	222	10.9	654	28	AQ319247	AQ319247 RPCI11-10
4	214	10.5	226	10	BF858371	BF858371 RCS-FT019

C	5	214	10.5	394	28	AQ206972	AQ206972 HS-3238.B
C	6	213	10.5	332	10	BF858286	BF858286 RCS-FT019
C	7	198	9.7	282	10	BF373581	BF373581 MRO-FT017
C	8	167	8.2	167	10	BF373406	BF373406 IL2-FT015
C	9	147	7.2	856	9	AI557225	AI557225 PT2.1-15-
C	10	124	6.1	441	10	BF858890	BF858890 RCS-FT019
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C	18	26	1.3	437	10	BE763867	BE763867 RC4-NT005
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C	26	26	1.3	766	13	BU623156	BU623156 UT-H-FLI-
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C	29	26	1.3	847	9	AL530074	AL530074 AL530074
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C	31	26	1.3	931	12	BM047350	BM047350 603628473
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ALIGNMENTS

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DEFINITION
ACCESSION AA578773
VERSION AA578773.1 GI:2356957
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 402)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@email.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquí, M.D.
, Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbrrp/image/image.html

Insert Length: 565 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 373.
Location/Qualifiers
1.402

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/clone="IMAGE:953262"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCL_CGAP_Prl"
/note="Vector: PAMP10; Site.1: NotI; Site.2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into PAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

BASE COUNT 128 a 86 c 84 g 104 t

ORIGIN

Query Match 18.0%; Score 367; DB 9; Length 402;

Best Local Similarity 100.0%; Pred.No.3.4e-147; Mismatches 0; Indels 0; Gaps 0;

Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

595 TATTGACGGATTACAGATTGAAATGATGACAAAGTGAGCATTTACCATGAGAG 654
|||||
36 TATTGACGGATTACAGATTGAAATGATGACAAAGTGAGCATTTACCATGAGAG 95
655 AAACAGAGAGAAAATCTTGATGCTTCAACAAGATGCAACAAACAAATGGAATPACT 714
|||||
96 AAACAGAGAGAAAATCTTGATGCTTCAACAAGATGCAACAAACAAATGGAATPACT 155
715 GTGATGATGAGAGCGAGCGAGGAGGAGATTAACAGGCGGAGAGGTCAGAGATT 774
|||||
156 GTGATGATGAGAGCGAGCGAGGAGGAGATTAACAGGCGGAGAGGTCAGAGATT 215
775 GTGGCCCTGCTGCTTAACCTGTCATTAACCAATCATTTCTTAACCTCA 834
|||||
216 GTGGCCCTGCTGCTTAACCTGTCATTAACCAATCATTTCTTAACCTCA 275
835 AAACAAAGCTGTTGATATCTGATCTTAACGTTCTTCTGGCCCAACATTTCCATA 894
|||||
276 AAACAAAGCTGTTGATATCTGATCTTAACGTTCTTCTGGCCCAACATTTCCATA 335
895 TATCCAGCCACATCTATTTTATATTTAGTCCAGATCTGACTGTGACCTTTTACA 954
|||||
336 TATCCAGCCACATCTATTTTATATTTAGTCCAGATCTGACTGTGACCTTTTACA 395
955 CTGTAGA 961
|||||
396 CTGTAGA 402

RESULT 2
BF373619 290 bp mRNA linear EST 24-NOV-2000

LOCUS BF373619
DEFINITION MR0-FT0175-310800-106-h09 FT0175 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF373619
VERSION BF373619.1 GI:11335644

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 290)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

TITLE
JOURNAL
MEDLINE
PUBMED

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR06t2-MR0-FT0175-
310800-106-h09&t3=2000-08-31&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 290.
Location/Qualifiers
1.290

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0175"
/note="Organ: prostate.tumor; Vector: puc18; Site.1: SmaI; Site.2: SmaI; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 78 a 73 c 53 g 86 t

ORIGIN

Query Match 11.7%; Score 238; DB 10; Length 290;

Best Local Similarity 100.0%; Pred.No.1.6e-91; Mismatches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

740 GGGAGAGATTAACCAAGGGGAGAGGCTAGAGATTGTGGCCCTGCTTAACCTGTGG 799
|||||
21 GGGAGAGATTAACCAAGGGGAGAGGCTAGAGATTGTGGCCCTGCTTAACCTGTGG 80
800 TTCAATACCAAAATCATTTATATTTCTTAACCCCAAAAGAGCTGTAATATCTGAT 859
|||||
81 TTCAATACCAAAATCATTTATATTTCTTAACCCCAAAAGAGCTGTAATATCTGAT 140
860 CTCTACGGTTCCTTCTGGGCCCAACATTCATATATATCCAGCCACATCTTTAATA 919
|||||
141 CTCTACGGTTCCTTCTGGGCCCAACATTCATATATATCCAGCCACATCTTTAATA 200
920 TTAGTTCACAGATCTGATCTGACCTTTCTACACTGTAGAAATAATACATTTCTATT 977
|||||
201 TTAGTTCACAGATCTGATCTGACCTTTCTACACTGTAGAAATAATACATTTCTATT 258

RESULT 3
AO319247/c 654 bp DNA linear GSS 06-MAY-1999

LOCUS AO319247
DEFINITION RPII11-10814.TV RPII-11 Homo sapiens genomic clone RPII-11-10814,
genomic survey sequence.

ACCESSION AO319247
VERSION AO319247.1 GI:4052212

KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 654)
AUTHORS Adams M.D., Rounsley S.D., Zhao S., Bass S., Linher K., Golden K., Berry K., Granger D., Suh E., Wible C., de Jong P. and Venter J.C.
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: 77
Class: BAC ends.

FEATURES
Source Location/Qualifiers
1..654
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7541355"
/db_xref="taxon:9606"
/clone="RPCI-11-108L4"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC library"

BASE COUNT 213 a 100 c 139 g 202 t

ORIGIN
Query Match 10.9%; Score 222; DB 28; Length 654;
Best Local Similarity 100.0%; Pred. No. 1.1e-84;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1195 TGCACATTCACAGACCTCAAAAGTCAATTCATTAAATACACAGATTAACTTTT 1254
DB 654 TGCACATTCACAGACCTCAAAAGTCAATTCATTAAATACACAGATTAACTTTT 595
QY 1255 TTAACCTGGAAGAAATTCATGTTACATGACGATGGAATTAATTCATATTTGTT 1314
DB 594 TTAACCTGGAAGAAATTCATGTTACATGACGATGGAATTAATTCATATTTGTT 535
QY 1315 TCCAGTGCAGAGTACTAAGTCTTATCCCTCCCTTTGTTGATTTTTCACGTA 1374
DB 534 TCCAGTGCAGAGTACTAAGTCTTATCCCTCCCTTTGTTGATTTTTCACGTA 475
QY 1375 TAAAGTTAAATGCTTACCTTTGATCTGAGGCTGTATACAGC 1416
DB 474 TAAAGTTAAATGCTTACCTTTGATCTGAGGCTGTATACAGC 433

RESULT 4
BF858371/c 226 bp mRNA linear EST 16-JAN-2001
LOCUS BF858371
DEFINITION RC5-FT0193-211100-012-E11 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF858371
VERSION BF858371.1 GI:12246115
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 226)
AUTHORS Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R., Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H., Brunstein A., deoliveira P.S., Bucher P., Jongeneel C.V., O'Hare

TITLE 'M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and Simpson A.J.
JOURNAL Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC5&c2=RC5-FT0193-211100-012-E11&t3=2000-11-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 226.

FEATURES
Source Location/Qualifiers
1..226
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0193"
/note="Organ: prostate_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 79 a 29 c 59 g 59 t

ORIGIN
Query Match 10.5%; Score 214; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.7e-81;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 787 CCTAAGTGTGCTTCATACCAATTCATATTTCTAACCCTCAAAAGAGCTGT 846
DB 226 CCTAAGTGTGCTTCATACCAATTCATATTTCTAACCCTCAAAAGAGCTGT 167
QY 847 TGTAAATATCTGATCTCTACGGTCTTCTGGGCCCAACATTCATATATCCAGCCACA 906
DB 166 TGTAAATATCTGATCTCTACGGTCTTCTGGGCCCAACATTCATATATCCAGCCACA 107
QY 907 CTCATTTTAAATATAGTTCAGATGCTGTCGACCTTCTACACTGTAGATATAC 966
DB 106 CTCATTTTAAATATAGTTCAGATGCTGTCGACCTTCTACACTGTAGATATAC 47
QY 967 ATTACTCATTTTGTCAAAAGACCTTCGTGTGC 1000
DB 46 ATTACTCATTTTGTTCAAAGACCTTCGTGTGC 13

RESULT 5
AQ206972/c 394 bp DNA linear GSS 17-SEP-1998
LOCUS AQ206972
DEFINITION HS_3238_B1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=21 Row=N, genomic survey sequence.
ACCESSION AQ206972
VERSION AQ206972.1 GI:3617542
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 394)

AUTHORS Mahatras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahatras GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3238 row: N column: 21
Class: BAC ends
High quality sequence stop: 394.
Location/Qualifiers
1. .394
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3238 Col=21 Row=N"
/sex="male"
/clone_lib="CIR Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 134 a 62 c 93 g 103 t 2 others

ORIGIN

Query Match 10.5%; Score 214; DB 28; Length 394;
Best Local Similarity 99.4%; Pred. No. 3,4e-81;
Matches 314; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 883 ACATTTCATATATCCAGCACATCTTTTAAATTTAGTCCAGATCTGACTGT 942
DB 381 ACATTTCATATATCCAGCACATCTTTTAAATTTAGTCCAGATCTGACTGT 322

QY 943 GACCTTTACACTAGATAGATATACATTTTGTTCAGAGACCTTCGTGCTG 1002
DB 321 GACCTTTACACTAGATAGATATACATTTTGTTCAGAGACCTTCGTGCTG 262

QY 1003 CCTAATATAGTACTGCTGCTTTTCTTAAGAGAGTCTGCGCCAGGGATCTGTGACA 1062
DB 261 CCTAATATAGTACTGCTGCTTTTCTTAAGAGAGTCTGCGCCAGGGATCTGTGACA 202

QY 1063 GGCTGGAGACATCTCAAGATCTTTCAGAGGTTATCTACTAGCACACAGCATGATCAT 1122
DB 201 GGCTGGAGACATCTCAAGATCTTTCAGAGGTTATCTACTAGCACACAGCATGATCAT 142

QY 1123 TACGAGTGAATATATCAACATCATCTCAGTGTCTTTCGCCATCTGAATTCAT 1182
DB 141 TACGAGTGAATATATCAACATCATCTCAGTGTCTTTCGCCATCTGAATTCAT 82

QY 1183 TTCCCACTTTGTGCC 1198
DB 81 TTCCCACTTTGTGCC 66

RESULT 6
BF858286 332 bp mRNA linear EST 16-JAN-2001
LOCUS BF858286
DEFINITION RC5-FT0193-201100-012-D06 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF858286
VERSION BF858286.1 GI:12246030
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 332)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsushima,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&tl=RC5-FT0193-201100-012-D06&tl=2000-11-20&tl=1)
Seq primer: puc 18 forward
High quality sequence stop: 332.
Location/Qualifiers
1. .332
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0193"
/note="Organ: prostate,tumor; Vector: puc18; Site:1; SmaI; Site:2; SmaI; A mini-library was made by cloning products derived from ORESNES PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 90 a 84 c 64 g 94 t

ORIGIN

Query Match 10.5%; Score 213; DB 10; Length 332;
Best Local Similarity 100.0%; Pred. No. 9,5e-81;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 741 GGAGGAGATACACAGGGGACAGAGGTCAGATTCGGCCCTGCTTAACATGTGCGT 800
DB 61 GGAGGAGATACACAGGGGACAGAGGTCAGATTCGGCCCTGCTTAACATGTGCGT 120

QY 801 TCATTAACCAATCATTTCTAATCTTCAACCTCAAAACAAAGCTGTGTAATATCGATC 860
DB 121 TCATTAACCAATCATTTCTAATCTTCAACCTCAAAACAAAGCTGTGTAATATCGATC 180

QY 861 TCTACGGTCTCTTCTGGGCCAATCTTCTCAATATATCCAGCACACTATTTTAAAT 920
DB 181 TCTACGGTCTCTTCTGGGCCAATCTTCTCAATATATCCAGCACACTATTTTAAAT 240

QY 921 TTAGTCCCAAGATCTGACTGATGACCTTCTAC 953
DB 241 TTAGTCCCAAGATCTGACTGATGACCTTCTAC 273

RESULT 7
BF373581 282 bp mRNA linear EST 24-NOV-2000
LOCUS BF373581
DEFINITION MRO-FT0175-210800-101-d05 FT0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF373581
VERSION BF373581.1 GI:11335606
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 282)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR0&t2=MR0-FT0175-210800-101-d05&t3=2000-08-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 35
High quality sequence stop: 282.

FEATURES
SOURCE
1..282
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0175"
/note="Organ: prostate,tumor; Vector: puc18; Site:1; Smai: Site:2; Smai: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 85 a 51 c 70 g 76 t
ORIGIN

Query Match 9.7%; Score 198; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.9e-74;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 753 CACGGGACAGAGGTCAGAGTTCGGCCCTGCGCTTAAGTGCCTTCAATACCAAT 812
Db |||||||
Oy 262 CACGGGACAGAGGTCAGAGTTCGGCCCTGCGCTTAACTGTGCTTCAATACCAAT 203
Db |||||||
Oy 813 CATTTCATATTTCTAACCCCAAAAGAGCTGTGTATATCTGATCTACAGGTTCT 872
Db |||||||
Oy 202 CATTTCATATTTCTAACCCCAAAAGAGCTGTGTATATCTGATCTACAGGTTCT 143
Db |||||||
Oy 873 TCTGGGCCCCAATTTCTCATATATCCAGCACACTATTTTAAATTTAGTCCCGA 932
Db |||||||
Oy 142 TCTGGGCCCCAATTTCTCATATATCCAGCACACTATTTTAAATTTAGTCCCGA 83
Db |||||||
Oy 933 TCTGTACTGTACCTTTC 950
Db |||||||
Oy 82 TCTGTACTGTACCTTTC 65

RESULT 8
BF373406 167 bp mRNA linear EST 24-NOV-2000
LOCUS BF373406
DEFINITION BF373406
ACCESSION BF373406
VERSION BF373406.1 GI:11335431
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 167)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=IL2&t2=IL2-FT0159-070800-120-H01&t3=2000-08-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 167.

FEATURES
SOURCE
1..167
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0159"
/note="Organ: prostate,tumor; Vector: puc18; Site:1; Smai: Site:2; Smai: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 47 a 38 c 49 g 33 t
ORIGIN

Query Match 8.2%; Score 167; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 7.2e-61;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 419 CACAGGAACCAAAAGAGACACAGATCCCTGGGGAATGCCGCCGCATCTTG 478
Db |||||||
Oy 1 CACAGGAACCAAAAGAGACACAGATCCCTGGGGAATGCCGCCGCATCTTG 60
Db |||||||
Oy 479 GGTATGATGATGAGCGCTCGCCCTGCGCGTGTGAGGGAAGACATTAGAAA 538
Db |||||||
Oy 61 GGTATGATGATGAGCGCTCGCCCTGCGCGTGTGAGGGAAGACATTAGAAA 120
Db |||||||
Oy 539 TGAATTCATGTTCTTAAAGATGGCAGAAACAGATCTGTT 585
Db |||||||
Oy 121 TGAATTCATGTTCTTAAAGATGGCAGAAACAGATCTGTT 167
Db |||||||

RESULT 9
A1557225 856 bp mRNA linear EST 09-AUG-1999
LOCUS A1557225
DEFINITION PT2.1.15_B05.r tumor2 Homo sapiens cDNA 3', mRNA sequence.
ACCESSION A1557225
VERSION A1557225.1 GI:4489588
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
Huang, G.M., Ng, W.L., Farkas, J., He, L., Liang, H.A., Gordon, D., Yu, J.

	a	c	g	t	others
BASE COUNT	237	191	180	214	34
ORIGIN					

Query Match 7.2%; Score 147; DB 9; Length 856;
Best Local Similarity 100.0%; Pred. No. 2,5e-52;
Matches 147; Conservative 0; Mismatches 0; Indels 0;
Gaps 0

QY	1564	TCTGAAATGATGAAAGTTTGGATTAAGTTGACATCTTACTTCTATCGAAGAACAGGAC	1622
	251	TCTGGAATGATGTAAGAGTTTGGAAATTAAGTTGACTTCTTACTTCATGCAAGAAAGGAC	310
QY	1624	CATATGAGATTCATCATCATGACATGAGACAGCAAAATCTTAAAGTGTAAATTTGATTTAACA	168
	311	CATATGAGATTCATCATCATGACATGAGACAGCAAAATCTTAAAGTGTAAATTTGATTTAACA	370
QY	1684	GTTTAGATTAATATATGAAATGCACA	1710
	371	GTTTAGATTAATATATGAAATGCACA	397

RESULT	10
BFE58890/c	
LOCUS	BFE58890 441 bp mRNA linear EST_16-JAN-2001
DEFINITION	RCS-FR0194-071200-023-G11 FT0194 Homo sapiens CDNA, mRNA sequence.
ACCESSION	BFE58890
VERSION	BFE58890.1 GI:12246634
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

BASE COUNT	142 a	67 c	97 g	135 t
ORIGIN				

Query Match	6.18;	Score 124;	DB 10;	Length 441;
Best local Similarity	100.0%;	Pred. No. 2.3e+42;		
Matches 124;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Accession	Sequence	Position
47		103
48		103
49		103
50		103
51		103
52		103
53		103
54		103
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166		103
167		103
168		103
169		103
170		103
171		

RESULT	11
BQ292550	BQ292550
LOCUS	572 bp mRNA linear EST 15-MAY-2002
DEFINITION	PMO-ANO087-240501-019-a06 ANO087 Homo sapiens CDNA, mRNA sequence.
ACCESSION	BQ292550
VERSION	BQ292550.1 GI:20801500
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&tc2=PMO-AN0087-240501-019-a06&tc3=2001-05-24&tc4=1)
Seq primer: puc 18 forward
High quality sequence stop: 572.

FEATURES

Location/Qualifiers

1..572

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_id="AN0087"
/note="Organ: amnion-normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 150 a 90 c 169 g 163 t

ORIGIN

Query Match 4.9%; Score 99; DB 13; Length 572;

Best Local Similarity 100.0%; Pred. No. 1.3e-31;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGAAGCTGCATCGAAGAAACAGAGGAGATTGTGCTGCAGCCGAGGAGACAG 60

Db 116 AGAAGCTGCATCGAAGAAACAGAGGAGATTGTGCTGCAGCCGAGGAGACAG 175

OY 61 GAAGATCTGCATGCTGGGAAAGACCTGATACACAGAG 99

Db 176 GAAGATCTGCATGCTGGGAAAGACCTGATACACAGAG 214

RESULT 12

AI557495

LOCUS AI557495 657 bp mRNA linear EST 09-AUG-1999

DEFINITION PT2.1.7.H12.r tumor2 Homo sapiens cDNA 3', mRNA sequence.

ACCESSION AI557495

VERSION AI557495.1 GI:4489858

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 657)

Authors Huang, G.M., Ng, W.L., Parkas, J., He, L., Liang, H.A., Gordon, D., Yu, J.

And Hood, L.

Prostate cancer expression profiling by cDNA sequencing analysis

Genomics 59 (2), 178-186 (1999)

JOURNAL 99339982

MEDLINE 10409429

PUBMED

COMMENT

Contact: Guyang Matthew Huang

Leroy Hood

University of Washington

Department of Molecular Biotechnology, Box 357730, University of

Washington, Seattle, WA 98195

Tel: 5106280100

Fax: 5106280108

Email: huangm@yahoo.com.

Location/Qualifiers

1..657

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_id="tumor2"

/note="Organ: Prostate; Vector: pBluescript; Directional

BASE COUNT 179 a 112 c 153 g 166 t 47 others

ORIGIN

Query Match 4.2%; Score 86; DB 9; Length 657;
Best Local Similarity 100.0%; Pred. No. 5.3e-26;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CAGAAAACAGAGGCGGAGATTGTGCTGCAGCCGAGGAGACCGAAGATCTGCAT 72

Db 14 CAGAAAACAGAGGCGGAGATTGTGCTGCAGCCGAGGAGACCGAAGATCTGCAT 73

OY 73 GGTGGGAAGACCTGATATACAGAG 98

Db 74 GGTGGGAAGACCTGATATACAGAG 99

RESULT 13

AO246715

LOCUS AO246715 451 bp DNA linear GSS 06-OCT-1998

DEFINITION HS-2059_B2_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2059 Col-16 Row-J, genomic survey sequence.

ACCESSION AO246715

VERSION AO246715.1 GI:3696897

KEYWORDS GSS.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 451)

Authors Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and

Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURN. 99380589

MEDLINE 10449764

PUBMED

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 2059 row: J column: 16

Class: BAC ends

High quality sequence stop: 451.

Location/Qualifiers

1..451

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate-2059 Col-16 Row-J"

/sex="male"

/clone_id="CIT Approved Human Genomic Sperm Library D"

/note="Organ: sperm; Vector: pBeloBAC11; BAC clones in

E-Coli DH10B"

BASE COUNT 133 a 101 c 86 g 130 t 1 others

ORIGIN

Query Match 2.1%; Score 43; DB 28; Length 451;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1910 TTGGCAATCATCTGCTCATCTTCTCCACCTTGAGATGCT 1952

Db 26 TTGGCAATCATCTGCTCATCTTCTCCACCTTGAGATGCT 68

RESULT	14
LOCUS	R01974
DEFINITION	R01974 305 bp mRNA linear EST 31-MAR-1995 ye85f01.r1 Soares fetal liver spleen INFLS Homo sapiens CDNA clone IMAGE:124537 5', mRNA sequence.
ACCESSION	R01974
VERSION	R01974.1 GI:751710
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 305) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman, M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maitra,M., Parsons,J., Rifkin,L., Roellig,T., Soares,M., Tan,F., Trevisakis,E., Waterston, T., Williamson,A., Woldmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished
AUTHORS	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 850L, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 864
TITLE	High quality sequence stops: 200 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 864 Std Error: 0.00 Seq primer: M13RP1
JOURNAL	High quality sequence stop: 200. Location/Qualifiers 1..305
COMMENT	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:477082" /db_xref="taxon:9606" /clone="IMAGE:124537" /sex="male" /dev_stage="20 week post conception fetus" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares fetal liver spleen INFLS" /note="Organ: Liver and Spleen; Vector: p7r3D (Pharmacia) with a modified polylinker; Site_1: Pac I - oligo(dT) primer 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAGAAATTAATTGAAGATCTTTTGTTCCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p7r3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	76 a 68 c 69 g 86 t 6 others
ORIGIN	
Query Match	1.3%; Score 26; DB 14; Length 305;
Best Local Similarity	100.0%; Pred. No. 4.4;
Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1142 TCACATCATCCTCGAGTGCTTTGCC 1167
Db	20 TCACATCATCCTCGAGTGCTTTGCC 45
RESULT	15
LOCUS	T79384 371 bp mRNA linear EST 15-MAR-1995
DEFINITION	ydf4g09.r1 Soares fetal liver spleen INFLS Homo sapiens CDNA clone IMAGE:114016 5', mRNA sequence.
ACCESSION	T79384
VERSION	T79384.1 GI:697893
KEYWORDS	EST.

SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 311)
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Ritzkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Woldmann,P. and Wilson,R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished
COMMENT	Other_ESTs: yd74g09.s1 Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 1236 High quality sequence stops: 275 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 1236 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 275. Location/Qualifiers 1..371 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:469633" /db_xref="taxon:9606" /clone="IMAGE:114016" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares fetal liver spleen INFLS" /note="Organ: Liver and Spleen; Vector: pTV73D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACGGAGAAATTAATTAAAGACTCTTTTTTTTTTTTTT 3'] , double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTV73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	105 a 81 c 70 g 113 t 2 others
ORIGIN	
Query Match	1.3%; Score 26; DB 14; Length 371;
Best Local Similarity	100.0%; Prid. No. 4.3;
Matches 26; Conservative 0; Mismatches 0; Gaps 0;	
OY	1142 TCACATCATCCTCAGTGCTCTTCCC 1167
db	
127 TCAACATCATCCTCAGTGCTCTTCCC 152	

Search completed: September 27, 2003, 11:35:43
Job time : 4278.73 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2003, 19:57:16 : Search time 3185 Seconds
(without alignments) 655.068 Million cell updates/sec

Title: US-09-402-713A-2

Perfect score: 51

Sequence: 1 MFHISSPFYPHPTQEAQKE.....HLGSSMSLALCLVPIVREGH 51

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 segs, 20454813386 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5773124

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-O=/cgn2_1/USPRO.spool/US09402713/runat_26092003_143059_16960/app-query.fasta_1.199
-DB=genembl -QPM=fastap -SUFFIX=olig.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCOR=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEARSIDE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09402713_GCGN1_1_3508_6runat_26092003_143059_16960 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESUBSTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Genembl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_com:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	812	6 AR261039	AR261039 Sequence
2	51	100.0	812	6 AR278570	AR278570 Sequence
3	51	100.0	812	6 AX1065207	AX1065207 Sequence
4	51	100.0	812	6 AX106690	AX106690 Sequence
5	51	100.0	812	6 AX140981	AX140981 Sequence
6	51	100.0	812	6 AX200841	AX200841 Sequence
7	51	100.0	812	6 AX267497	AX267497 Sequence
8	51	100.0	820	6 BD082484	BD082484 PCA3, PCA
9	51	100.0	1872	6 BD082483	BD082483 PCA3, PCA
10	51	100.0	2037	6 BD082482	BD082482 PCA3, PCA
11	51	100.0	2229	6 AR261037	AR261037 Sequence
12	51	100.0	2229	6 AR278568	AR278568 Sequence
13	51	100.0	2229	6 AX1066205	AX1066205 Sequence
14	51	100.0	2229	6 AX106688	AX106688 Sequence
15	51	100.0	2229	6 AX140979	AX140979 Sequence
16	51	100.0	2229	6 AX200839	AX200839 Sequence
17	51	100.0	2229	6 AX267495	AX267495 Sequence
18	51	100.0	2426	6 AR261038	AR261038 Sequence
19	51	100.0	2426	6 AR278569	AR278569 Sequence
20	51	100.0	2426	6 AX1066206	AX1066206 Sequence
21	51	100.0	2426	6 AX106689	AX106689 Sequence
22	51	100.0	2426	6 AX140980	AX140980 Sequence
23	51	100.0	2426	6 AX200840	AX200840 Sequence
24	51	100.0	2426	6 AX267496	AX267496 Sequence
25	51	100.0	3112	6 AR261036	AR261036 Sequence
26	51	100.0	3112	6 AR278567	AR278567 Sequence
27	51	100.0	3112	6 AX1066204	AX1066204 Sequence
28	51	100.0	3112	6 AX106687	AX106687 Sequence
29	51	100.0	3112	6 AX140978	AX140978 Sequence
30	51	100.0	3112	6 AX200838	AX200838 Sequence
31	51	100.0	3112	6 AX267494	AX267494 Sequence
32	51	100.0	3582	6 BD082485	BD082485 PCA3, PCA
33	51	100.0	3923	6 AR261166	AR261166 Sequence
34	51	100.0	3923	6 AR278697	AR278697 Sequence
35	51	100.0	3923	6 AX200988	AX200988 Sequence
36	51	100.0	3923	6 AX267716	AX267716 Sequence
37	51	100.0	3923	6 AF103907	AF103907 Homo sapi
38	43	84.3	718	6 AR260894	AR260894 Sequence
39	43	84.3	718	6 AR260894	AR260894 Sequence
40	43	84.3	718	6 AR278425	AR278425 Sequence
41	43	84.3	718	6 AX1066203	AX1066203 Sequence
42	43	84.3	718	6 AX106532	AX106532 Sequence
43	43	84.3	718	6 AX140823	AX140823 Sequence
44	43	84.3	718	6 AX200683	AX200683 Sequence
45	43	84.3	718	6 AX267339	AX267339 Sequence

RESULT 1

ALIGNMENTS

AR261039/c
LOCUS AR261039 812 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 471 from patent US 6321716.
ACCESSION AR261039
VERSION AR261039.1 GI:28071802
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 812)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 471 27-NOV-2001;
FEATURES
source
1. 812
Location/Qualifiers
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-402-713A-2 (1-51) x AR261039 (1-812)

QY 1 MetPheLeuHisIleSerSerProphelysTyrProHisThrGlnGluAaGlnLysGlu 20
Db 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAAAGCAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTGGGTCAATGATGAGCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 484 CTGTGCTGCTGCCCTGTGTGAGGAGAGACAT 452

RESULT 2
AR278570/c
LOCUS AR278570 812 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 471 from patent US 6512094.
ACCESSION AR278570
VERSION AR278570.1 GI:29712816
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 812)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalis,M.D., Fanger,G.R., Better,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 471 28-JAN-2003;
FEATURES
source
1. 812
Location/Qualifiers
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-402-713A-2 (1-51) x AR278570 (1-812)

QY 1 MetPheLeuHisIleSerSerProphelysTyrProHisThrGlnGluAaGlnLysGlu 20
Db 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAAAGCAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTGGGTCAATGATGAGCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 484 CTGTGCTGCTGCCCTGTGTGAGGAGAGACAT 452

RESULT 3
AX106207/c
LOCUS AX106207 812 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 345 from Patent WO0125273.
ACCESSION AX106207
VERSION AX106207.1 GI:13921896
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1
AUTHORS Skeiky,Y.A., Xu,J., Cheever,M.A. and Reed,S.G.
TITLE Compositions and methods for wtl specific immunotherapy
JOURNAL Patent: WO 0125273-A 345 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. 812
Location/Qualifiers
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-402-713A-2 (1-51) x AX106207 (1-812)

QY 1 MetPheLeuHisIleSerSerProphelysTyrProHisThrGlnGluAaGlnLysGlu 20
Db 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAAAGCAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTGGGTCAATGATGAGCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
Db 484 CTGTGCTGCTGCCCTGTGTGAGGAGAGACAT 452

RESULT 4
AX106690/c
LOCUS AX106690 812 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 471 from Patent WO0125272.
ACCESSION AX106690
VERSION AX106690.1 GI:13922355
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1
AUTHORS Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE Compositions and methods for wtl specific immunotherapy
JOURNAL Patent: WO 0125272-A 471 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. 812
Location/Qualifiers
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0125272-A 471 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..812
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713A-2 (1-51) x AX106690 (1-812)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
Db 604 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAACAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCGACATCTTGGGTCAATCATGATGAGCCTCC 485

QY 41 LeuCysLeuValProLeuValArgGluLysHis 51
Db 484 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 452

RESULT 5
AX140981 812 bp DNA linear PAT 31-MAY-2001
LOCUS AX140981
DEFINITION Sequence 471 from Patent WO0134802.
ACCESSION AX140981
VERSION AX140981.1 GI:14281078
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0134802-A 471 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..812
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713A-2 (1-51) x AX140981 (1-812)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
Db 604 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAACAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCGACATCTTGGGTCAATCATGATGAGCCTCC 485

QY 41 LeuCysLeuValProLeuValArgGluLysHis 51
Db 484 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 452

RESULT 7
AX267497 812 bp DNA linear PAT 26-OCT-2001
LOCUS AX267497
DEFINITION Sequence 471 from Patent WO0173032.
ACCESSION AX267497
VERSION AX267497.1 GI:16516261
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.

Db 604 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAACAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCGACATCTTGGGTCAATCATGATGAGCCTCC 485

QY 41 LeuCysLeuValProLeuValArgGluLysHis 51
Db 484 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 452

RESULT 6
AX200841 812 bp DNA linear PAT 29-AUG-2001
LOCUS AX200841
DEFINITION Sequence 471 from Patent WO0151633.
ACCESSION AX200841
VERSION AX200841.1 GI:15390744
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skelky,Y.A., Wang,A. and Mesghar,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0151633-A 471 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..812
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:
Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713A-2 (1-51) x AX200841 (1-812)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
Db 604 ATGTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAACAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 544 GCACAGAGATCCCTGGGAGAAATGCCCGCCGACATCTTGGGTCAATCATGATGAGCCTCC 485

QY 41 LeuCysLeuValProLeuValArgGluLysHis 51
Db 484 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 452

RESULT 7
AX267497 812 bp DNA linear PAT 26-OCT-2001
LOCUS AX267497
DEFINITION Sequence 471 from Patent WO0173032.
ACCESSION AX267497
VERSION AX267497.1 GI:16516261
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.

TITLE
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T., and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL
Patent: WO 0173032-A 471 04-OCT-2001;
CORIXA CORPORATION (US)

FEATURES
source
1. .812
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN

Alignment Scores:

Pred. No.: 2.37e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713a-2 (1-51) x AX267497 (1-812)

QY 1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAglInLysGlu 20
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Db 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGAA 545
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QY 21 AlaGlnArgSerLeuGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||
Db 544 GCACAGAGATCCCTGGAGAAATGCCGCGCCATCTGGTCATGATGAGACCTCGCC 485
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QY 41 LeuCysLeuValProLeuValArgGluGlnHis 51
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Db 484 CTGTGCTGTGTCCTGTTGTGAGGAGAGACAT 452
|||||

RESULT 8
LOCUS BD082484 820 bp DNA linear PAT 27-AUG-2002
DEFINITION PCA3, PCA3 genes, and methods of use.
ACCESSION BD082484
VERSION BD082484.1 GI:22628094
KEYWORDS JP 2001522240-A/3.
SOURCE JP 2001522240-A/3.
ORGANISM Mastadenovirus
Mastadenovirus
Virus; dsDNA viruses, no RNA stage; Adenoviridae.

REFERENCE 1 (bases 1 to 820)
AUTHORS Bussemakers, M.J.G.
TITLE PCA3, PCA3 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 3 13-NOV-2001;
DIAGNOCURE INC

COMMENT
PN JP 2001522240-A/3

PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC
C12Q1/68,
PC G01N33/577, A61K39/395, A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.

FEATURES
source
1. .820
Location/Qualifiers
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"

BASE COUNT 262 a 169 c 191 g 198 t
ORIGIN

Alignment Scores:

Pred. No.: 2.38e-44 Length: 820
Score: 51.00 Matches: 51

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713a-2 (1-51) x BD082484 (1-820)

QY 1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAglInLysGlu 20
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Db 214 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGAA 273
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QY 21 AlaGlnArgSerLeuGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||
Db 274 GCACAGAGATCCCTGGAGAAATGCCGCGCCATCTGGTCATGATGAGACCTCGCC 333
|||||
QY 41 LeuCysLeuValProLeuValArgGluGlnHis 51
|||||
Db 334 CTGTGCTGTGTCCTGTTGTGAGGAGAGACAT 366
|||||

RESULT 9
LOCUS BD082483 1872 bp DNA linear PAT 27-AUG-2002
DEFINITION PCA3, PCA3 genes, and methods of use.
ACCESSION BD082483
VERSION BD082483.1 GI:22628093
KEYWORDS JP 2001522240-A/2.
SOURCE JP 2001522240-A/2.
ORGANISM Mastadenovirus
Mastadenovirus
Virus; dsDNA viruses, no RNA stage; Adenoviridae.

REFERENCE 1 (bases 1 to 1872)
AUTHORS Bussemakers, M.J.G.
TITLE PCA3, PCA3 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 2 13-NOV-2001;
DIAGNOCURE INC

COMMENT
PN JP 2001522240-A/2

PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC
C12Q1/68,
PC G01N33/577, A61K39/395, A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.

FEATURES
source
1. .1872
Location/Qualifiers
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"

BASE COUNT 567 a 389 c 369 g 539 t 8 others
ORIGIN

Alignment Scores:

Pred. No.: 4.51e-44 Length: 1872
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-402-713a-2 (1-51) x BD082483 (1-1872)

QY 1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAglInLysGlu 20
|||||
Db 214 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGAA 273
|||||
QY 21 AlaGlnArgSerLeuGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||
Db 274 GCACAGAGATCCCTGGAGAAATGCCGCGCCATCTGGTCATGATGAGACCTCGCC 333
|||||
QY 41 LeuCysLeuValProLeuValArgGluGlnHis 51
|||||

DB 334 CTGTGCTGTGTCGCCGCTTGTGAGGAGACAT 366

RESULT 10
BD082482

LOCUS BD082482 2037 bp DNA linear PAT 27-AUG-2002

DEFINITION PC3, PCA3 genes, and methods of use.

ACCESSION BD082482

VERSION BD082482.1 GI:22628092

KEYWORDS JP 2001522240-A/1.

SOURCE Mastadenovirus

ORGANISM Mastadenovirus

REFERENCE 1 (bases 1 to 2037)
Virus; dsDNA viruses, no RNA stage; Adenoviridae.
AUTHORS Bussemakers, M.J.G.
TITLE PC3, PCA3 genes, and methods of use
JOURNALS Patent: JP 2001522240-A 1 13-NOV-2001;
DINGNOURE INC SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES
COMMENT PN JP 2001522240-A/1
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC
C12O1/68,
PC G01N33/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH key Location/Qualifiers
FT CDS Location/Qualifiers
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/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"

BASE COUNT 622 a 426 c 406 g 575 t 8 others

ORIGIN

Alignment Scores:
Pred. No.: 4.82e-44 Length: 2037
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x BD082482 (1-2037)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
|||||
DB 379 ATGTTTTCGACATTTCCAGCCCTTTAAATATCCACACACAGAGCAACAAAGAA 438

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||
DB 439 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTATCGATGAGCCTCGCC 498

QY 41 LeuCysLeuValProLeuValArgGlnGlyHis 51
|||||
DB 499 CTGTGCTGTGTCGCCGCTTGTGAGGAGACAT 531

RESULT 11
AR261037/c 2229 bp DNA linear PAT 29-JAN-2003

LOCUS AR261037

DEFINITION Sequence 469 from patent US 6321716.

ACCESSION AR261037

VERSION AR261037.1 GI:28071800

KEYWORDS

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2229)
Mashiki, Z., and Harada, J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 469 27-NOV-2001;

FEATURES
source Location/Qualifiers
1..2229
/organism="unknown"

BASE COUNT 654 a 447 c 481 g 647 t

ORIGIN

Alignment Scores:
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x AR261037 (1-2229)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
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DB 1659 ATGTTTTCGACATTTCCAGCCCTTTAAATATCCACACACAGAGCAACAAAGAA 1600

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||
DB 1599 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTATCGATGAGCCTCGCC 1540

QY 41 LeuCysLeuValProLeuValArgGlnGlyHis 51
|||||
DB 1539 CTGTGCTGTGTCGCCGCTTGTGAGGAGACAT 1507

RESULT 12
AR278568/c 2229 bp DNA linear PAT 10-APR-2003

LOCUS AR278568

DEFINITION Sequence 469 from patent US 6512094.

ACCESSION AR278568

VERSION AR278568.1 GI:29712814

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2229)
Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Reltter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A.W.,
Hepler, W.T., and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 469 28-JAN-2003;
FEATURES
source Location/Qualifiers
1..2229
/organism="unknown"

BASE COUNT 654 a 447 c 481 g 647 t

ORIGIN

Alignment Scores:
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-402-713a-2 (1-51) x AR278568 (1-2229)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu 20
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DB 1659 ATGTTTTCGACATTTCCAGCCCTTTAAATATCCACACACAGAGCAACAAAGAA 1600

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
|||||
DB 1599 GCACAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGTATCGATGAGCCTCGCC 1540

QY 41 LeuCysLeuValProLeuValArgGlnGlyHis 51
|||||
DB 1539 CTGTGCTGTGTCGCCGCTTGTGAGGAGACAT 1507

RESULT 13
LOCUS AX106205/c 2229 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 343 from Patent WO0125273.
ACCESSION AX106205
VERSION AX106205.1 GI:13921894
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Skelky,Y.A., Xu,J., Cheever,M.A. and Reed,S.G.
TITLE Compositions and methods for wt1 specific immunotherapy
JOURNAL Patent: WO 0125273-A 343 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
Alignment Scores:
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-402-713a-2 (1-51) x AX106205 (1-2229)
QY 1 MetPhleuHisIleSerSerProphelysTYrProHisThrgInuIaGlnySgu 20
DB 1659 ATGTTTTCACATTTCCAGCCCCCTTAATATCCACACACAGGAGCAAAAGGAA 1600
QY 21 AlaGlnArgSerLeuGlyLumetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 1599 GCACAGAGATCCCTGGAGAAATGCCGCGCCGACATCTGGTGCATGATGAGCCTCGCC 1540
QY 41 LeuCySLeuValProLeuValArgGluGlyHis 51
DB 1539 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 1507
RESULT 14
LOCUS AX106688/c 2229 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 469 from Patent WO0125272.
ACCESSION AX106688
VERSION AX106688.1 GI:13922353
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Xu,J., Skelky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0125272-A 469 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..2229
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
Alignment Scores:
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-402-713a-2 (1-51) x AX106688 (1-2229)
QY 1 MetPhleuHisIleSerSerProphelysTYrProHisThrgInuIaGlnySgu 20
DB 1659 ATGTTTTCACATTTCCAGCCCCCTTAATATCCACACACAGGAGCAAAAGGAA 1600
QY 21 AlaGlnArgSerLeuGlyLumetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 1599 GCACAGAGATCCCTGGAGAAATGCCGCGCCGACATCTGGTGCATGATGAGCCTCGCC 1540
QY 41 LeuCySLeuValProLeuValArgGluGlyHis 51
DB 1539 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 1507
Search completed: September 26, 2003, 21:01:01
Job time : 3188 secs

Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-402-713a-2 (1-51) x AX106688 (1-2229)
QY 1 MetPhleuHisIleSerSerProphelysTYrProHisThrgInuIaGlnySgu 20
DB 1659 ATGTTTTCACATTTCCAGCCCCCTTAATATCCACACACAGGAGCAAAAGGAA 1600
QY 21 AlaGlnArgSerLeuGlyLumetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 1599 GCACAGAGATCCCTGGAGAAATGCCGCGCCGACATCTGGTGCATGATGAGCCTCGCC 1540
QY 41 LeuCySLeuValProLeuValArgGluGlyHis 51
DB 1539 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 1507
RESULT 15
LOCUS AX140979/c 2229 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 469 from Patent WO0134802.
ACCESSION AX140979
VERSION AX140979.1 GI:14281076
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 469 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..2229
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
Alignment Scores:
Pred. No.: 5.17e-44 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-402-713a-2 (1-51) x AX140979 (1-2229)
QY 1 MetPhleuHisIleSerSerProphelysTYrProHisThrgInuIaGlnySgu 20
DB 1659 ATGTTTTCACATTTCCAGCCCCCTTAATATCCACACACAGGAGCAAAAGGAA 1600
QY 21 AlaGlnArgSerLeuGlyLumetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 1599 GCACAGAGATCCCTGGAGAAATGCCGCGCCGACATCTGGTGCATGATGAGCCTCGCC 1540
QY 41 LeuCySLeuValProLeuValArgGluGlyHis 51
DB 1539 CTGTGCTGTGTCCTGCTGTGAGGAGAGACAT 1507
Search completed: September 26, 2003, 21:01:01
Job time : 3188 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2003, 19:55:06 ; Search time 301 Seconds
(without alignments)
457.380 Million cell updates/sec

Title: US-09-402-713A-2

Perfect score: 51
Sequence: 1 MFLHSSPFKYPHTQEAQKE.....HLGSSMSLALCLVPLVREGH 51

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 segs, 1349719017 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5103471

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq.19jun03 -QPM=fastlap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR.SCORE=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09402713.ecgn.1_1_0.6runat_26092003_143059_16949 -NCPV=6 -ICPV=3
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FCGAPOP=6
-FCGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
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21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	51	100.0	812	21	AAA06690
c 2	51	100.0	812	22	AA563899
c 3	51	100.0	812	22	AAH93806
c 4	51	100.0	812	22	AAH85120
c 5	51	100.0	812	22	AAH02871
c 6	51	100.0	812	22	AAH69949
c 7	51	100.0	812	24	ABL95270
c 8	51	100.0	812	25	ACA59707
c 9	51	100.0	820	19	AAV62429
c 10	51	100.0	876	24	AAD38815
c 11	51	100.0	1872	19	AAV62428
c 12	51	100.0	2037	19	AAV62427
c 13	51	100.0	2229	21	AAA06688
c 14	51	100.0	2229	22	AA563897
c 15	51	100.0	2229	22	AAH93804
c 16	51	100.0	2229	22	AAH85118
c 17	51	100.0	2229	22	AAH02869
c 18	51	100.0	2229	22	AAH69947
c 19	51	100.0	2229	24	ABL95268
c 20	51	100.0	2229	25	ACA59705
c 21	51	100.0	2426	21	AAA06689
c 22	51	100.0	2426	22	AA563898
c 23	51	100.0	2426	22	AAH93805
c 24	51	100.0	2426	22	AAH85119
c 25	51	100.0	2426	22	AAH02870
c 26	51	100.0	2426	22	AAH69948
c 27	51	100.0	2426	24	ABL95269
c 28	51	100.0	2426	25	ACA59706
c 29	51	100.0	3112	21	AAA06687
c 30	51	100.0	3112	22	AA563896
c 31	51	100.0	3112	22	AAH93803
c 32	51	100.0	3112	22	AAH85117
c 33	51	100.0	3112	22	AAH02868
c 34	51	100.0	3112	22	AAH69947
c 35	51	100.0	3112	24	ABL95267
c 36	51	100.0	3112	25	ACA59704
c 37	51	100.0	3582	19	AAV62430
c 38	51	100.0	3923	22	AA564026
c 39	51	100.0	3923	22	AAH93861
c 40	51	100.0	3923	24	ABL92196
c 41	51	100.0	3923	24	ABL95397
c 42	51	100.0	3923	25	ACA59834
c 43	46	90.2	449	23	ABV36763
c 44	46	90.2	550	23	ABV49867
c 45	43	84.3	718	21	AAA06545

RESULT 1

AAA06690/C

AAA06690 standard; cDNA; 812 BP.

AAA06690;

13-JUN-2000 (first entry)

Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:471.

Human prostate cancer; diagnosis; tumour; gene therapy; detection;

Human; prostate; cytostatic; vaccine; ss.

Homo sapiens.

XX

XX

XX

PN

XX

WO200004149-A2.

ALIGNMENTS

PD 27-JAN-2000.
XX
XX 14-JUL-1999; 99MO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
XX
XX Claim 1; Page 262; 263pp; English.
XX
XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AA82000 to AA82020 represent sequences used in the exemplification of
XX the present invention.
XX
XX Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 7.03e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
XX
US-09-402-713A-2 (1-51) x AA06690 (1-812)
QY 1 MetPheLeuHisIleSerSerProPheIysTYrProHisThrgIngluAaInlysglu 20
DB 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAACACAAAAGGAA 545
QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAa 40
DB 544 GCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCCACTTGGGTCAATCGATGAGCCTCGCC 485
QY 41 LeuCysLeuValProLeuValArgGluGlnHis 51
DB 484 CTGTGCCTGTGCCGCTGTGAGGGAAGACAT 452
RESULT 2
AA063899/c
ID AA063899 standard; cDNA; 812 BP.
XX
XX AA063899;
XX
XX 29-JAN-2002 (first entry)
XX
XX Human prostate cDNA sequence #433.
XX
XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX

OS Homo sapiens.
XX
XX
XX WO200173032-A2.
XX
XX 04-OCT-2001.
XX
XX 27-MAR-2001; 2001MO-US09919.
XX
XX 27-MAR-2000; 2000US-0536857.
XX 09-MAY-2000; 2000US-0568100.
XX 12-MAY-2000; 2000US-0570737.
XX 13-JUN-2000; 2000US-0593793.
XX 27-JUN-2000; 2000US-0605783.
XX 10-AUG-2000; 2000US-0636215.
XX 29-AUG-2000; 2000US-0651236.
XX 06-SEP-2000; 2000US-0657279.
XX 02-OCT-2000; 2000US-0679426.
XX 10-OCT-2000; 2000US-0685166.
XX
XX (CORI-) CORIXA CORP.
XX
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedrick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX WPI; 2001-639232/73.
XX
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX
XX Claim 1; Page 386-387; 579pp; English.
XX
XX
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
XX polynucleotide of the invention.
XX
SQ Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
Alignment Scores:
Pred. No.: 7.03e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
XX
US-09-402-713A-2 (1-51) x AA063899 (1-812)
QY 1 MetPheLeuHisIleSerSerProPheIysTYrProHisThrgIngluAaInlysglu 20
DB 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAACACAAAAGGAA 545
QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAa 40
DB 544 GCACAGAGATCCCTGGGAGAAATGCCCGGCCGCCCACTTGGGTCAATCGATGAGCCTCGCC 485
QY 41 LeuCysLeuValProLeuValArgGluGlnHis 51
DB 484 CTGTGCCTGTGCCGCTGTGAGGGAAGACAT 452
RESULT 3
AA093806/c
ID AA093806 standard; cDNA; 812 BP.
XX

XX AAH93806;
AC
XX 04-OCT-2001 (first entry)
DT
XX Human prostate-specific cDNA sequence P710P #4.
DE
XX Human prostate cancer; prostate-specific; diagnosis; vaccine;
KW cyrostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX W0200151633-A2.
PN
XX 19-JUL-2001.
PD
XX 16-JAN-2001; 2001WO-US01574.
PE
XX 14-JAN-2000; 2000US-0483672.
PR
XX (CORI-) CORIXA CORP.
PA
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW;
PI Wang A, Meagher MJ;
XX
XX WPI; 2001-425873/45.
DR
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; Page 385; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cyrostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnosis and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
SQ

Alignment Scores:
Pred. No.: 7.03e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-402-713a-2 (1-51) x AAH93806 (1-812)
QY 1 MetPheLeuHsIleSerProPhelystyrProHsIsthrGIngluaIaGlnLysGlu 20
DB 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAAACAAAGAA 545
QY 21 AlaGlnArgSerLeuGluMetProGlyARghIsleuGlySerSerMetSerLeuAla 40
DB 544 GCACAGAGATCCCGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCGCTCGCC 485
QY 41 LeuGlyLeuValProLeuValArgGluGlyHis 51
DB 484 CTGTGCTGGTCCCGCTTGAGGAGAAAGACAT 452

RESULT 4
ID AAH85120/c
XX AAH85120 standard; CDNA; 812 BP.
XX
XX AAH85120;
AC
XX 25-SEP-2001 (first entry)
DT
XX Human prostate-specific cDNA sequence P710P #4.
DE
XX Human prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
XX Homo sapiens.
XX W0200134802-A2.
PN
XX 17-MAY-2001.
PD
XX 09-NOV-2000; 2000WO-US30904.
PE
XX 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX
XX (CORI-) CORIXA CORP.
PA
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skelky YAW, Wang A;
PI WPI; 2001-308785/32.
DR
XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of a
PT prostate cancer -
XX
PS Claim 5; Page 284-285; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cyrostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAC99000 to AAC99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
XX Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
SQ

Alignment Scores:
Pred. No.: 7.03e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-402-713a-2 (1-51) x AAH85120 (1-812)
QY 1 MetPheLeuHsIleSerProPhelystyrProHsIsthrGIngluaIaGlnLysGlu 20
DB 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAAACAAAGAA 545
QY 21 AlaGlnArgSerLeuGluMetProGlyARghIsleuGlySerSerMetSerLeuAla 40
DB 544 GCACAGAGATCCCGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCGCTCGCC 485
QY 41 LeuGlyLeuValProLeuValArgGluGlyHis 51
DB 484 CTGTGCTGGTCCCGCTTGAGGAGAAAGACAT 452

DB 484 CTGTGCTGGTCCGCTTGTGAGGAGACAT 452

RESULT 5
ID AAH02871/c
ID AAH02871 standard; cDNA; 812 BP.
AC AAH02871;
DT 14-JUN-2001 (first entry)
XX
DE Prostate tumour antigen cDNA sequence for P710P #4.
XX
KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
KW Prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN W0200125272-A2.
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000MO-US27464.
XX
PR 04-OCT-1999; 99US-0157455.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Skelky YAM, Reed SG, Cheever MA;
XX
DR WPI; 2001-245062/25.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer -
XX
PS Claim 4; Page 267; 276pp; English.
XX
CC The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;

Alignment Scores:
Pred. No.: 7.03e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-402-713A-2 (1-51) x AAH02871 (1-812)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThGlnGluAaGlnLysGlu 20
DB 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 544 GCACAGAGATCCCTGGAGAGAAATGCCGCGCCCATCTTGGGTCAATGATGACCTCGCC 485

QY 41 LeuGlyLeuValProLeuValArgGlnGlyHis 51
DB 484 CTGTGCTGGTCCGCTTGTGAGGAGACAT 452

RESULT 6
ID AAF86949/c
ID AAF86949 standard; cDNA; 812 BP.
AC AAF86949;
DT 06-JUL-2001 (first entry)
XX
DE Human P710P inventive antigen coding sequence SEQ ID NO: 345.
XX
KW Human; mouse; immunotherapy; cancer; leukemia; WTI; Wilm's tumour gene;
KW Chromosome 11p13; zinc finger transcription factor; ss.
XX
OS Homo sapiens.
XX
PN W0200125273-A2.
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000MO-US27465.
XX
PR 04-OCT-1999; 99US-0157459.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skelky YAM, Xu J, Cheever MA, Reed SG;
XX
DR WPI; 2001-328324/34.
XX
PT Polypeptide comprising part of the Wilm's Tumour gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
XX
PS Disclosure; Page 220; 228pp; English.
XX
CC The present invention describes compositions comprising peptides derived
CC from the Wilm's tumour protein WTI and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WTI
CC proteins are provided. The human WTI gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukemia. The present sequence is
CC a coding sequence used in the exemplification of the invention.
XX
SQ Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;

Alignment Scores:
Pred. No.: 7.03e-44 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-402-713A-2 (1-51) x AAF86949 (1-812)

QY 1 MetPheLeuHisIleSerSerProPheLysTyrProHisThGlnGluAaGlnLysGlu 20
DB 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
DB 544 GCACAGAGATCCCTGGAGAGAAATGCCGCGCCCATCTTGGGTCAATGATGACCTCGCC 485

QY 41 LeuGlyLeuValProLeuValArgGlnGlyHis 51
DB 484 CTGTGCTGGTCCGCTTGTGAGGAGACAT 452

RESULT 7
ID ABL95270/c
ID ABL95270 standard; cDNA; 812 BP.
XX

AC ABL95270;
XX
XX 19-JUL-2002 (first entry)
XX
DE Human P710P cDNA sequence SEQ ID NO 471.
XX
XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX US2002022248-A1.
XX
XX 21-FEB-2002.
XX
XX 12-JAN-2001; 2001US-0759143.
XX
XX 25-FEB-1997; 97US-0806099.
XX 01-AUG-1997; 97US-0904804.
XX 09-FEB-1998; 98US-0020956.
XX 25-FEB-1998; 98US-0030607.
XX 14-JUL-1998; 98US-0115453.
XX 23-SEP-1998; 98US-013812.
XX 15-JAN-1999; 99US-0232149.
XX 09-APR-1999; 99US-0288946.
XX 13-JUL-1999; 99US-0352616.
XX 12-NOV-1999; 99US-0439313.
XX 18-NOV-1999; 99US-0443686.
XX 14-JAN-2000; 2000US-0483672.
XX 27-MAR-2000; 2000US-0536857.
XX 09-MAY-2000; 2000US-0568100.
XX 12-MAY-2000; 2000US-0570737.
XX 13-JUN-2000; 2000US-0593793.
XX 27-JUN-2000; 2000US-0605783.
XX 10-AUG-2000; 2000US-0636215.
XX 29-AUG-2000; 2000US-0651236.
XX 06-SEP-2000; 2000US-0657279.
XX 02-OCT-2000; 2000US-0679426.
XX 10-OCT-2000; 2000US-0685166.
XX
XX (XUJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPT; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
XX diseases, in particular prostate cancer, and as markers for the
XX progression of cancer
XX
XX Claim 1: SEQ ID NO 471; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
XX their encoded proteins. These can be used in the diagnosis and treatment
XX of cancers, particularly prostate cancer. The present sequence is a cDNA

CC described in the invention.
XX
XX SQ Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 7.03e-44 Length: 812
XX Score: 51.00 Matches: 51
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-09-402-713A-2 (1-51) x ABL95270 (1-812)
XX
XX QY 1 MethpheleuHISlleSerSerProphelysTyRProHISthngIngluAlagInlySGlu 20
XX DB 604 ATGTTTGGACATTTCAGCCCTTTAAATTCACACACACAGAGGACCAAAAGGAA 545
XX QY 21 AAGlnArSerLeuGlyGluMetProGlyArGHisLeuGlySerSerMetSerLeuAa 40
XX DB 544 GCACAGACATCCCTGGAGAAATGCCCGCCCATCTTGGGTATCGATGAGCTCGCC 485
XX QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
XX DB 484 CTGTGCTGTGTCCTCCCTGTGTGAGGAGAGGACAT 452
XX
XX RESULT 8
XX ACA59707/c
XX ID ACA59707 standard; cDNA; 812 BP.
XX
XX AC ACA59707;
XX
XX DT 10-JUN-2003 (first entry)
XX
XX DE Prostate cancer therapy associated cDNA #450.
XX
XX KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
XX immunogen; cancer; prostate specific antigen; PSA;
XX prostatic acid phosphatase; PAP; prostate specific membrane antigen;
XX PSMa; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN US2002192763-A1.
XX
XX PD 19-DEC-2002.
XX
XX PF 29-JUN-2001; 2001US-0895793.
XX
XX PR 17-APR-2000; 2000US-157455P.
XX PR 04-OCT-2000; 2000US-0679272.
XX PR 28-MAR-2001; 2001US-0822827.
XX
XX (XUJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX (HURA/) HURAL J.
XX (MCNE/) MCNEILL P D.
XX (HOUN/) HOUGHTON R L.

PA	(DBAS/) Y DE BASSOLS C V.	
PA	(FOYT/) FOY T M.	
XX		
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;	
PI	Fanger GR, Retter MW, Stolk JA, Day CH, Veddyck TS, Carter D;	
PI	Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;	
PI	McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;	
XX		
DR	WPI: 2003-352711/33.	
XX		
PT	New fusion protein comprising prostate-specific polypeptides, or its	
PT	immunogenic portions, useful for diagnosing, preventing and/or treating	
PT	cancer, particularly prostate cancer	
XX		
PS	Example 16; SEQ ID NO 471; 85pp; English.	
XX		
CC	The invention describes a fusion protein comprising at least one amino	
CC	acid sequence of immunogenic portions of any of the 3 sequences not	
CC	defined in the specification, or sequences having at least 70 or 90 %	
CC	sequence identity to any one of the 35 sequences defined in the USPTO	
CC	web site, which is encoded by any of the 4 nucleotide sequences not	
CC	defined in the specification. The fusion protein, composition and	
CC	methods are useful for diagnosing, preventing and/or treating cancer,	
CC	particularly prostate cancer. The proteins are useful as markers to	
CC	indicate the presence or absence of cancer. This sequence	
CC	represents a prostate cancer therapy associated cDNA.	
CC	Note: The sequence data for this patent did not form part of the	
CC	printed specification, but was obtained in electronic format directly	
CC	from the US patent office at	
XX	seqdata.uspto.gov/sequence.html?DocID=US20020192763.	
XX		
SQ	Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;	
	Alignment Scores:	
	Pred. NO: 7.03e-44 Length: 812	
	Score: 51.00 Matches: 51	
	Percent Similarity: 100.00% Conservatived: 0	
	Best Local Similarity: 100.00% Mismatches: 0	
	Query Match: 100.00% Indels: 0	
	DB: 25 Gaps: 0	
US-09-402-713A-2 (1-51) x ACA59707 (1-812)		
OY	1 MetPheLeuHisTleSerSerProPheLysTyrProHisTngInuAlaGlnLysGlu 20	
DB	ATGTTTTCGCACATTTCACGCCCTTTAAATATTCACACACAGGAAGCAAAAGGAA 545	
OY	21 AlaGlnArgSerLeuGlnLysMetProGlyArgHisLeuGlnLysSerMetSerLeuAla 40	
DB	544 GCACAGAGATCCCTGGGAGAAATATGCCCGGCCCATCTTGGGTATCATGATAGCCCTGCC 485	
OY	41 LeuGlnLysValProLeuValArgGlnLysHis 51	
DB	484 CTGTGCTGTGCTCCGCTGTGAGGAGAGACAT 452	
RESULT 9		
AAV62429	standard; cDNA; 820 BP.	
AAV62429:		
AC	30-DEC-1998 (first entry)	
XX		
DT	Prostate cancer antigen (PCa3) cDNA splice variant 3.	
XX		
DE	Prostate cancer antigen cDNA splice variant 3; PCA3; prostatic cancer;	
XX		
KW	PC; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9845420-A1.	
XX		
DB	15-OCT-1998	

XX	09-APR-1998:	98MO-CA00346.
PF		
XX	10-APR-1997:	97US-0041836.
XX		
PA	(DIAG-)	DIAGNOCURE INC.
XX		
PI	Bussemakers MJG;	
XX		
DR	WPI; 1998-568347/48.	
XX		
PT	New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,	
PT	prevention and treatment of prostatic cancer	
PS	Claim 4; Pages 77-78; 11pp; English.	
XX		
CC	The present sequence represents the prostate cancer antigen (PCA3)	
CC	cDNA splice variant 3 sequence comprising of exons 1, 3, and 4a	
CC	of the PCA3 gene. The PCA3 cDNA splice variant 3 sequence,	
CC	isolated from a human primary prostatic tumor tissue cDNA library,	
CC	was found in approximately 1% of the cDNA clones isolated. The	
CC	invention claims for PCA3 cDNA variants and the proteins they encode.	
CC	The invention also claims for antibodies against PCA3 protein. The	
CC	antibodies are claimed to be useful for detecting PCA3 protein in	
CC	immunoassay tests, for diagnosing, assessing and prognosing of	
CC	prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin	
CC	or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed	
CC	to be useful for treating PC, while determining elevated levels of	
CC	PCA3 (as RNA or protein) is useful for detecting a predisposition	
CC	to development of PC, e.g. in prenatal tests. Detecting PCA3 protein	
CC	allows differentiation between malignant and benign prostatic disease,	
CC	and the level of PCA3 expression allows correlation with the grade of	
CC	tumour. PCA3 protein and its fragments are also claimed to be useful	
CC	in vaccines for preventing PC; in drug screens for identifying	
CC	specific (ant)agonists (potentially useful therapeutically) and for	
CC	studying protein-DNA interactions.	
XX		
SQ	Sequence 820 BP; 262 A; 169 C; 191 G; 198 T; 0 other;	
US		
Alignment Scores:		
Pred. NO.:	7.09e-44	Length: 820
Score:	51.00	Matches: 51
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
	19	Gaps: 0
US-09-402-713A-2 (1-51) x AAV62429 (1-820)		
OY	1 MetPheIeuHisIleSerSerProPheIySTYTPRoHISthngInGluAlaGlnIySglu 20	
Db	214 ATGTTTTTGCACATTTTCAGCCCTTTAAATTCACACACACAGGAAGCACAAGAA 273	
OY	21 AlIGlAArgSerIeuGlnIuMetProGlyAArgHISlanguIySerSerMetSerIeuAla 40	
Db	274 GCACAGAGATCCCTGGGAGAAATAGCCCGCCCATTTTGGGTCAATGATAGCCTCGCC 333	
OY	41 LeuCySteuValProIeuValAArgGluGlyHIS 51	
Db	334 CTGTGCTGTGCTCCCGCTTGTGTGAGGAGAGACAT 366	
RESULT 10		
AAD38815		
ID	AAD38815 standard; cDNA; 876 BP.	
XX		
AC	AAD38815;	
XX		
DT	23-SEP-2002 (first entry)	
XX		
DE	Human PSNA cDNA, Prol23.	
XX		
TM	Human; prostate specific protein; PSP; prostate specific nucleic acid;	
XX	vaccine; transgenic; prostate cancer; gene therapy; transgenic animal;	

KM PSNA; ss.
 XX Homo sapiens.
 OS WO200224718-A1.
 PN 28-MAR-2002.
 PD 19-SEP-2001; 2001WO-US29386.
 XX 19-SEP-2000; 2000US-233746P.
 PR (DIAD-) DIADEXUS INC.
 XX Sun Y, Recipon H, Cafertkey R, All S;
 PI WPI; 2002-471216/50.
 DR
 XX Novel isolated prostate specific polypeptide useful for identifying,
 PT diagnosing, monitoring, staging, imaging, and treating prostate cancer
 PT and non-cancerous disease states in prostate
 PS Claim 1; Page 179; 210pp; English.
 XX The invention relates to prostate specific proteins (PSP) and prostate
 CC specific nucleic acids (PSNA). Sequences of the invention are useful
 CC for identifying, diagnosing, monitoring, staging, imaging and treating
 CC prostate cancer and non-cancerous disease states in prostate. They are
 CC also useful for producing engineered prostate tissue for treatment and
 CC research. The PSNA sequences are used in gene therapy and for producing
 CC transgenic animals and cells. The invention is also used as vaccines.
 CC The present sequence is human PSNA CDNA.
 XX
 SQ Sequence 876 BP; 275 A; 183 C; 207 G; 211 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 7,55e-44 Length: 876
 Score: 51.00 Matches: 51
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-402-713A-2 (1-51) x AAD38815 (1-876)
 QY 1 MetpHeuHsIlSeSerProPhelystyrProHstHngInglAlaGlnysGlu 20
 DB 243 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACAAAGGAA 302
 QY 21 AlaGlnArGserLeuGlyGluMetProGlyArGhIsLeuGlySerSerMetSerLeuAla 40
 DB 303 GCACAGAGATCCCTGGGAGAAATGCCCGCCCACTTGGGTGATCGATGACCTCCGC 362
 QY 41 LeuCysLeuValProLeuValArGIngluYhIs 51
 DB 363 CTGTGCCGTGCTCCGCTGTGAGGGAAGACAT 395
 RESULT 11
 AAV62428
 ID AAV62428 standard; cDNA: 1872 BP.
 AC AAV62428;
 XX 30-DEC-1998 (first entry)
 XX Prostate cancer antigen (PCA3) cDNA splice variant 2.
 DE Prostate cancer antigen cDNA splice variant 2; PCA3; prostatic cancer;
 KW PC; ds.
 XX Homo sapiens.
 OS
 XX MO9845420-A1.

XX 15-OCT-1998.
 PD 09-APR-1998; 98WO-CA00346.
 PF 10-APR-1997; 97US-0041836.
 PR (DIAG-) DIAGNOCURE INC.
 XX Bussemakers MUG;
 PI WPI; 1998-568347/48.
 DR
 XX New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
 PT prevention and treatment of prostatic cancer
 PT
 PS Claim 4; Pages 76-77; 111pp; English.
 XX The present sequence represents the prostate cancer antigen (PCA3)
 CC cDNA splice variant 2 sequence comprising of exons 1, 3, 4a and
 CC 4b of the PCA3 gene. The PCA3 cDNA splice variant 2 sequence,
 CC isolated from a human primary prostatic tumour tissue cDNA library,
 CC was found in approximately 65% of the cDNA clones isolated. The
 CC invention claims for PCA3 cDNA variants and the proteins they encode.
 CC The invention also claims for antibodies against PCA3 protein. The
 CC antibodies are claimed to be useful for detecting PCA3 protein in
 CC immunosassay tests, for diagnosing, assessing and prognosing of
 CC prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
 CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed
 CC to be useful for treating PC, while determining elevated levels of
 CC PCA3 (as RNA or protein) is useful for detecting a predisposition
 CC to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
 CC allows differentiation between malignant and benign prostatic disease,
 CC and the level of PCA3 expression allows correlation with the grade of
 CC tumour. PCA3 protein and its fragments are also claimed to be useful
 CC in vaccines for preventing PC; in drug screens for identifying
 CC specific (ant)agonists (potentially useful therapeutically) and for
 CC studying protein-DNA interactions.
 XX
 SQ Sequence 1872 BP; 567 A; 389 C; 369 G; 539 T; 8 other;
 XX
 Alignment Scores:
 Pred. No.: 1,55e-43 Length: 1872
 Score: 51.00 Matches: 51
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 19 Gaps: 0
 US-09-402-713A-2 (1-51) x AAV62428 (1-1872)
 QY 1 MetpHeuHsIlSeSerProPhelystyrProHstHngInglAlaGlnysGlu 20
 DB 214 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACAAAGGAA 273
 QY 21 AlaGlnArGserLeuGlyGluMetProGlyArGhIsLeuGlySerSerMetSerLeuAla 40
 DB 274 GCACAGAGATCCCTGGGAGAAATGCCCGCCCACTTGGGTGATCGATGACCTCCGC 333
 QY 41 LeuCysLeuValProLeuValArGIngluYhIs 51
 DB 334 CTGTGCCGTGCTCCGCTGTGAGGGAAGACAT 366
 RESULT 12
 AAV62427
 ID AAV62427 standard; cDNA: 2037 BP.
 AC AAV62427;
 XX 30-DEC-1998 (first entry)
 XX Prostate cancer antigen (PCA3) cDNA splice variant 1.

KW	Prostate cancer antigen CDNA splice variant 1; PCA3; prostatic cancer; PC; ds.	
KM		
XX	Homo sapiens.	
OS		
FH	Key	Location/Qualifiers
FT	CDS	379..534
FT		/*tag= a
FT		/*product= "PCA3 protein variant 1"
FT	polyA_signal	2019..2024
FT		/*tag= b
XX		
XX	WO9845420-A1.	
PD		
XX	15-OCT-1998.	
XX		
PF	09-APR-1998; 98WO-Ca00346.	
XX		
PR	10-APR-1997; 97US-0041836.	
XX		
PA	(DIAG-) DIAGNOCURE INC.	
XX		
PI	Bussemakers MJG;	
XX		
DR	WPI; 1998-568347/48.	
DR	P-PSDB; AAW79736.	
XX		
PT	New nucleic acid encoding prostate cancer antigen 3 - for diagnosis, prevention and treatment of prostatic cancer	
XX		
PS	Claim 3; Fig 2B-2J; 11pp; English.	
XX		
CC	The present sequence represents the prostate cancer antigen (PCA3)	
CC	CDNA splice variant 1 sequence comprising of exons 1, 2, 3, 4a and	
CC	4b of the PCA3 gene. The PCA3 CDNA splice variant 1 sequence,	
CC	isolated from a human primary prostatic tumor tissue CDNA library,	
CC	was found in approximately 5% of the CDNA clones isolated. The	
CC	invention claims for PCA3 CDNA variants and the proteins they encode.	
CC	The invention also claims for antibodies against PCA3 protein. The	
CC	antibodies are claimed to be useful for detecting PCA3 protein in	
CC	immunoassay tests, for diagnosing, assessing and prognosing of	
CC	prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin	
CC	or radioisotope, and nucleic acids antisense to PCA3 CDNA are claimed	
CC	to be useful for treating PC, while determining elevated levels of	
CC	PCA3 (as RNA or protein) is useful for detecting a predisposition	
CC	to development of PC, e.g. in prenatal tests. Detecting PCA3 protein	
CC	allows differentiation between malignant and benign prostatic disease,	
CC	and the level of PCA3 expression allows correlation with the grade of	
CC	tumour. PCA3 protein and its fragments are also claimed to be useful	
CC	in vaccines for preventing PC; in drug screens for identifying	
CC	specific (ant)agonists (potentially useful therapeutically) and for	
CC	studying protein-DNA interactions.	
XX		
XX		
SO	Sequence 2037 BP; 622 A; 426 C; 406 G; 575 T; 8 other;	
Alignment Scores:		
Pred. NO.:	1,67e-43	Length: 2037
Score:	51.00	Matches: 51
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	19	Gaps: 0
US-09-402-713A-2 (1-51) x AAV62427 (1-2037)		
OY	1 MetPheLeuHisIleSerSerProPheIstYrProHisThnGlnAlaGlnIysGln	20
Db	379 ATGTTTTCACACATTTTCAGACCCCTTTAAATATTCACACACACAGAGAAAGCAAAAGAA	438
OY	21 AlIGlAarSerLeuGlnIyGlnuMetProGlyAaGhIstauGlySerSerMetSerLeuAla	40
Db	439 GCACAGAGATCCCTGGAGAAATAGCCGGCCGACATCTTGAGTATGATGATGAGCTCGC	498

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QY      41 LeucylleuValProleuValArgIngluYHis 51
        |||
Db      499 CTGTCCCTGTGTCCTCGCTTGTGAGGAGACAT 531

RESULT 13
AAA06688/c
ID      AAA06688 standard; cDNA; 2229 BP.
XX
XX      AAA06688;
XX
XX      13-JUN-2000 (first entry)
XX
XX      Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:469.
XX
XX      Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW      immunogenic; cytosolic; vaccine; ss.
XX
XX      Homo sapiens.
XX
XX      WO200004149-A2.
XX
XX      27-JAN-2000.
XX
XX      14-JUL-1999; 99WO-US15838.
XX
XX      14-JUL-1998; 98US-0115453.
XX      14-JUL-1998; 98US-0116134.
XX      23-SEP-1998; 98US-0159812.
XX      23-SEP-1998; 98US-0159822.
XX      15-JAN-1999; 99US-0232149.
XX      15-JAN-1999; 99US-0232880.
XX      09-APR-1999; 99US-0286946.
XX
XX      (CORI-) CORIXA CORP.
XX
XX      Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
XX      WPI: 2000-171268/15.
XX
XX      New polypeptide useful for treating and diagnosing prostate cancer
XX      comprises an immunogenic portion of prostate tumor protein -
XX
XX      Claim 1; Page 260-261; 263pp; English.
XX
XX      The present invention describes isolated polypeptides, comprising an
XX      immunogenic portion of a prostate tumour protein (PTP). The polypeptides
XX      and polynucleotides encoding them have cytostatic activity and can be
XX      used in vaccines and in gene therapy. The polypeptides and
XX      polynucleotides encoding them, antigen presenting cells which express
XX      the polypeptides, antibodies against the polypeptides and vaccines
XX      comprising them can be used for inhibiting the development of prostate
XX      cancer in a patient. The polypeptides can be used to generate antibodies
XX      or anti-idiotypic antibodies for passive immuno therapy. A portion of
XX      the polynucleotides encoding the polypeptides can be used as a probe or
XX      to modulate the expression of the polypeptides. AAA06241 to AAA0651 and
XX      AAA82000 to AAA82020 represent sequences used in the exemplification of
XX      the present invention.
XX
XX      SEQ      Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;

Alignment Scores:
Pred. No.:      1,82e-43      Length:      2229
Score:          51.00      Matches:      51
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:            21      Gaps:        0

US-09-402-713A-2 (1-51) x AAA06688 (1-2229)

QY      1 MethPheLeuHisIleSerSerProPheIysTyrProHisThrIngluAlaGlnIysGlu 20
        |||
Db      1659 ATGTTTTGGCAATTTTCCAGGCCCTTTAAATATCCACACACAGGAAGCACAAAAGGAA 16000

```

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisIleuGlySerSerMetSerLeuAla 40
 |||
 Db 1599 GCACAGAGATCCCTGGGAGAAATGCCCGCCGTCATCTGGTCATGATAGAGCTCGCC 1540
 |||
 OY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
 |||
 Db 1539 CTGTGCTGTGCTCGCTTGTGAGGAAAGACAT 1507
 |||
 RESULT 14
 AAS63897/c
 ID AAS63897 standard; cDNA; 2229 BP.
 XX
 AC AAS63897;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human prostate cDNA sequence #431.
 XX
 KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
 XX
 OS Homo sapiens.
 XX
 PN W0200173032-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09919.
 XX
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593783.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
 XX
 DR WPI; 2001-639232/73.
 XX
 PT New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer -
 PS Claim 1; Page 385; 579pp; English.
 XX
 XX The invention relates to isolated prostate-specific
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
 CC antibodies raised against the polypeptides (or antigenic epitopes
 CC derived from them) and antigen-presenting cells expressing the
 CC polypeptides. The antibodies are useful for detecting the presence of
 CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
 CC the antigen-presenting cells are useful for stimulating and/or expanding
 CC T cells specific for a tumour protein, and for inhibiting the development
 CC of cancer especially prostate cancer. Compositions comprising the
 CC polynucleotide and/or polypeptide are useful for stimulating an immune
 CC response, and for treating cancer. The oligonucleotide is useful for
 CC detecting cancer. The present sequence is a prostate specific
 CC polynucleotide of the invention.
 XX
 SO Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;

Alignment Scores:
 Pred. No.: 1.82e-43 Length: 2229
 Score: 51.00 Matches: 51
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-402-713a-2 (1-51) x AAS63897 (1-2229)
 QY 1 MethLeuHisIleSerSerProPheIysTyrProHisThrGlnJuaAlaGlnGlu 20
 |||
 Db 1659 ATGTGTTGGACATTTCCAGCCCTTTAAATATCCACACACACAGAAACAAAGGAA 1600
 |||
 QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisIleuGlySerSerMetSerLeuAla 40
 |||
 Db 1599 GCACAGAGATCCCTGGGAGAAATGCCCGCCGTCATCTGGTCATGATAGAGCTCGCC 1540
 |||
 OY 41 LeuCysLeuValProLeuValArgGluGlyHis 51
 |||
 Db 1539 CTGTGCTGTGCTCGCTTGTGAGGAAAGACAT 1507
 |||
 RESULT 15
 AAH93804/c
 ID AAH93804 standard; cDNA; 2229 BP.
 XX
 AC AAH93804;
 XX
 DT 04-OCT-2001 (first entry)
 XX
 DE Human prostate-specific cDNA sequence P710P #2.
 XX
 KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
 KW cytostatic; gene therapy; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200151633-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 16-JAN-2001; 2001WO-US01574.
 XX
 PR 14-JAN-2000; 2000US-0483672.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
 PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAM;
 PI Wang A, Meagher MJ;
 XX
 DR WPI; 2001-425873/45.
 XX
 PT New polynucleotide encoding a prostate-specific protein, for
 PT diagnosing, monitoring and treating prostate cancer in a patient and
 PT for use in vaccines -
 PS Claim 1; Page 383-384; 543pp; English.
 XX
 XX The present invention describes polynucleotide sequences (I) which encode
 CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
 CC and can be used in vaccine production and gene therapy. (I), (II),
 CC antibodies to (II), fusion proteins comprising (II), and isolated
 CC T cells prepared using (I) or (II) are used treat cancer in a patient.
 CC (I) and the antibodies are also used in the detection of cancer in a
 CC patient. The cancer that is diagnosed or treated is particularly
 CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
 CC (I) can be used for monitoring the progression of cancer in a patient.
 CC (I) and (II) can also be used to improve diagnostic and therapeutic
 CC methods for prostate cancer. They can indicate the level of metastasis
 CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
 CC AAH01318 represent polynucleotide and amino acid sequences used in the
 CC exemplification of the present invention.
 XX
 SO Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;

Alignment Scores:

Pred. No.:	1.82e-43	length:	2229
Score:	51.00	Matches:	51
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-402-713a-2 (1-51) x AAH93804 (1-2229)

QY	1	MetPheLeuHisIleSerSerProPheLysTyrProHisThrGlnGluAlaGlnLysGlu	20
Db	1659	ATGTTTTCACATTTCCAGCCCCCTTTAAATATCCACACACAGAGAGCAAAAGAA	1600
QY	21	AlaGlnArgSerLeuGlnMetProGlyArgHisLeuGlySerSerMetSerLeuAla	40
Db	1599	GCACAGAGATCCCTGGGAGAAATGCCGCCCATCTTGCTCATCATGATGAGAGCTCGCC	1540
QY	41	LeuCysLeuValProLeuValArgGlnGlyHis	51
Db	1539	CTGTGCCCTGGTCCCGCTGTGAGGAGAGACAT	1507

Search completed: September 26, 2003, 20:07:46
 Job time : 303 secs


```
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-471

Alignment Scores:
Pred. No.: 2.3e-43      Length: 812
Score: 51.00           Matches: 51
Best Local Similarity: 100.00%      Conservative: 0
Query Match: 100.00%      Mismatches: 0
DB: 100.00%             Indels: 0
                          Gaps: 0

US-09-402-713a-2 (1-51) x US-09-759-143-471 (1-812)

QY      1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAlaGlnLysGlu 20
        |||TTTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA
Db      604 ATGTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA 545

QY      21 AlaGlnArgSerLeuGlnMetProGlyArgHisLeuGlnLysSerMetSerLeuAla 40
        |||TTTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA
Db      544 GCACAGAGATCCCTGGAGAAATGCCGCCGCATCTGGTCATGATGAGACCTCGCC 485

QY      41 LeuCysLeuValProLeuValArgGlnGlyHis 51
        |||TTTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA
Db      484 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 452

RESULT 2
US-09-780-669-471/c
; Sequence 471, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-471

Alignment Scores:
Pred. No.: 2.3e-43      Length: 812
Score: 51.00           Matches: 51
Best Local Similarity: 100.00%      Conservative: 0
Query Match: 100.00%      Mismatches: 0
DB: 100.00%             Indels: 0
                          Gaps: 0
```

```
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 100.00%             Gaps: 0

US-09-402-713a-2 (1-51) x US-09-780-669-471 (1-812)

QY      1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAlaGlnLysGlu 20
        |||TTTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA
Db      604 ATGTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA 545

QY      21 AlaGlnArgSerLeuGlnMetProGlyArgHisLeuGlnLysSerMetSerLeuAla 40
        |||TTTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA
Db      544 GCACAGAGATCCCTGGAGAAATGCCGCCGCATCTGGTCATGATGAGACCTCGCC 485

QY      41 LeuCysLeuValProLeuValArgGlnGlyHis 51
        |||TTTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA
Db      484 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 452

RESULT 3
US-09-822-827-471/c
; Sequence 471, Application US/09822827
; Patent No. US2002008180A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-471

Alignment Scores:
Pred. No.: 2.3e-43      Length: 812
Score: 51.00           Matches: 51
Best Local Similarity: 100.00%      Conservative: 0
Query Match: 100.00%      Mismatches: 0
DB: 100.00%             Indels: 0
                          Gaps: 0

US-09-402-713a-2 (1-51) x US-09-822-827-471 (1-812)

QY      1 MetPheLeuHisIleSerSerProPheLysTYrProHisThrGlnGluAlaGlnLysGlu 20
        |||TTTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA
Db      604 ATGTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA 545

QY      21 AlaGlnArgSerLeuGlnMetProGlyArgHisLeuGlnLysSerMetSerLeuAla 40
        |||TTTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA
Db      544 GCACAGAGATCCCTGGAGAAATGCCGCCGCATCTGGTCATGATGAGACCTCGCC 485

QY      41 LeuCysLeuValProLeuValArgGlnGlyHis 51
        |||TTTTTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGCAAAAGGAA
Db      484 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 452

RESULT 4
US-09-895-793-471/c
; Sequence 471, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-471
```

APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 471
LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-793-471

Alignment Scores:
Pred. No.: 2.3e-43 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-402-713A-2 (1-51) x US-09-895-793-471 (1-812)

OY 1 MethpLeuHISLIESerProPhelySTYrProHISrHrGInGInuAlaGInLySGLu 20
DB 604 ATGTTTGGCACATTTCAGCCCTTTAAATATCCACACACAGGAAGCAAAAGGAA 545
OY 21 AlaGInArSerLeuGInGInuMetProGInArGInHISLeuGInLySerMetSerLeuA 40
DB 544 GCACAGAGATCCCTGGGGAATGCGCGCCCATCTTGGGTATCATGAGCCTCGCC 485
OY 41 LeuCySeuValProLeuValArgGInuGInHIS 51
DB 484 CTGTGCTGTGTCGCGCTGTGAGGGAAGACAT 452

RESULT 5

US-09-895-814-471/C
Sequence 471, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.

APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 471
LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-814-471

Alignment Scores:
Pred. No.: 2.3e-43 Length: 812
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-402-713A-2 (1-51) x US-09-895-814-471 (1-812)

OY 1 MethpLeuHISLIESerProPhelySTYrProHISrHrGInGInuAlaGInLySGLu 20
DB 604 ATGTTTGGCACATTTCAGCCCTTTAAATATCCACACACAGGAAGCAAAAGGAA 545
OY 21 AlaGInArSerLeuGInGInuMetProGInArGInHISLeuGInLySerMetSerLeuA 40
DB 544 GCACAGAGATCCCTGGGGAATGCGCGCCCATCTTGGGTATCATGAGCCTCGCC 485
OY 41 LeuCySeuValProLeuValArgGInuGInHIS 51
DB 484 CTGTGCTGTGTCGCGCTGTGAGGGAAGACAT 452

RESULT 6

US-10-144-678A-471/C
Sequence 471, Application US/10144678A
Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 471
LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
US-10-144-678a-471

Alignment Scores:

Pred. No.:	2.3e-43	Length:	812
Score:	51.00	Matches:	51
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-402-713a-2 (1-51) x US-10-144-678a-471 (1-812)

QY 1 MetPhleuH1s1leSerSerProphelysTyProH1sthrGlnGluAlaGlnGlu 20

DB 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40

DB 544 GCACAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGTCATCGATGAGCCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51

DB 484 CTGTGCTGTGCTCCGCTTGAGGAGAGACAT 452

RESULT 7

US-10-012-896-471/c

Sequence 471, Application US/10012896

Publication No. US20020183251A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvyck, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carloca
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshinori
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 471
LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-471

Alignment Scores:

Pred. No.:

2.3e-43

Length:

812

Score:	51.00	Matches:	51
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-402-713a-2 (1-51) x US-10-012-896-471 (1-812)

QY 1 MetPhleuH1s1leSerSerProphelysTyProH1sthrGlnGluAlaGlnGlu 20

DB 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40

DB 544 GCACAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGTCATCGATGAGCCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51

DB 484 CTGTGCTGTGCTCCGCTTGAGGAGAGACAT 452

RESULT 8

US-10-010-940-471/c

Sequence 471, Application US/10010940

Publication No. US2003008062A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqiu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427D3
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 471
LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
US-10-010-940-471

Alignment Scores:

Pred. No.:	2.3e-43	Length:	812
Score:	51.00	Matches:	51
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-402-713a-2 (1-51) x US-10-010-940-471 (1-812)

QY 1 MetPhleuH1s1leSerSerProphelysTyProH1sthrGlnGluAlaGlnGlu 20

DB 604 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGGAA 545

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40

DB 544 GCACAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGTCATCGATGAGCCTCGCC 485

QY 41 LeuCysLeuValProLeuValArgGluGlyHis 51

DB 484 CTGTGCTGTGCTCCGCTTGAGGAGAGACAT 452

RESULT 9

US-09-957-708-3

```
; Sequence 3, Application US/09957708
; Publication No. US20030031678A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Heve
; APPLICANT: Caferey, Robert
; APPLICANT: Ali, Shujath
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific
; TITLE OF INVENTION: Genes
; FILE REFERENCE: DEX-0239
; CURRENT APPLICATION NUMBER: US/09/957,708
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,746
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-957-708-3

Alignment Scores:
Pred. No.: 2.45e-43 Length: 876
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-402-713A-2 (1-51) x US-09-957-708-3 (1-876)

Qy 1 MethelenuHisIleSerSerProphelysTyProhIsthrngIngluaIaGlnlySglu 20
Db 243 ATGTTTTCACATTTCCAGCCCTTAATATCCACACACAGGAAGCAAAAGGAA 302
Qy 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 303 GCACAGAGATCCCTGGGAGAAATGCCCGCCGCATCTTGGTCATGATGAGCTCCGCC 362
Qy 41 LeuCySleuValProLeuValArgGluGlyHis 51
Db 363 CTGTGCTGTGTCGCCGCTTGTGAGGAGAGACAT 395

RESULT 10
US-09-759-143-469/c
; Sequence 469, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-469

Alignment Scores:
Pred. No.: 5.34e-43 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-402-713A-2 (1-51) x US-09-759-143-469 (1-2229)

Qy 1 MethelenuHisIleSerSerProphelysTyProhIsthrngIngluaIaGlnlySglu 20
Db 1659 ATGTTTTCACATTTCCAGCCCTTAATATCCACACACAGGAAGCAAAAGGAA 1600
Qy 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
Db 1599 GCACAGAGATCCCTGGGAGAAATGCCCGCCGCATCTTGGTCATGATGAGCTCCGCC 1540
Qy 41 LeuCySleuValProLeuValArgGluGlyHis 51
Db 1539 CTGTGCTGTGTCGCCGCTTGTGAGGAGAGACAT 1507

RESULT 11
US-09-780-669-469/c
; Sequence 469, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-469

Alignment Scores:
Pred. No.: 5.34e-43 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-09-402-713a-2 (1-51) x US-09-780-669-469 (1-2229)
QY      1 MetPheLeuHisIleSerSerProPheLysTYRProHisThrGlnGluAlaGlnLysGlu 20
      |||||||
Db      1659 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAGGACAAAGGAA 1600
QY      21 AlaGlnArgSerLeuGlyMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
      |||||||
Db      1599 GCACAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGATCATGATGAGCCTCGCC 1540
QY      41 LeuCysLeuValProLeuValArgGlnGlyHis 51
      |||||||
Db      1539 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 1507

RESULT 12
US-09-822-827-469/c
; Sequence 469, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-469

Alignment Scores:
Pred. No.:      5,34e-43      Length:      2229
Score:          51.00      Matches:      51
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             9      Gaps:      0

US-09-402-713a-2 (1-51) x US-09-822-827-469 (1-2229)
QY      1 MetPheLeuHisIleSerSerProPheLysTYRProHisThrGlnGluAlaGlnLysGlu 20
      |||||||
Db      1659 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAGGACAAAGGAA 1600
QY      21 AlaGlnArgSerLeuGlyMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
      |||||||
Db      1599 GCACAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGATCATGATGAGCCTCGCC 1540
QY      41 LeuCysLeuValProLeuValArgGlnGlyHis 51
      |||||||
Db      1539 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 1507

RESULT 13
US-09-895-793-469/c
; Sequence 469, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.

US-09-402-713a-2 (1-51) x US-09-895-793-469 (1-2229)
QY      1 MetPheLeuHisIleSerSerProPheLysTYRProHisThrGlnGluAlaGlnLysGlu 20
      |||||||
Db      1659 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAGGACAAAGGAA 1600
QY      21 AlaGlnArgSerLeuGlyMetProGlyArgHisLeuGlySerSerMetSerLeuAla 40
      |||||||
Db      1599 GCACAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGATCATGATGAGCCTCGCC 1540
QY      41 LeuCysLeuValProLeuValArgGlnGlyHis 51
      |||||||
Db      1539 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 1507

RESULT 14
US-09-895-814-469/c
; Sequence 469, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Heppler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```

```
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-469

Alignment Scores:
Pred. No.: 5.34e-43 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-402-713a-2 (1-51) x US-09-895-814-469 (1-2229)

QY 1 MetPheLeuHsIleSerSerProPhelystyrProHsIsthrGlnGluAlaGlnLysGlu 20
Db 1659 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGGAA 1600

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHsIleuGlySerSerMetSerLeuAla 40
Db 1599 GCACAGAGATCCCTGGGAGAAATGCCGCGCCCATCTTGTCATCGATGAGCCTCGCC 1540

QY 41 LeuCySLeuValProLeuValArgGluGlyHis 51
Db 1539 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 1507

RESULT 15
US-10-144-678A-469/C
; Sequence 469, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlotia
; APPLICANT: Foy, Teresa M.
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-10-144-678A-469

Alignment Scores:
Pred. No.: 5.34e-43 Length: 2229
Score: 51.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-402-713a-2 (1-51) x US-10-144-678A-469 (1-2229)

QY 1 MetPheLeuHsIleSerSerProPhelystyrProHsIsthrGlnGluAlaGlnLysGlu 20
Db 1659 ATGTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGGAA 1600

QY 21 AlaGlnArgSerLeuGlyGluMetProGlyArgHsIleuGlySerSerMetSerLeuAla 40
Db 1599 GCACAGAGATCCCTGGGAGAAATGCCGCGCCCATCTTGTCATCGATGAGCCTCGCC 1540

QY 41 LeuCySLeuValProLeuValArgGluGlyHis 51
Db 1539 CTGTGCTGTGCTCCGCTTGTGAGGAGAGACAT 1507

Search completed: September 26, 2003, 21:44:11
Job time : 280 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2003, 19:58:16 ; Search time 2216 Seconds
(without alignments)
559.354 Million cell updates/sec

Title: US-09-402-713A-2
Perfect score: 51
Sequence: 1 MFLHSSPFKPHQEAQKE.....HLGSSMALCLVPLVREGH 51

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 segs, 1215238056 residues

Word size: 1

Total number of hits satisfying chosen parameters: 45562604

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-O=/cgn2.1/USPRO.spool/US09402713/runat_26092003_143059_16972/app-query.fasta.1.199
-DB=EST -QFMT=fastap -SUFFIX=olig.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro
-NORR=ext -HEARST=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09402713-EGCN.1.12810-terunat_26092003_143059_16972 -NCPU=6 -ICPU=3
-NO.MAP -LARGESUBSTR=NEG.SCOR=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_tod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	72.5	176	10 BF373406	BF373406 IL2-FT015
2	37	72.5	167	9 A1780885	A1780885 EST621764
3	37	72.5	382	10 BG631598	BG631598 CC-estfcl
4	37	72.5	438	29 FR0024676	AL017520 F.tubripe
5	37	72.5	494	13 BY641551	BY641551 BY641551
6	37	72.5	528	9 AM093357	AM093357 EST286537
7	37	72.5	531	12 B1801819	B1801819 H061G05 E
8	37	72.5	572	9 AM624953	AM624953 EST313782
9	37	72.5	741	10 BB634056	BB634056 BB634056
10	37	72.5	754	12 BM410648	BM410648 EST584975
11	37	72.5	132	10 BG527932	BG527932 602556894
12	37	72.5	174	13 BY370977	BY370977 BY370977
13	37	72.5	239	13 BQ368838	BQ368838 PM1-GN051
14	37	72.5	243	13 BY370387	BY370387 BY370387
15	37	72.5	266	10 BF887863	BF887863 QV2-TN017
16	37	72.5	273	28 A2113501	A2113501 RPL1-23-4
17	37	72.5	292	28 AQ006096	AQ006096 C1T-HSP-2
18	37	72.5	314	13 BY688754	BY688754 BY688754
19	37	72.5	318	29 BZ765908	BZ765908 SALK_1354
20	37	72.5	332	14 C80550	C80550 C80550 Mous
21	37	72.5	361	13 BY088994	BY088994 BY088994
22	37	72.5	388	14 CB779343	CB779343 AMGNNUC:S
23	37	72.5	389	10 BF455095	BF455095 UT-M-B21-
24	37	72.5	401	28 A2238755	A2238755 RPL1-23-8
25	37	72.5	411	29 BZ917002	BZ917002 CH240_102
26	37	72.5	416	12 BG979998	BG979998 PM3-CN010
27	37	72.5	418	14 BY694175	BY694175 BY694175
28	37	72.5	421	10 BB786885	BB786885 BB786885
29	37	72.5	422	12 B1319624	B1319624 1e13f04.y
30	37	72.5	429	14 CA725167	CA725167 wds3f.pko
31	37	72.5	437	14 CA045471	CA045471 ssa1plc15
32	37	72.5	469	10 BB829415	BB829415 BB829415
33	37	72.5	488	29 AG248548	AG248548 locus_jap
34	37	72.5	497	14 CA564802	CA564802 K0330009-
35	37	72.5	510	10 BB766938	BB766938 BB766938
36	37	72.5	518	9 AA756841	AA756841 vu20b03.f
37	37	72.5	521	10 BB283541	BB283541 BB283541
38	37	72.5	527	28 AQ975708	AQ975708 RPL1-23-3
39	37	72.5	537	9 A1235734	A1235734 EST232296
40	37	72.5	558	14 CB500521	CB500521 ssa1g8503
41	37	72.5	558	28 AQ727566	AQ727566 HS_5456_A
42	37	72.5	569	12 B1342171	B1342171 369865 MA
43	37	72.5	576	10 BE065497	BE065497 RC3-BT031
44	37	72.5	576	13 B0194674	B0194674 UI-R-CN1-
45	37	72.5	577	14 C80499	C80499 C80499 Mous

ALIGNMENTS

RESULT 1
BF373406
LOCUS BF373406 167 bp mRNA linear EST 24-NOV-2000
DEFINITION IL2-FT0159-070800-120-H01 FT0159 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF373406
VERSION BF373406.1 GI:11335431
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 167)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

TITLE	Shougen sequencing of the human transcriptome with ORF expressed Sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
PUBMED	10737800
COMMENT	Contact: Simpson A.J.G.

Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/getcdm2.pl?file=IL2c2-IL2-FT0159.070800-120-H01c3-2000-08-07c4c4-1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 167.

FEATURES	source
Location/Qualifiers	
1. .167	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/dev_stage="Adult"	
/clone_lib="FT0159"	
/note="Organ: prostate; tumor: Vector: puc18; site:1: Sma1; site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	
BASE COUNT	
ORIGIN	
47 a	
38 c	
49 g	
33 t	

Alignment Scores:	
Pred. No.:	1.29e-27
Score:	37.00
Percent Similarity:	100.00%
Best local Similarity:	100.00%
Query Match:	72.55%
DB:	10
Length:	167
Matches:	37
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-402-713A-2 (1-51) X BF373406 (1-167)

[illegible]

RESULT 2	LOCUS	DEFINITION
AI780885/c	AI780885	176 bp mRNA linear EST 18-MAY-2001
	EST261764	tomato susceptible, Cornell Lycopersicon esculentum cDNA
	clone cGSL1302,	mRNA sequence.

ACCESSION	A1780885	
VERSION	A1780885.1	GI:5278926
KEYWORDS	EST.	

SOURCE Lycopersicon esculentum (tomato)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE 1 (bases 1 to 176)

AUTHORS
D. Asencio, M., He, X., Lyman, J., Materon, A. L., Vision, T., Holt, I. E.,
Ilang, F., Upton, J., Rönning, C. M., Craven, M. B., Fujii, C. Y., Bommaran,
C. L., Nieman, W., Fraser, C. M., Venter, J. C., Tanksley, S. D.,
Giovannoni, J. J. and Martin, G. B.
TITLE
Generation of ESTs from *Pseudomonas* susceptible tomato
JOURNAL
Unpublished
COMMENT
Contact: CUGI

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES		source
Location/Qualifiers	1. 176	
	/organism="Lycopersicon esculentum"	
	/mol_type="mRNA"	
	/cultivar="R1-13 (Rio Grande x Money Maker)"	
	/db_xref="taxon:4081"	
	/clone="cDES1302"	
	/tissue_type="leaf"	
	/dev_stage="4-week old"	
	/lab_host="SOLR"	
	/clone_lib="tomato susceptible, Cornell"	
	/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; cDES - Tomato Pseudomonas Susceptible EST library. Directionally cloned cDNAs inserted into pBluescript SK(-) at 5' end with EcoRI and 3' end with XhoI site"	
BASE COUNT	74 a	35 c 27.9 40 t
ORIGIN		

Alignment Scores:	
Pred. No.:	14.7
Score:	9.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	17.65%
DB:	9
Length:	176
Matches:	9
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-402-713A-2 (1-51) x A1780885 (1-176)

QY	38	SerLeuAlaLeucCysLeuValProLeu	46
Db	53	TCAATTGGCATTTGTTAGTCCCATTA	27

RESULT 3	
BG631598/c	
LOCUS	BG631598
DEFINITION	cc-eflicleBt81d Tomato flower library from a mixture of
	382 bp mRNA linear EST 19-Apr-2001

cc-esf1cLEL8L8ld1, mRNA sequence

ACCESSION	BG631598	
VERSION	BG631598.1	GI:13683072
KEYWORDS	EST.	
SOURCE	Lycopersicon esculentum	(tomato)
ORGANISM	Lycopersicon esculentum	

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 382)

AUTHORS van der Hoeven, R.S. and Tanksley, S.D.

TITLE ESTS from a tomato flower library

Journal
Unpublished
Contact: Butzer & van der Meer

COMMENT
Contact: Rutgers S. van der Hoeven
Cornell University

252 Emerson Hall, Ithaca, NY 14850, USA

Tel: 607 255 7886

Fax: 607 255 6683

Email: rv19@cornell.edu

3 prime sequence.

FEATURES	Location/Qualifiers
source	1. . 382

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/organism="Lycopersicon esculentum"
/mol_type="mRNA"
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/cultivar="E6203"
 /db_xref="taxon:4081"
 /clone="cc-esficle8L81d1"
 /tissue_type="developing flower buds and open flowers"
 /dev_stage="4-8 week old plants"
 /lab_host="X10LR"
 /clone_id="Tomato flower library from a mixture of
 developmental stages"
 /note="Vector: pBK_CMV; Site_1: EcoRI; Site_2: XhoI;
 Flowers and flower buds were collected from greenhouse
 grown plants and used for library construction (cLEL)."
 BASE COUNT 124 a 94 c 56 g 108 t
 ORIGIN

Alignment Scores:

Pred. No.: 35 6 Length: 382
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.65% Indels: 0
 DB: 10 Gaps: 0

US-09-402-713A-2 (1-51) x BG631598 (1-382)

OY 38 SerleuAlaLeuCySLeuAlaProleu 46
 DB 106 TCATTCGCACTGTGTTCATTCACATTA 80

RESULT 4

FR0024676/c FR0024676 438 bp DNA linear GSS 10-DEC-1997
 LOCUS F.rubripes GSS sequence, clone 127M03aA4, genomic survey sequence.
 DEFINITION AL017520.1 GI:2683888
 ACCESSION
 VERSION
 KEYWORDS GSS: genome survey sequence.
 SOURCE Takifugu rubripes
 ORGANISM

REFERENCE 1 (bases 1 to 438)
 AUTHORS Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranta,Y.,
 Williams,G. and Brenner,S.
 TITLE Direct Submission
 JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
 Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmrc.ac.uk

COMMENT

DESCR:

One pass dye-terminator sequencing of cosmid cloned genomic
 sequence.

FEATURES

source location/Qualifiers
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 /organism="Takifugu rubripes"
 /mol_type="genomic DNA"
 /db_xref="taxon:31033"
 /clone="127M03aA4"
 /clone_id="cosmid 127M03"
 BASE COUNT 119 a 95 c 74 g 149 t 1 others
 ORIGIN

Alignment Scores:

Pred. No.: 41.6 Length: 438
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.65% Indels: 0
 DB: 29 Gaps: 0

US-09-402-713A-2 (1-51) x FR0024676 (1-438)

OY 34 glySerSermetSerleuAlaLeuCyS 42
 DB 175 GGTTCACACATGACGCTTACACTTGT 149

RESULT 5

BY641551 494 bp mRNA linear EST 15-DEC-2002
 LOCUS BY641551
 DEFINITION BY61551 RIKEN full-length enriched, visual cortex Mus musculus
 CDNA clone K4303435F21 3', mRNA sequence.
 ACCESSION BY641551
 VERSION BY641551.1 GI:26976733
 KEYWORDS EST.

Mus musculus (house mouse)
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 494)
 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
 Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamana,I., Kiyosawa,H.,
 Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
 Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
 Quackenbush,J., Schriml,L.M., Kanapi,A., Matsuda,H., Batalov,S.,
 Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chochila,C., Corbani,
 L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,
 A., Frazer,K.S., Gaasterland,T., Gaidbold,M., Gissi,C., Godzik,A.,
 Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
 Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
 King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,
 P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,
 H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
 Pesole,G., Petrosky,N., Pillai,R., Pontus,J.U., Qi,D.,
 Ramchandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,
 B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempere,C.A., Setou,
 M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,
 R.D., Tomita,M., Verardo,R., Wagner,L., Walstedt,C., Wang,Y.,
 Watanabe,Y., Wells,C., Wilming,L.G., Wyszew-Boriss,A., Yanagisawa,
 M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
 Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Kono,H., Nakamura,
 M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Alizawa,K.,
 Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,
 Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,
 E.S., Rogers,J.J., Birney,E. and Hayashizaki,Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

TITLE

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
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 The Institute of Physical and Chemical Research (RIKEN)
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 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 UR: http://genome.gsc.riken.go.jp/
 Alizawa,K., Akimura,T., Arakawa,T.,
 T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Kono,H., Miyazaki,A.,
 Murata,M., Nakamura,M., Nomura,K., Nomura,K., Ohno,M., Sakai,K.,
 Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
 M., Waki,K., Watanabe,A., Muramatsu,M. and Hayashizaki,Y. Direct
 Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Michela Fagioli and Takao K. Henshi (
 Laboratory for Neuronal Circuit Development Brain Science Institute
 RIKEN 2-1 Hirotsawa, Mako-shi, Saitama 351-0198 Japan) whose
 assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

source

Location/Qualifiers

1. 494

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="K430345f21"

/tissue_type="visual cortex"

/clone_lib="RIKEN full-length enriched, visual cortex"

BASE COUNT 147 a 109 c 98 g 139 t 1 others

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	47.8	9	494	0	0	0
Percent Similarity:	9.00	100.00%	100.00%	0	0	0
Best Local Similarity:	100.00%	100.00%	100.00%	0	0	0
Query Match:	17.65%	17.65%	17.65%	0	0	0
DB:	13	13	13	0	0	0

US-09-402-713a-2 (1-51) x BY641551 (1-494)

Qy 18 GlnlysgluAlaGlnaArgSerLeugly 26

Db 350 CAGAAAGAGGCCCAAGAGACTTTGGCA 376

RESULT 6

LOCUS

AM093357 528 bp mRNA linear EST 18-MAY-2001

DEFINITION EST286537 tomato mixed elicitor, B71 Lycopersicon esculentum cDNA

clone cLET24J3, mRNA sequence.

AM093357.1 GI:6058952

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum (tomato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asterids; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 528)

D'Ascenzo, M., He, X., Lyman, J., Holt, I. E., Jiang, F., Upton, J.,

Romano, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Niernman, W.,

Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and Giovannoni

TITLE

JOURNAL

COMMENT

unpublished

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

Location/Qualifiers

1. 528

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="Rio Grande PtoR"

/db_xref="taxon:4081"

/clone="cLET24J3"

/tissue_type="leaf"

/dev_stage="4-6 week old plants"

/lab_host="XLI-Blue MRF"
 /clone_lib="tomato mixed elicitor, B71"
 /note="Vector: pBluescript SK(-); site 1: EcoRI; site 2:
 XhoI; cLET - Inoculated with a variety of disease response
 elicitors. Plants exposed to 2,6 dichloroisocitric
 acid, BTH, jasmonic acid, ethylene, fenthion, ELX,
 okadaic acid, or systemin prior to tissue harvest. EcoRI
 site was destroyed during cloning."

BASE COUNT 144 a 88 c 130 g 166 t

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	51.5	9	528	0	0	0
Percent Similarity:	9.00	100.00%	100.00%	0	0	0
Best Local Similarity:	100.00%	100.00%	100.00%	0	0	0
Query Match:	17.65%	17.65%	17.65%	0	0	0
DB:	9	9	9	0	0	0

US-09-402-713a-2 (1-51) x AM093357 (1-528)

Qy 38 SerLeuAlaLeuGlySerLeuValProLeu 46

Db 442 TCATGCGATTGTGTAGTCCATTGA 468

RESULT 7

LOCUS

BI801819/c 531 bp mRNA linear EST 01-NOV-2001

DEFINITION H061G05 Endosperm library from Oryza sativa (10 days after anthesis

) Oryza sativa cDNA clone H061G05, mRNA sequence.

BI801819 GI:16574523

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Eriarthridae; Oryzaceae; Oryza.

1 (bases 1 to 531)

Dong, H. T., Li, D. B., Zhuang, X. F., Dai, C. G., Sun, L. X., Pei, Y. X., Wu

, H. F., Jiang, Y. X., Yu, F. C., Gao, Q. K. and Lou, Y. C.

A Gene Expression Screen in Oryza sativa

unpublished

Contact: Dong HT

Laboratory of Functional Genetics

Bio-Technology Institute of Zhejiang University

Kaixuan Road 268#, Hangzhou, Zhejiang, P. R. China

Tel: 0086-571-86892051

Fax: 0086-571-86961525

Email: htdong@zju.edu.cn

Seq primer: M13 forward primer.

Location/Qualifiers

1. 531

/organism="Oryza sativa"

/mol_type="mRNA"

/db_xref="taxon:4530"

/clone="H061G05"

/tissue_type="Endosperm"

/dev_stage="10 days after anthesis"

/clone_lib="Endosperm library from Oryza sativa (10 days

after anthesis)"

/note="Vector: pSport2"

BASE COUNT 163 a 116 c 123 g 129 t

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	51.9	9	531	0	0	0
Percent Similarity:	9.00	100.00%	100.00%	0	0	0
Best Local Similarity:	100.00%	100.00%	100.00%	0	0	0
Query Match:	17.65%	17.65%	17.65%	0	0	0
DB:	12	12	12	0	0	0

```

US-09-402-713a-2 (1-51) x B1801819 (1-531)
QY      33 LeuglySerMetSerLeuAlaLeu 41
      |||||
Db      366 CTGCTACCTCTATGTCATTCGCAATTG 340.

RESULT 8
LOCUS   AM624953
DEFINITION AM624953 572 bp mRNA linear EST 18-MAY-2001
          ESR313782 tomato radicle, 5 d post-imbibition, Cornell University
          Lycopersicon esculentum cDNA clone CLE29C13 5', mRNA sequence.
ACCESSION AM624953
VERSION   AM624953.1 GI:7337980
KEYWORDS EST.
SOURCE    Lycopersicon esculentum (tomato)
          Lycopersicon esculentum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 572)
          van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,
          Hansen,T., Craven,M.B., Bowman,C.L., Roming,C.M., Nieman,W.,
          Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
          Generation of ESTs from tomato radicle tissue (etiolated)
          Unpublished
          Contact: CUGI
          Clemson University Genomics Institute
          Clemson University
          100 Jordan Hall, Clemson, SC 29634, USA
          Email: http://www.genome.clemson.edu/orders/index.html
          5 prime sequence.
FEATURES
    source             1..572
                        location/Qualifiers
                        /organism="Lycopersicon esculentum"
                        /mol_type="mRNA"
                        /cultivar="TA496"
                        /db_xref="taxon:4081"
                        /clone="CLE29C13"
                        /tissue_type="radicle"
                        /dev_stage="seedlings 5 days post-imbibition"
                        /clone_1lb="tomato radicle, 5 d post-imbibition, Cornell
                        University"
                        /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
                        XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin
                        (USDA-ARS, Ithaca, NY 14850)."
BASE COUNT  165 a 94 c 140 g 173 t
ORIGIN
Alignment Scores:
Pred. No.:      56.4      Length:      572
Score:          9.00      Matches:      9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    17.65% Indels:      0
DB:             9 Gaps:      0

US-09-402-713a-2 (1-51) x AM624953 (1-572)
QY      38 SerLeuAlaLeuCysLeuValProLeu 46
      |||||
Db      486 TCATTGGCATGTGTGTTAGTCCCAATTA 512

RESULT 9
LOCUS   BB634056/c
DEFINITION BB634056 741 bp mRNA linear EST 26-OCT-2001
          BB634056 RIKEN full-length enriched, adult male spinal cord Mus
          musculus cDNA clone A330099N22 5', mRNA sequence.
ACCESSION BB634056
VERSION   BB634056.1 GI:16470372
KEYWORDS EST.
SOURCE    Mus musculus (house mouse)
          Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
AUTHORS
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 741)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Koude
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,
Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamana,I., Atzawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
    source             1..741
                        location/Qualifiers
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /db_xref="taxon:10090"
                        /clone="A330099N22"
                        /sex="male"
                        /tissue_type="spinal cord"
                        /dev_stage="adult"
                        /lab_host="DH10B"
                        /clone_1lb="RIKEN full-length enriched, adult male spinal
                        cord"
                        /note="Site 1: SalI; Site 2: BamHI. cDNA library was
                        prepared and sequenced in Mouse Genome Encyclopedia
                        Project of Genome Exploration Research Group in Riken
                        Genomic Sciences Center and Genome Science Laboratory in
                        RIKEN. Division of Experimental Animal Research in Riken
                        contributed to prepare mouse tissues. 1st strand cDNA was
                        primed with a primer [5'
                        GAGACAGACAGATCCAGACCTCTTTTCTTTTCTTTTCTTTN 3']. cDNA was
                        prepared by using Trenaose Thermo-activated reverse
                        transcriptase and subsequently enriched for full-length by
                        cap-trapper. cDNA went through one round of normalization
                        to Rot = 10.0 and subtraction to Rot = 459.0. Second
                        strand cDNA was prepared with the primer adapter of
                        sequence [5' GAGACAGACATTCGAGTTAATTAATATCCCCCCCCCC
                        3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                        modified pBluescript KS(+) after bulk excision from Lambda

```

```

BASE COUNT      223 a      45 c      270 g      203 t
ORIGIN
Alignment Scores:
Pred. No.:      75.8      Length:      741
Score:          9.00      Matches:      9
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    17.65%      Indels:      0
DB:             10      Gaps:      0

US-09-402-713a-2 (1-51) x BB634056 (1-741)
Oy      5 11eSerSerProPhelystyrProHis 13
Db      584 ATATCATCTCCCTTCAAAATATCCCAT 558

RESULT 10
BM410648      754 bp      mRNA      linear      EST 22-JAN-2002
LOCUS      EST584975 tomato breaker fruit Lycopersicon esculentum cDNA clone
DEFINITION      CLE54K11 5' end, mRNA sequence.
ACCESSION      BM410648
VERSION      BM410648.1 GI:18262278
KEYWORDS      EST.
SOURCE      Lycopersicon esculentum (tomato)
ORGANISM      Lycopersicon esculentum
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
asterids: lamiales: Solanales: Solanaceae: Solanum; Lycopersicon.
1 (bases 1 to 754)
Alcala,J., Vredalov,J., White,R., Visions,T., Karamycheva,S.A., Tsai
,J., Bougri,O., Kirkness,E., Uteback,T., Van Aken,S., Roming
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished
Contact: CGCI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
Location/Qualifiers
1..754
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/db_xref="taxon:4081"
/clone="CLE54K11"
/tissue_type="Pericarp"
/dev_stage="Breaker"
/lab_host="SOLR"
/clone_lib="tomato breaker fruit"
/Note="Vector: pBluescriptSK(-)Mudapt; site_1: EcoRI;
site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."

BASE COUNT      221 a      135 c      177 g      221 t
ORIGIN
Alignment Scores:
Pred. No.:      77.3      Length:      754
Score:          9.00      Matches:      9
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    17.65%      Indels:      0
DB:             12      Gaps:      0

```

```

US-09-402-713a-2 (1-51) x BM410648 (1-754)
Oy      38 SerLeuAlaLeuCysLeuValProLeu 46
Db      702 TCATTGGCATTGTGTAGTCCCATTA 728

RESULT 11
BG527932      132 bp      mRNA      linear      EST 03-APR-2001
LOCUS      602556894F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4685735 5',
DEFINITION      mRNA sequence.
ACCESSION      BG527932
VERSION      BG527932.1 GI:13519469
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
1 (bases 1 to 132)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Invitae Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM495 row: 1 column: 24
High quality sequence stop: 104.
Location/Qualifiers
1..132
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4685735"
/tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_59"
/Note="Organ: Lung; Vector: pDNR-LIB (Clontech); site_1:
SfiI (ggcgccctcgcc); site_2: SfiI (ggccatctggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGACATG-dT(30)BN-3'
sequence (where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
Library."

BASE COUNT      32 a      40 c      31 g      29 t
ORIGIN
Alignment Scores:
Pred. No.:      106      Length:      132
Score:          8.00      Matches:      8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    15.69%      Indels:      0
DB:             10      Gaps:      0

US-09-402-713a-2 (1-51) x BG527932 (1-132)
Oy      34 GlySerSerMetSerLeuAlaLeu 41
Db      29 GGSTCTCGATGTCCCTGTGCTCTG 52

RESULT 12

```

BY370977 174 bp mRNA linear EST 12-DEC-2002
 LOCUS BY370977
 DEFINITION musculus full-length enriched, kidney CCL-142 RAG CDNA Mus
 ACCESSION BY370977
 VERSION BY370977.1 GI:26600465
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 174)
 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
 Nakai,I., Otsu,N., Saito,R., Suzuki,H., Yamanaoka,T., Kiyosawa,H.,
 Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
 Gojobori,T., Baldarelli,R., Hill,D.P., Bul,C., Hume,D.A.,
 Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
 Belset,K.W., Blake,J.A., Bradt,D., Brusic,V., Choitha,C., Corbani,
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 A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.,
 Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
 Jarvis,E.D., Kanai,A., Kawai,H., Kawasawa,Y., Kedzierski,R.M.,
 King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,
 P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,
 H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Perleca,G.,
 Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D.,
 Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,
 B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempile,C.A., Setou,
 M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,
 R.D., Tomita,M., Verardo,R., Wagner,T., Wahlstedt,C., Wang,Y.,
 Watanabe,Y., Wells,C., Wilming,L.G., Wyshaw-Boris,A., Yanagisawa,
 M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
 Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,
 M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
 Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,
 Y., Itoh,M., Kagawa,I., Yasunishi,A., Sakai,K., Sasaki,D., Shibata,
 K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,
 E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 JOURNAL NATURE
 MEDLINE 22354683
 PUBMED 12466851
 COMMENT
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 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,
 T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
 Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
 Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
 M., Waki,K., Watabiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
 Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1737-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
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 ACCESSION B0368838
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 KEYWORDS EST.
 SOURCE
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 239)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL 20202663
 MEDLINE 10737800
 PUBMED 10737800
 COMMENT
 CONTACT Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1<2=PM1-GN0514-310501-006-h01<3=2001-05-31<4=1>)
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products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT      83 a      51 c      61 g      44 t
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DB:              13      Gaps:      0

US-09-402-713A-2 (1-51) x BQ368838 (1-239)
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ACCESSION      BY370387      cDNA clone G430009005 3', mRNA sequence.
VERSION      BY370387.1      GI:26599875
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 243)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,T., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
Gojbori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,
L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,
A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,
Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,
P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Mikl,
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Ramchandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,
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M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,
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Watanabe,Y., Wells,C., Wilming,L.G., Wyszewski-Boris,A., Yanagisawa,
M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
Carinci,P., Hayatsu,N., Hirozane-Kishikawa,T., Kono,H., Nakamura,
M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Aizawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,
Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,
K., Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,
E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL      Nature 420, 563-573 (2002)
MEDLINE      22354683
PUBMED      12466851
COMMENT      Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute

```

```

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Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Aizawa,T., Carninci,P., Fukuda,S., Hirozane,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Kono,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
M., Waki,K., Watanabe,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipillar sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
source      Location/Qualifiers
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US-09-402-713A-2 (1-51) x BY370387 (1-243)
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VERSION      BY370387.1      GI:12279109
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SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 266)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bais,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

```


TITLE Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=QV2&t2=QV2-TN0171-
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Location/Qualifiers

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derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
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low stringency conditions."
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GenCore version 5.1.6
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Post-processing: Listing first 45 summaries

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SUMMARIES

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11	1155	61.7	2426	6	AR278569	AR278569 Sequence
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ALIGNMENTS

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DEFINITION PCA3, PCA3 genes, and methods of use.
ACCESSION BD082483
VERSION BD082483.1 GI:22628093
KEYWORDS JP 2001522240-A/2.
SOURCE Mastadenovirus
ORGANISM Mastadenovirus
VIRUSES: dsDNA viruses, no RNA stage; Adenoviridae.
1 (bases 1 to 1872)
REFERENCE Bussemakers,M.J.G.
AUTHORS PCA3, PCA3 genes, and methods of use
TITLE Patent: JP 2001522240-A 2 13-NOV-2001;
JOURNAL DIAGNOCURE INC

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PI		MARION J G		BUSSEMAKERS			
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						Gaps 0;	
QY	1	AGAGGTGGCATGAGAAAAACAGAGGAGATTTGTGTGCTGCAGCCGAGGAGACAG	60				
DB	1	AGAGGCTGGCATGAGAAAAACAGAGGAGATTTGTGTGCTGCAGCCGAGGAGACAG	60				
QY	61	GAAGATCTGCATGTGGGAAGACCTGATGATACAGAGTGAGAAATTAAGAAAGCTGCT	120				
DB	61	GAAGATCTGCATGTGGGAAGACCTGATGATACAGAGTGAGAAATTAAGAAAGCTGCT	120				
QY	121	GACTTTACATCTGAGGCCACACATCTGCTGAAATGGAGVAAATTAACATCCTAGAAC	180				
DB	121	GACTTTACATCTGAGGCCACACATCTGCTGAAATGGAGVAAATTAACATCCTAGAAC	180				
QY	181	AGCAAGTGCATATATATGTCTAAGTAGTACATGTTTGGACATTTCCACATCCCTTT	240				
DB	181	AGCAAGTGCATATATATGTCTAAGTAGTACATGTTTGGACATTTCCACATCCCTTT	240				
QY	241	AAATATCCACACACAGAGAAAGCAAAAGGAAGACAGATCCCTGGAGAAATGCC	300				
DB	241	AAATATCCACACACAGAGAAAGCAAAAGGAAGACAGATCCCTGGAGAAATGCC	300				
QY	301	GGCCGCCATCTTGGGTCATGATGAGCCTGCCCTGCTGGCTCCGCTTGGAGGAA	360				
DB	301	GGCCGCCATCTTGGGTCATGATGAGCCTGCCCTGCTGGCTCCGCTTGGAGGAA	360				
QY	361	GGCATTAGAAATGATGATGTCTCTTAAGGATGGGAGGAAACAGATCCTGTT	420				
DB	361	GGCATTAGAAATGATGATGTCTCTTAAGGATGGGAGGAAACAGATCCTGTT	420				
QY	421	GTGATATTTTATTTGAACGGGATTACAGATTTGAATGAAGTACAAAGTGACATTAC	480				
DB	421	GTGATATTTTATTTGAACGGGATTACAGATTTGAATGAAGTACAAAGTGACATTAC	480				
QY	481	AATGAGAGGAAACACAGACGAGAAATCTTGATGGCTTCACAGACATGCAACAAACAAA	540				
DB	481	AATGAGAGGAAACACAGACGAGAAATCTTGATGGCTTCACAGACATGCAACAAACAAA	540				
QY	541	TGGAATACGTGTGATGATGAGGACGACCAAGCTGGGAGAGAGATTAACAGGGGCGAGG	600				
DB	541	TGGAATACGTGTGATGATGAGGACGACCAAGCTGGGAGAGAGATTAACAGGGGCGAGG	600				
QY	601	GTGAGATTTCTGCGCTGCTGCTTAACAGTGGCTTCATTAACCAATCATTTATATTTTC	660				
DB	601	GTGAGATTTCTGCGCTGCTGCTTAACAGTGGCTTCATTAACCAATCATTTATATTTTC	660				
QY	661	TAACTCTCAAAACAAAGCTGTGTATATCTGATCTAGAGTTCTTCTGGGCCCAACA	720				
DB	661	TAACTCTCAAAACAAAGCTGTGTATATCTGATCTAGAGTTCTTCTGGGCCCAACA	720				
QY	721	TTCCTCATATATTCAGGACACATCTTTTAAATTTAGTCCCAAGTCTGTACTGAC	780				
DB	721	TTCCTCATATATTCAGGACACATCTTTTAAATTTAGTCCCAAGTCTGTACTGAC	780				
QY	781	CTTTTACACTGATGAGATTAACATTAATCTGATTTGTTCAAGACCTTCGCTGCTGCT	840				
DB	781	CTTTTACACTGATGAGATTAACATTAATCTGATTTGTTCAAGACCTTCGCTGCTGCT	840				
QY	841	AATATGAGCTGACTGTTTTTCCMAAGGAGTGTGCGCCAGGAGATCTGTGAACAGC	900				
DB	841	AATATGAGCTGACTGTTTTTCCMAAGGAGTGTGCGCCAGGAGATCTGTGAACAGC	900				
QY	901	TGGAGACATCTCAAGATCTTTCCAGGCTTATCTTACTAGCACACAGCATCATTTAC	960				
DB	901	TGGAGACATCTCAAGATCTTTCCAGGCTTATCTTACTAGCACACAGCATCATTTAC	960				
QY	961	GGAGTGAATATCAATCAACATCATCTGAGTGTCTTCCCATCTGAAATTCATTTTC	1020				
DB	961	GGAGTGAATATCAATCAACATCATCTGAGTGTCTTCCCATCTGAAATTCATTTTC	1020				
QY	1021	CCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCAATTCATTAATCAAGATTTAA	1080				
DB	1021	CCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCAATTCATTAATCAAGATTTAA	1080				
QY	1081	CTTTTCTTTTAACTCGGAAGATTCAGATGTACATGACGCTATGGGAATTTATTAAGT	1140				
DB	1081	CTTTTCTTTTAACTCGGAAGATTCAGATGTACATGACGCTATGGGAATTTATTAAGT	1140				
QY	1141	ATTTTGTCTTCCAGTCAAGATGACATAGCTTATCCCTCCCTTGTGTGATTTT	1200				
DB	1141	ATTTTGTCTTCCAGTCAAGATGACATAGCTTATCCCTCCCTTGTGTGATTTT	1200				
QY	1201	TTTCCAGTATTAAGTTAAATGCTTAGCCTTGTACTGAGGCTGTATACAGACAGCTCT	1260				
DB	1201	TTTCCAGTATTAAGTTAAATGCTTAGCCTTGTACTGAGGCTGTATACAGACAGCTCT	1260				
QY	1261	CCCCATCCCGCAGCCTTATCTGATCAACATCAACCCCTCCCATNTVSCCTAAACAA	1320				
DB	1261	CCCCATCCCGCAGCCTTATCTGATCAACATCAACCCCTCCCATNTVSCCTAAACAA	1320				
QY	1321	ATCTAATCTGTAATCTCTGTAACATGTCAGAGNATACATTTCTTCTGCTCGAGAAAG	1380				
DB	1321	ATCTAATCTGTAATCTCTGTAACATGTCAGAGNATACATTTCTTCTGCTCGAGAAAG	1380				
QY	1381	TCTTCTTCTGCTTAAATCTAGATGATGTAAGTTTGAATTAAGTGAATCTTACT	1440				
DB	1381	TCTTCTTCTGCTTAAATCTAGATGATGTAAGTTTGAATTAAGTGAATCTTACT	1440				
QY	1441	TCAATGAAAGGAGGACATATGAGATTCATACATGACAGACAGCAATCTTAAAG	1500				
DB	1441	TCAATGAAAGGAGGACATATGAGATTCATACATGACAGACAGCAATCTTAAAG	1500				
QY	1501	TGTAAATTTGATTAAGAGTTTGAATTAATATATGAATGCAAGACCAAGAGGAATG	1560				
DB	1501	TGTAAATTTGATTAAGAGTTTGAATTAATATATGAATGCAAGACCAAGAGGAATG	1560				
QY	1561	TTTATGGGCGACITTTGTAAGCCTGGGATGTGAAGAAAGGCGAGACCTCATATATC	1620				
DB	1561	TTTATGGGCGACITTTGTAAGCCTGGGATGTGAAGAAAGGCGAGACCTCATATATC	1620				
QY	1621	TTTATTAATATCTTCAATTTCTATCTCATGACATATCAACAAAGCTTTCAAGAA	1680				
DB	1621	TTTATTAATATCTTCAATTTCTATCTCATGACATATCAACAAAGCTTTCAAGAA	1680				
QY	1681	TTTATGACAGTCAAAATCCCAAGGTAACCTTATTCATTTCAATGCTGAGTGGCTTTAG	1740				
DB	1681	TTTATGACAGTCAAAATCCCAAGGTAACCTTATTCATTTCAATGCTGAGTGGCTTTAG	1740				
QY	1741	AAATTTGGCAAAATCACTAGTCACTTATCTCAATCTTGAAGATGTGCTGCTTACT	1800				
DB	1741	AAATTTGGCAAAATCACTAGTCACTTATCTCAATCTTGAAGATGTGCTGCTTACT	1800				
QY	1801	TAAATTAAGAAATTAAGGACCTTGTGAGCCACTTTAGGCTTCACTCTGGCAATTAAG	1860				
DB	1801	TAAATTAAGAAATTAAGGACCTTGTGAGCCACTTTAGGCTTCACTCTGGCAATTAAG	1860				

RESULT 2
BD082482
LOCUS BD082482 2037 bp DNA linear PAT 27-AUG-2002
DEFINITION PC3, PCA3 genes, and methods of use.
ACCESSION BD082482
VERSION BD082482.1 GI:22628092
KEYWORDS JP 2001522240-A/1.
SOURCE Mastadenovirus
ORGANISM Mastadenovirus
REFERENCE
1 (bases 1 to 2037)
AUTHORS Bussemakers, M.J.G.
TITLE PC3, PCA3 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 1 13-NOV-2001;
DIAGNOCURE INC SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES
COMMENT
PN JP 2001522240-A/1
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC
C1201/68,
PC G01N33/577,A61K39/395,A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 379..531.
Location/Qualifiers
1..2037
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"
BASE COUNT 622 a 426 c 406 g 575 t 8 others
ORIGIN
Query Match 94.8%; Score 1775; DB 6; Length 2037;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 GGTGAGAAATGAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 157
DB 263 GGTGAGAAATGAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATGG 322
QY 158 AGATAATTACATCTAGAAAGACAGATGACATATTAATGCTAGTAGTGATGT 217
DB 323 AGATAATTACATCTAGAAAGACAGATGACATATTAATGCTAGTAGTGATGT 382
QY 218 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGAAACACAAAAGAGAC 277
DB 383 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGAGAAACACAAAAGAGAC 442
QY 278 AGAATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCAATGATGAGCCTCGCCCTGT 337
DB 443 AGAATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCAATGATGAGCCTCGCCCTGT 502
QY 338 GCCTGTGCTCCGCTGTGAGGAGAGACATTTAGAAAATGAATTGATGTTCTTTAAAGA 397
DB 503 GCCTGTGCTCCGCTGTGAGGAGAGACATTTAGAAAATGAATTGATGTTCTTTAAAGA 562
QY 398 TGGGAGGAAAAAGATCCTGTGTGATATTTATTGTAACGGGATTTACAGATTTGAAT 457
DB 563 TGGGAGGAAAAAGATCCTGTGTGATATTTATTGTAACGGGATTTACAGATTTGAAT 622
QY 458 GAATGCACAAGTAGCATTTACCAATGAGAGAAAAACAGAGAAAAATCTTGATGGCTT 517
DB 623 GAATGCACAAGTAGCATTTACCAATGAGAGAAAAACAGAGAAAAATCTTGATGGCTT 682

QY 518 CACAAGATGCAACAACAATAATGATTAAGTACTGTGATGATGATGAGAGCCAGCAGCTGGGG 577
DB 683 CACAAGATGCAACAACAATAATGATTAAGTACTGTGATGATGATGAGAGCCAGCAGCTGGGG 742
QY 578 AGAGATTAACCAAGGGGAGAGAGGTGAGATTTGGCCCTGCTGCTTAAGTGTGCTTC 637
DB 743 AGAGATTAACCAAGGGGAGAGAGGTGAGATTTGGCCCTGCTGCTTAAGTGTGCTTC 802
QY 638 ATAACCAATATCTTATTTATTTTATTAACCTTCAACCAACAAAGCTGTTGTAATATGATGTC 697
DB 803 ATAACCAATATCTTATTTATTTTATTAACCTTCAACCAACAAAGCTGTTGTAATATGATGTC 862
QY 698 TACGTTCTCTTGCGGCCCAACATTTCTCATATATCCAGCCACACTCATTTTATATTT 757
DB 863 TACGTTCTCTTGCGGCCCAACATTTCTCATATATCCAGCCACACTCATTTTATATTT 922
QY 758 AGTTCCAGATCTGTACTGTGACCTTTCTACAGCTGATGATTAACATTAATCTATTTTGTTC 817
DB 923 AGTTCCAGATCTGTACTGTGACCTTTCTACAGCTGATGATTAACATTAATCTATTTTGTTC 982
QY 818 AAAGACCTTGTGCTGCTGCTTAATATGATGATGATGATGATGATGATGATGATGATG 877
DB 983 AAAGACCTTGTGCTGCTGCTTAATATGATGATGATGATGATGATGATGATGATGATG 1042
QY 878 GCCCAGGGGATCTGTGAACAGGCTGGAGAGATCTCAAGATCTTCCAGGGTTATACCTTA 937
DB 1043 GCCCAGGGGATCTGTGAACAGGCTGGAGAGATCTCAAGATCTTCCAGGGTTATACCTTA 1102
QY 938 CTAGACACACAGATGATTAAGAGATTAATTAATCAATCAATCAATCAATCAATCAATCA 997
DB 1103 CTAGACACACAGATGATTAAGAGATTAATTAATCAATCAATCAATCAATCAATCAATCA 1162
QY 998 TTGGCCATACATGAATTAATTTCCACATTTTGTGGCCATTTCTCAAGACCTCAAAAATGTC 1057
DB 1163 TTGGCCATACATGAATTAATTTCCACATTTTGTGGCCATTTCTCAAGACCTCAAAAATGTC 1222
QY 1058 TTCCATTAATATCAAGATTAATTTTAACTTGAAGAGATTAATTAATTAATTAATTAAT 1117
DB 1223 TTCCATTAATATCAAGATTAATTTTAACTTGAAGAGATTAATTAATTAATTAATTAAT 1282
QY 1118 CAGCTAGGGAATTAATTAATTAATTTTCCAGTGAACAGATGATGATGATGATGATGATG 1177
DB 1283 CAGCTAGGGAATTAATTAATTAATTTTCCAGTGAACAGATGATGATGATGATGATGATG 1342
QY 1178 TCCCTCCCTTGTGATTTTTCACAGTAATTAATTAATTAATTAATTAATTAATTAATTA 1237
DB 1343 TCCCTCCCTTGTGATTTTTCACAGTAATTAATTAATTAATTAATTAATTAATTAATTA 1402
QY 1238 AGGCTGTATACAGACAGCCTCTCCCATCTCCAGCCTTATCTGATCAGCATCAAC 1297
DB 1403 AGGCTGTATACAGACAGCCTCTCCCATCTCCAGCCTTATCTGATCAGCATCAAC 1462
QY 1298 CCTCCCATATTAACCAAAATCTAATTTGTAATTTCTTGAACATGTCAGGATGATG 1357
DB 1463 CCTCCCATATTAACCAAAATCTAATTTGTAATTTCTTGAACATGTCAGGATGATG 1522
QY 1358 ATTTTCCTCTGCTGAGAGCTCTCTGCTGCTTAATTAATTAATTAATTAATTAATTA 1417
DB 1523 ATTTTCCTCTGCTGAGAGCTCTCTGCTGCTTAATTAATTAATTAATTAATTAATTA 1582
QY 1418 TTGAATTAATTAATTAATTAATTTCAAAAGAGGACATTAATGATTCATCATCA 1477
DB 1583 TTGAATTAATTAATTAATTTCAAAAGAGGACATTAATGATTCATCATCA 1642
QY 1478 CATGACACAGCAATTAATAAGTGAATTTGATTTAATGAAGTTTGAATTAATTAATGA 1537
DB 1643 CATGACACAGCAATTAATAAGTGAATTTGATTTAATGAAGTTTGAATTAATTAATGA 1702
QY 1538 ATGCAAGKCCACAGAGGAGATGTTATGGGACAGTTGTAAGCCGCGGATGTAAGTA 1597
DB 1703 ATGCAAGKCCACAGAGGAGATGTTATGGGACAGTTGTAAGCCGCGGATGTAAGTA 1762
QY 1598 AAGCAGGAACTCATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1657

Db	1763	AAGCAGAGGAACCCATCATGTATCTATTAATATATACCTTCTCTATCTATACAA	18222
Qy	1658	TATCCAAACAGCTTTTCACAGAAATTCATGACAGTGCAAATCCCAAGSTAACCTTATCC	17171
Db	1823	TATCCAAACAGCTTTTCACAGAAATTCATGACAGTGCAAATCCCAAGSTAACCTTATCC	18822
Qy	1718	ATTTCATGCGTAGTGGCGCTTTTAAATTTTGGCAATCATATCTGGTCACTTATTCACACT	17777
Db	1883	ATTTCATGCGTAGTGGCGCTTTTAAATTTTGGCAATCATATCTGGTCACTTATTCACACT	19422
Qy	1778	TGAGATGTGTGTGTCTGTAGTAATTTGAAGAATATAGGCGACTCTGTAGGCACATT	18372
Db	1943	TGAGATGTGTGTGTCTGTAGTAATTTGAAGAATATAGGCGACTCTGTAGGCACATT	20022
Qy	1838	AGGTTCACTCTCTGGCAATTAAGAATTTTACAAAG	1872
Db	2003	AGGTTCACTCTCTGGCAATTAAGAATTTTACAAAG	2037
RESULT 3			
BD082485			
LOCUS	BD082485	3582 bp	DNA
DEFINITION	PCa3, PCa3 genes, and methods of use.		linear
ACCESSION	BD082485.1		
VERSION	BD082485.1 GI:22628095		
KEYWORDS	JP 2001522240-A/4.		
SOURCE	JP 2001522240-A/4.		
ORGANISM	Mastadenovirus		
REFERENCE	Mastadenovirus		
AUTHORS	1 (bases: dsDNA viruses, no RNA stage; Adenoviridae.		
TITLE	Bussemakers, M.J.G.		
JOURNAL	Patent: JP 2001522240-A 4 13-NOV-2001;		
COMMENT	DIAGNOCURE INC		
	PN JP 2001522240-A/4		
	PD 13-NOV-2001		
	PF 09-APR-1998 JP 1998542194		
	PR 10-APR-1997 US 60/041836		
	PI MARION J G BUSSEMAKERS		
	PC C12NM15/00.C12NM15/12.C12NM15/21.C07K14/47.C07K16/18, PC		
	C12O1/68.		
	PC G01N33/577, A61K39/395, A01K67/027		
	CC Strandedness: Double;		
	CC Topology: Linear;		
	CC Key		
	EH Location/Qualifiers		
	FT CDS		
FEATURES			
source	1..3582	Location/Qualifiers	
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	/db_xref="taxon:10509"		
BASE COUNT	1052 a	787 c	680 g 1063 t
ORIGIN			
Query Match	73.0%; Score 1367; DB 6; Length 3582;		
Best Local Similarity	99.5%; Pred. No. 0;		
Matches 1767; Conservative	0; Mismatches 8; Indels 0; Gaps 0;		
Qy	98	GGTGAGAAATTAAGAAAGGCTGCTACCTTACCATCTGAGGCCACACATCTGCTGAATATGG	157
Db	285	GGTGAGAAATTAAGAAAGGCTGCTGCTACCTTACCATCTGAGGCCACACATCTGCTGAATATGG	344
Qy	158	AGATTAATTAACATCTAGAAACAGCAAGATGACATATATATGCTTAAGTAGTACATGT	217
Db	345	AGATTAATTAACATCTAGAAACAGCAAGATGACATATATATGCTTAAGTAGTACATGT	404
Qy	218	TTTTGCACATTTTCAGCCCTTTTAATATATCCACACACACAGGAAGCAAAAGGAAGCAC	277
Db	405	TTTTGCACATTTTCAGCCCTTTTAATATATCCACACACACAGGAAGCAAAAGGAAGCAC	464
Qy	278	AGAGATCCCTGGGAGAAATGCCGGCCCATCTTGGGTATCGATGATGACGCTGGCCTGT	337

Db	465	AGAGATTCCTGGGAGAAATGCCCGCGCCATCTTGGGTCATGAGATGAGCCTGGCCCTGT	524
QY	338	GCCTGCTCCGCTGTGTGAGGAGAGACATTAGAAAAATGAATTGATGTCTTCTTAAAGA	397
Db	525	GCCTGCTCCGCTGTGTGAGGAGAGACATTAGAAAAATGAATTGATGTCTTCTTAAAGA	584
QY	338	TGGGAGAGAAACAGATCCTGTGTGTGTGATATTATTGAAACGGGATTTACGATTTGAAAT	457
Db	565	TGGGAGAGAAACAGATCCTGTGTGTGTGATATTATTGAAACGGGATTTACGATTTGAAAT	644
QY	458	GAAGTCACAAAGTGCATTTACCAATGAGAGGAAAAACACAGAGAAATCTTGATGGCTT	517
Db	645	GAAGTCACAAAGTGCATTTACCAATGAGAGGAAAAACACAGAGAAATCTTGATGGCTT	704
QY	518	CACAGAACATGCAACAACAAATGGAATACTGTGATGACATGAGCAGCCAGCTGGGG	577
Db	705	CACAGAACATGCAACAACAAATGGAATACTGTGATGACATGAGCAGCCAGCTGGGG	764
QY	578	AGGACATTAACACAGGGGGCAGAGGGTCAAGATTTGACCCTGGCGCTTAAACGTGGGTTG	637
Db	765	AGGACATTAACACAGGGGGCAGAGGGTCAAGATTTGACCCTGGCGCTTAAACGTGGGTTG	824
QY	638	ATTAACCAATCATTTTCATTTTCTTAACCTTCACAAACAAAGCTGTGTAATCTGATCTC	697
Db	825	ATTAACCAATCATTTTCATTTTCTTAACCTTCACAAACAAAGCTGTGTAATCTGATCTC	884
QY	698	TACGGTTCCTTCTGGGGCCACACATTCCTCAATATATCCAGCCACATCATTTTAAATATT	757
Db	885	TACGGTTCCTTCTGGGGCCACACATTCCTCAATATATCCAGCCACATCATTTTAAATATT	944
QY	758	AGTTCGCCAGATGTGATCTGTGACCTTCTACACTGTAGAAATTAACATTACTCATTTGCTC	817
Db	945	AGTTCGCCAGATGTGATCTGTGACCTTCTACACTGTAGAAATTAACATTACTCATTTGCTC	1004
QY	818	AAAGACCCCTGCTGTGTGCTGCTAAATATAGTGTGCTGCTTTTCTTAAGAGATGTTCTG	877
Db	1005	AAAGACCCCTGCTGTGTGCTGCTAAATATAGTGTGCTGCTTTTCTTAAGAGATGTTCTG	1064
QY	878	GCCCCAGGGGATCTGGAACAGGCTGGGAGACATCTCAAGATCTTTCAGGGTTATACTTA	937
Db	1065	GCCCCAGGGGATCTGGAACAGGCTGGGAGACATCTCAAGATCTTTCAGGGTTATACTTA	1124
QY	938	CTAGACACACAGATGATCATTTACGGAGTGAATTTATTAACAACATCATCTCTAGTGTCT	997
Db	1125	CTAGACACACAGATGATCATTTACGGAGTGAATTTATTAACAACATCATCTCTAGTGTCT	1184
QY	998	TTGCCATACACAAATTCATTTCCCACTTTGGCCATTCGCAACACCTCAAAAATGTCA	1057
Db	1185	TTGCCATACACAAATTCATTTCCCACTTTGGCCATTCGCAACACCTCAAAAATGTCA	1244
QY	1058	TTCCATTAAATACAGAGATTAACTTTTCTTAACTCGAAGAAATTCATATGTTACATG	1117
Db	1245	TTCCATTAAATACAGAGATTAACTTTTCTTAACTCGAAGAAATTCATATGTTACATG	1304
QY	1118	CAGCATATGGGAATTTAATTACATATTTTGTTCACAGTCAAAAGATGACTAGTCTTTA	1177
Db	1305	CAGCATATGGGAATTTAATTACATATTTTGTTCACAGTCAAAAGATGACTAGTCTTTA	1364
QY	1178	TCCCTCCCTTGTGTGATTTTCTTCCAGTAAAGTAAAGTAAAGTGTAGCCCTGTAGCTG	1237
Db	1365	TCCCTCCCTTGTGTGATTTTCTTCCAGTAAAGTAAAGTAAAGTGTAGCCCTGTAGCTG	1424
QY	1238	AGGCTGTATACAGCACAGCCTCTCTCCCACTCCCTCCAGCCTTATCTGTCAATCAACATCAAC	1297
Db	1425	AGGCTGTATACAGCACAGCCTCTCTCCCACTCCCTCCAGCCTTATCTGTCAACATCAAC	1484
QY	1298	CCCTCCCATNTSACCTAAACAAATCTAATCTGTGTAATCTTGAACATGTCAAGNCATAC	1357
Db	1485	CCCTCCCATNTSACCTAAACAAATCTAATCTGTGTAATCTTGAACATGTCAAGNCATAC	1544
QY	1358	ATTATTCCTTCTGCTGTGAGAGCTCTCTCTGTCTTAATCTGAAGATGATTAAGTT	1417
Db	1545	ATTATTCCTTCTGCTGTGAGAGCTCTCTCTGTCTTAATCTGAAGATGATTAAGTT	1604

OY	1418	TTGAATAAGTGCATCTACTTCTCATGCAAGAAGGACACATATGAGATTCAATCA	1477
Db	1605	TTGATAATAGTTGATATCTTACTTCATGCAAGAAGGACACATATGAGATTCAATCA	1664
OY	1478	CATGAGACAGCAATACTAAAGAGTAATTGATTATATAGAGTTAGATAATATATGA	1537
Db	1665	CATGAGACAGCAATACTAAAGAGTAATTGATTATATAGAGTTAGATAATATATGA	1724
OY	1538	ATGCAAGACCACAGAGGAATGTTTATGSGGACGTTTGTAAOCTTGAGATGGAAG	1597
Db	1725	ATGCAAGAGCCACAGAGGAATGTTTATGSGGACGTTTGTAAOCTTGAGATGGAAG	1784
OY	1598	AAGCAGGGAACCATATGATATCTATATATATATACCTATTCCTATATCTATACAA	1655
Db	1785	AAGCAGGGAACCATATGATATCTATATATATATACCTATTCCTATATCTATACAA	1844
OY	1658	TATCCAAACAACTTTTCACAGAAATTCATGATGATCCCAATCCCAAGGTAACTTATCC	1717
Db	1845	TATCCAAACAACTTTTCACAGAAATTCATGATGATCCCAATCCCAAGGTAACTTATCC	1904
OY	1718	ATTTCATGAGTAGAGCGCTTATGAATTTTGGCAATCATACTGGTCACTTATCTCACTT	1777
Db	1905	ATTTCATGAGTAGAGCGCTTATGAATTTTGGCAATCATACTGGTCACTTATCTCACTT	1964
OY	1778	TGAGATGATGTTGTCCTGTAGTAATTTGAAGAATATGGGCACTCTGTGAGCACCTTT	1837
Db	1965	TGAGATGATGTTGTCCTGTAGTAATTTGAAGAATATGGGCACTCTGTGAGCACCTTT	2024
OY	1838	AGGCTTCACTCTTGCAATTAAGAATTTACAAAG	1872
Db	2025	AGGCTTCACTCTTGCAATTAAGAATTTACAAAG	2059

RESULT 4				
AR261166				
LOCUS	AR261166	3923 bp	DNA	linear
DEFINITION	Sequence 690 from patent US 6321716.			PAT 29-JAN-2003
ACCESSION	AR261166			
VERSION	AR261166.1	GI:28071929		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
	Unclassified.			
REFERENCE	1 (bases 1 to 3923)			
AUTHORS	Mashiki,Z. and Harada,J.			
TITLE	Negative pressure control apparatus for engine mounted in vehicle			
JOURNAL	Patent: US 6321716-A 690 27-NOV-2001;			
FEATURES	location/qualifiers			
	1..3923			
SOURCE	/organism="unknown"			
BASE COUNT	1157 a	840 c	740 g	1186 t
ORIGIN				

	Query Match	73.0%	Score 1367;	DB 6;	Length 3923;
	Best Local Similarity	99.5%	Prod. No. 0;		
	Matches 167;	Conservative	0;	Mismatches 8;	Indels 0;
				Gaps	0;
OY	98	GGTGAGAAATTAAGAAAGGCTGCTACTTACATCTGAGGCGACACATCTGCTGAATAGG	157		
Db	285	GGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCGACACATCTGCTGAATAGG	344		
OY	158	AGATTAATTACATCACTTGAAGAACAGCAAGATGACAAATTAATGTCTTAAGTGTGATCATGT	217		
Db	345	AGATTAATTACATCACTTGAAGAACAGCAAGATGACAAATTAATGTCTTAAGTGTGATCATGT	404		
OY	218	TTTTGCACATTTCCAGCCCTTTTAAATPPTCCACACACACAGAGAACACAAAAGGAAGTAC	277		
Db	405	TTTTGCACATTTCCAGCCCTTTTAAATPPTCCACACACACAGAGAACACAAAAGGAAGTAC	464		
OY	278	AGAGATCCCTGGAGAAATTCGCCGCGCCACTTTGGGTGCATCGATGAGGCTCGCCCTGT	337		
Db	465	AGAGATCCCTGGAGAAATTCGCCGCGCCACTTTGGGTGCATCGATGAGGCTCGCCCTGT	524		

QY	338	GCTGTGTC	CCGCTTGTG	GGGAGGACATTG	AAAAATGATGTG	CTTCCCTTAAGGA	397
Db	525	GCTGTGTC	CCGCTTGTG	GGGAGGACATTG	AAAAATGATGTG	CTTCCCTTAAGGA	584
QY	398	TGGGAGGAAA	CACATCTGTG	TGGATATTTATTTAG	GGGGTTACAGTTTGAAT		457
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QY	518	CACAAGACAT	GCACAAACAAATG	AGATCTGTATACAT	ATGAGGAGCCCAAGCTGGGG		577
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QY	578	AGAGATTAAC	ACGAGGGGAGAGGG	GTGACAGATTTTGCCCTGCTG	CTTAACGTGTCGCTG		637
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QY	638	ATACCAAAAT	CATTTTCATATTTCT	TAACCTCAAAACAAAGCTG	TTGTAAATCTGATCTC		697
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QY	818	AAAGACCCCT	GTGTGCTGCTATAT	GTAGTACACTGTTTCTTA	AGAGAGTGTCTG		877
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QY	998	TTGCCATAC	TGAATTCATTTCC	CACTTTGTGCCATTTCT	CAAGACCTCAAAATGTCA		1057
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QY	1058	TTCCATTAA	TATCACAGATTA	ACTTTTTTTTTTA	ACCTGGAGAAATGTACATG		1117
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Db	1485	CCCTTCCAT	NTSACCTAAACAAA	ATCTAATCTGTAATTC	CTTGAACATGTAGGNCATAC		1544
QY	1358	ATTATTCCT	TCTGTGCTGAGAAG	CTTCTCTGTCTCTTA	NTCTTAAGATGTATAAGTT		1417
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RESULT 5
LOCUS AR278697 3923 bp DNA linear PAT 10-Apr-2003
DEFINITION Sequence 690 from patent US 6512094.
ACCESSION AR278697
VERSION AR278697.1 GI:29712943
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3923)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 690 28-JAN-2003;
FEATURES
source Location/Qualifiers
BASE COUNT 1157 a 840 c 740 g 1186 t
ORIGIN

Query Match 73.0%; Score 1367; DB 6; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 6
AX200988 3923 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 618 from Patent W00151633.
DEFINITION AX200988
ACCESSION AX200988
VERSION AX200988.1 GI:15390814
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skelky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 618 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..3923
Location/Qualifiers
/organism="Homo sapiens"
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/db_xref="taxon:9606"
BASE COUNT 1157 a 840 c 740 g 1186 t
ORIGIN

Query Match 73.0%; Score 1367; DB 6; Length 3923;
Best Local Similarity 99.5%; Freq. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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DEFINITION	Sequence 690 from Patent WO0173032.	linear	PAT 26-OCT-2001
ACCESSION	AX267716		
VERSION	AX267716.1	GI:16516388	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1		
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,		
	Kalos,M.D., Fanger,G.R., Rether,M.W., Stolk,J.A., Day,C.H.,		
	Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A., Hepler,W.T.		
	and Henderson,R.A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate		
	Cancer		
JOURNAL	Patent: WO 01/3032-A 690 04-OCT-2001;		
FEATURES	CORIXA CORPORATION (US)		
SOURCE	Location/Qualifiers		
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BASE COUNT	1157 a 840 c 740 g 1186 t		
ORIGIN			
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Best Local Similarity	99.5%;	Pred. No. 0;	
Matches 1767; Conservative	0;	Mismatches 8;	Indels 0;
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RESULT 9
AF103908

LOCUS AF103908 5435 bp DNA linear PRI 14-AUG-2000
DEFINITION Homo sapiens non-coding RNA DD3 gene, exons 2, 3, and 4.
ACCESSION AF103908
VERSION AF103908.1 GI:6165974
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Bussemakers,M.J., van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Kathaus,H.F., Schalken,J.A., Debruyne,F.M., Ru.N. and Isaacs,W.B.
TITLE Bussemakers,M.J., van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Kathaus,H.F., Schalken,J.A., Debruyne,F.M., Ru.N. and Isaacs,W.B.
DOI: a new prostate-specific gene, highly overexpressed in prostate
cancer
JOURNAL Cancer Res. 59 (23), 5975-5979 (1999)
MEDLINE 20072260
PUBMED 10606244
REFERENCE 2 (bases 1 to 5435)
AUTHORS Bussemakers,M.J., Van Bokhoven,A., Verhaegh,G.W., Smit,F.P.,
Kathaus,H.F.M., Schalken,J.A., Debruyne,F.M.J., Ru.N. and
Isaacs,W.B.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) Urology Research Laboratory, University
Hospital Nijmegen, P.O. Box 9101, Nijmegen 6500 HB, Netherlands
FEATURES
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BASE COUNT 1546 a 1188 c 1036 g 1654 t 11 others
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Best Local Similarity 99.5%; Pred. No. 0;
Matches 1585; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 400 GGCAGGAAACGATCGTTGTGATATTTTGAACGGGATACGATTTGAATGA 459
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RESULT 10
AR261038/c
LOCUS AR261038 2426 bp DNA linear PART 29-JAN-2003
DEFINITION Sequence 470 from patent US 6321716.
ACCESSION AR261038
VERSION AR261038.1 GI:28071801
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2426)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 470 27-NOV-2001;
FEATURES
source
1..2426
/organism="unknown"
BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN

Query Match 61.7%: Score 1155; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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D 630 GAGGCTGTATACAGC 616

RESULT 11
AR278569/c 2426 bp DNA linear PAT 10-Apr-2003
LOCUS AR278569 Sequence 470 from patent US 6512094.

ACCESSION AR278569
VERSION AR278569.1 GI:29712815
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2426)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6512094-A 470 28-JAN-2003;
FEATURES Location/Qualifiers
source 1..2426
BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN
Query Match 61.7%; Score 1155; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGAGAAATTAAGAAAGCTGCTGACTTACCATCTGAGGCCACACATCTGTAATG 156
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Qy 1237 GAGGCTGTATACAGC 1251
Db 630 GAGGCTGTATACAGC 616

RESULT 12
AX106206/c 2426 bp DNA linear PAT 30-APR-2001
LOCUS AX106206 Sequence 344 from Patent W00125273.
DEFINITION AX106206
ACCESSION AX106206
VERSION AX106206.1 GI:13921895
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Skelley Y.A., Xu J., Cheever M.A. and Reed S.G.
TITLE Compositions and methods for wtl specific immunotherapy
JOURNAL Patent: WO 0125273-A 344 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN

Query Match 61.7%; Score 1155; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 AGGTGAGAAATAGAAAGGCTGCTGACTTTTACCATCTGAGCCACACATCTGTAATG 156
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Qy 1237 GAGGCTGTATACAGC 1251
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AX106689/c 2426 bp DNA linear PAT 30-APR-2001
LOCUS AX106689 Sequence 470 from Patent W00125272.
DEFINITION AX106689
ACCESSION AX106689

VERSION AX106689.1 GI:13922354
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
AUTHORS Xu, J., Skelky, Y.A., Reed, S.G. and Cheever, M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0125272-A 470 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1.2426
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/db_xref="taxon:9606"

BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN

Query Match 61.7%; Score 1155; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 156
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DB 810 ATTCATTAATATACAGAGATTAATCTTTTATTTTACCTGGAAGATTCATATGTTTCAAT 751

QY 1117 GCAGCTATGGGAATTTATTAATATTTTTCAGTGCAGTCAAGAGATGATGATGATGATGAT 1176
DB 750 GCAGCTATGGGAATTTATTAATATTTTTCAGTGCAGTCAAGAGATGATGATGATGATGAT 691

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DB 690 ATCCCTCCCTTTGTTGATTTTTCAGTATTAAGTTAAATGCTTAGCCTTGATCT 631

QY 1237 GAGGCTGATACAGC 1251
DB 630 GAGGCTGATACAGC 616

RESULT 14
AX140980/c 2426 bp DNA linear PAT 31-MAY-2001
LOCUS AX140980
DEFINITION Sequence 470 from Patent W00134802.
ACCESSION AX140980
VERSION AX140980.1 GI:14281077
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.B., Skelky, Y.A. and Wang, A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0134802-A 470 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 717 a 476 c 548 g 685 t
ORIGIN

Query Match 61.7%; Score 1155; DB 6; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 156
DB 1770 AGGTGAGAAATAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 1711

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DB 1710 GAGATATTAACATCACTAGAACAGACAGATGACATATATGTCTAAGTAGACATG 1651

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QY 397 ATGGCAGAGAAAACAGATCTGTGTGATATTTATTTGACGGATTAACAGATTTGAAA 456
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Db 1350 TCACAAGACATGCAACAAACAAATGGAATGATCTGATGACATGAGGACAGCAAGCTGGG 1291
QY 577 GAGGAGATPACACAGGGGAGAGGTCAGGATTCGGCCCTGCTGCTTAACCTGTGCGTT 636
Db 1290 GAGGAGATPACACAGGGGAGAGGTCAGGATTCGGCCCTGCTGCTTAACCTGTGCGTT 1231
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Db 1170 CTACGGTTCCTTCTGGGCCCAACATTTCTCATATATACAGCCACATCTATTTTAAATAT 1111
QY 757 TAGTTCACAGATCTGTACTGTGACCTTTTACACTGTAGATTAACATTTCTGTT 816
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AX200840/c

LOCUS AX200840 2426 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 470 from Patent WO0151633.
ACCESSION AX200840
VERSION AX200840.1 GI:15390743
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Rietter,M.W.,
Stolk,J.A., Skelly,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
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Patent: WO 0151633-A 470 19-JUL-2001;
CORIXA CORPORATION (US)
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BASE COUNT 717 a 476 c 348 g 685 t
ORIGIN
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Best Local Similarity 100.0%; Pred No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGGAATTAAGAAAGGCTGCTGACCTTACCATCTGAGGCCACACATCTGCTGAATG 156
Db 1770 AGGTGGAATTAAGAAAGGCTGCTGACCTTACCATCTGAGGCCACACATCTGCTGAATG 1711
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Db 1290 GAGGAGATPACACAGGGGAGAGGTCAGGATTCGGCCCTGCTGCTTAACCTGTGCGTT 1231
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OY 817 CAAGACCCCTCGTGTGCTGCTAATATATGAGCTGTTTCCCTAAGAGTGTCT 876
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Db 1050 CAAGACCCCTCGTGTGCTGCTAATATATGAGCTGTTTCCCTAAGAGTGTCT 991
OY 877 GGGCCAGGGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGGTTATACTT 936
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Db 990 GGGCCAGGGGATCTGTGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGGTTATACTT 931
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OY 1117 GCAGCTATGGGAATTTATACATATTTGTTTCCAGTGCAGAAAGATGACTAAGTCTT 1176
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Searched: 2552756 seqs, 1349719017 residues

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4	1367	73.0	3923	22	AAH64026	Human cDNA encodin
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6	1367	73.0	3923	24	ABK92196	Prostate cancer-as
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						Prostate cancer th

C	9	1155	61.7	2426	21	AA06689	Human immunogenic
C	10	1155	61.7	2426	22	AA56388	Human prostate cDN
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C	13	1155	61.7	2426	22	AAH02870	Prostate tumour an
C	14	1155	61.7	2426	22	AAAF6694	Human P710P invent
C	15	1155	61.7	2426	24	ABL95629	Human P710P cDNA s
C	16	1155	61.7	2426	25	ACA59706	Prostate cancer th
C	17	1155	61.7	3112	21	AAAO6687	Human immunogenic
C	18	1155	61.7	3112	22	AA563896	Human prostate cDN
C	19	1155	61.7	3112	22	AAH93803	Human prostate-spe
C	20	1155	61.7	3112	22	AAH85117	Human prostate-spe
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C	37	812	43.4	812	22	AAH93806	Human prostate-spe
C	38	812	43.4	812	22	AAH85120	Human prostate-spe
C	39	812	43.4	812	22	AAH02871	Prostate tumour an
C	40	812	43.4	812	22	AAAF6694	Human P710P invent
C	41	812	43.4	812	24	ABL95270	Human P710P cDNA s
C	42	812	43.4	812	25	ACA59707	Prostate cancer th
C	43	475	25.4	658	23	ABV42450	Human prostate exp
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ALIGNMENTS

RESULT 1

ID AAV62428 standard; cDNA; 1872 BP.

AC AAV

DT 30-DEC-1998 (first entry)

DE Prostate cancer antigen (PCA3) cDNA splice variant 2.

KW Prostate cancer antigen CDNA splice variant 2; PCA3; prostatic cancer;

PC;

OS
HOM

PN W09845420-A1.

PD 15-OCT-1998.

PF 09-APR-1998;

PR 10-APR-1997; 97US-0041836

PA (DIAG-) DIAGNOCURE INC.

PI Bussemakers MJC,

DR WPI; 1998-568347/48.

PT New nucleic acid encoding prostate cancer antigen 3 - for diagnosis
PT prevention and treatment of prostatic cancer

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Db	1741	AAATTTGGCAATATATCTGCTACCTATCTCAACTTGGATGATGTGTCCTTAGT	1800
OY	1801	TAAATGAAGAAATAGGCACTCTTGAGCCACTTATAGGGTTCATCTGCAATTAAG	1860
Db	1801	TAAATGAAGAAATAGGCACTCTTGAGCCACTTATAGGGTTCATCTGCAATTAAG	1860
OY	1861	AATTTACAAAGA	1872
Db	1861	AATTTACAAAGA	1872
RESULT 2			
AAV62427	standard; cDNA: 2037 BP.		
XX	AAV62427;		
XX	AC		
XX	DT		
XX	30-DEC-1998	(first entry)	
DE	Prostate cancer antigen (PCa3) cDNA splice variant 1.		
XX			
KW	Prostate cancer antigen cDNA splice variant 1; PCa3; prostatic cancer;		
KM	PC; ds.		
XX			
OS	Homo sapiens.		
XX			
XX	Key	Location/Qualifiers	
FT	CDS	379..534	
FT	/*tag= a		
FT	/*product= "PCa3 protein variant 1"		
FT	2019..2024		
FT	/*tag= b		
XX			
PN	W09845420-A1.		
PD	15-OCT-1998.		
XX			
XX	09-APR-1998;	98WO-CA00346.	
PF			
PR	10-APR-1997;	97US-0041836.	
XX			
PA	(DIAG-) DIAGNOCURE INC.		
PI	Bussemakers MJG;		
XX			
DR	WPI: 1998-568347/48.		
XX	P-PSDB; AAW79736.		
PT			
XX			
PS	Claim 3; Fig 2B-2J; 11pp; English.		
XX			
CC	The present sequence represents the prostate cancer antigen (PCa3)		
CC	cDNA splice variant 1 sequence comprising of exons 1, 2, 3, 4a and		
CC	4b of the PCa3 gene. The PCa3 cDNA splice variant 1 sequence,		
CC	isolated from a human primary prostatic tumour tissue cDNA library,		
CC	was found in approximately 5% of the cDNA clones isolated. The		
CC	invention claims for PCa3 cDNA variants and the proteins they encode.		
CC	The invention also claims for antibodies against PCa3 protein. The		
CC	antibodies are claimed to be useful for detecting PCa3 protein in		
CC	immunossay tests, for diagnosing, assessing and prognosing of		
CC	prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin		
CC	or radioisotope, and nucleic acids antisense to PCa3 cDNA are claimed		
CC	to be useful for treating PC, while determining elevated levels of		
CC	PCa3 (as RNA or protein) is useful for detecting a predisposition		
CC	to development of PC, e.g. in prenatal tests. Detecting PCa3 protein		
CC	allows differentiation between malignant and benign prostatic disease,		
CC	and the level of PCa3 expression allows correlation with the grade of		
CC	tumour. PCa3 protein and its fragments are also claimed to be useful		
CC	in vaccines for preventing PC; in drug screens for identifying		

[illegible]

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QY 1058 TTCCATTAAATACACAGGATTAACCTTTTTTTTAACTGGAAGAAATTCATGTTACATG 1117
Db 1223 TTCCATTAAATACACAGGATTAACCTTTTTTTTAACTGGAAGAAATTCATGTTACATG 1282
QY 1118 CAGCTATGGAATTTAATTAATATTTGTTTCCAGTGCAGAAAGATGACTAAGTCTTTA 1177
Db 1283 CAGCTATGGAATTTAATTAATATTTGTTTCCAGTGCAGAAAGATGACTAAGTCTTTA 1342
QY 1178 TCCCTCCCTTTGTTGTTGATTTTTTTTCCAGTATTAAGTTAAATGCTTAGCCCTGTA 1237
Db 1343 TCCCTCCCTTTGTTGTTGATTTTTTTTCCAGTATTAAGTTAAATGCTTAGCCCTGTA 1402
QY 1238 AGGCTGATACAGACAGCCCTCCGCCATCCCTCCAGCCCTATCTGATCACCATCAAC 1297
Db 1403 AGGCTGATACAGACAGCCCTCCGCCATCCCTCCAGCCCTATCTGATCACCATCAAC 1462
QY 1298 CCGTCCCATNYSACCTTAACAAAATCTAATCTGTAATCTCTGAACTGTCAGGNCATAC 1357
Db 1463 CCGTCCCATNYSACCTTAACAAAATCTAATCTGTAATCTCTGAACTGTCAGGNCATAC 1522
QY 1358 ATTTTCTCTCTGCTGAGAAAGCTCTTCTCTCTTAAATCTAGAAATGTAAGTT 1417
Db 1523 ATTTTCTCTCTGCTGAGAAAGCTCTTCTCTCTTAAATCTAGAAATGTAAGTT 1582
QY 1418 TTGATAATAGTGAATCTACTTCAATGCAAAAGGAGGACATATGATTCATCA 1477
Db 1583 TTGATAATAGTGAATCTACTTCAATGCAAAAGGAGGACATATGATTCATCA 1642
QY 1478 CATGAGACACCAATATAAGTATTAATGATTAAGAGTTAGATTAATATGAA 1537
Db 1643 CATGAGACACCAATATAAGTATTAATGATTAAGAGTTAGATTAATATGAA 1702
QY 1538 ATGCAAGAKCCACAGAGGGAATGTTATGGGCAAGCTTTGAAGCTGGGATGGAAGMA 1597
Db 1703 ATGCAAGAKCCACAGAGGGAATGTTATGGGCAAGCTTTGAAGCTGGGATGGAAGMA 1762
QY 1598 AAGGACAGGAAACCATAGTATCTTAATATATATCTCAATCTCTATCTATCA 1657
Db 1763 AAGGACAGGAAACCATAGTATCTTAATATATATCTCAATCTCTATCTATCA 1822
QY 1658 TATCCAAACAAGCTTTTCCAGAAATTCATGCAAGTGCAAATCCCAAGAGTAACCTTTATCC 1717
Db 1823 TATCCAAACAAGCTTTTCCAGAAATTCATGCAAGTGCAAATCCCAAGAGTAACCTTTATCC 1882
QY 1718 ATTTCAATGGAGTGGCTTTAGAAATTTTGGCAATCATACTGGTCACTTATCTCAACTT 1777
Db 1883 ATTTCAATGGAGTGGCTTTAGAAATTTTGGCAATCATACTGGTCACTTATCTCAACTT 1942
QY 1778 TGAGATGTGTTTGTCTGTAGTAAATGTAAGAAATAGGGCACTCTTGAGCCCACTTT 1837
Db 1943 TGAGATGTGTTTGTCTGTAGTAAATGTAAGAAATAGGGCACTCTTGAGCCCACTTT 2002
QY 1838 AGGGTTCACCTCTGGCAATTAAGAAATTTACAAAGA 1872
Db 2003 AGGGTTCACCTCTGGCAATTAAGAAATTTACAAAGA 2037

RESULT 3
AAV62430
ID AAV62430 standard; cDNA; 3582 BP.
XX
AC AAV62430;
XX
DT 30-DEC-1998 (first entry)
XX
DE Prostate cancer antigen (PCA3) wild-type cDNA.
XX
KM Prostate cancer antigen cDNA; PCA3; prostatic cancer;
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
```

```
FT CDS 401..556
FT /*tag= a
FT /product= "PCA3 protein"
FT polyA_signal 983..987
FT /*tag= b
FT polyA_signal 2041..2046
FT /*tag= c
FT polyA_signal 2597..2602
FT /*tag= d
FT polyA_signal 3494..3496
FT /*tag= e
XX
XX MO9845420-A1.
XX
XX 15-OCT-1998.
XX
XX 09-APR-1998; 98MO-CA00346.
XX
XX 10-APR-1997; 97US-0041836.
XX
XX (DIAG-) DIAGNOCURE INC.
XX
XX Bussemakers MJG;
XX
XX WPI; 1998-568347/48.
XX
XX P-PSDB; AAW/9738.
XX
XX New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
XX prevention and treatment of prostatic cancer
XX
XX Claim 3; Fig 5B-5F; 11pp; English.
XX
XX The present sequence represents the prostate cancer antigen (PCA3)
XX wild-type cDNA sequence comprising of exons 1, 2, 3, 4a-4d of the
XX PCA3 gene. The invention claims for PCA3 cDNA variants and the
XX proteins they encode. The invention also claims for antibodies
XX against PCA3 protein. The antibodies are claimed to be useful for
XX detecting PCA3 protein in immunoassay tests, for diagnosing, assessing
XX and prognosing of prostatic cancer (PC). Antibodies, optionally
XX coupled to a cytotoxin or radioisotope, and nucleic acids antisense
XX to PCA3 cDNA are claimed to be useful for treating PC, while determining
XX elevated levels of PCA3 (as RNA or protein) is useful for detecting a
XX predisposition to development of PC, e.g. in prenatal tests. Detecting
XX PCA3 protein allows differentiation between malignant and benign
XX prostatic disease, and the level of PCA3 expression allows correlation
XX with the grade of tumour. PCA3 protein and its fragments are also
XX claimed to be useful in vaccines for preventing PC; in drug screens
XX for identifying specific (ant)agonists (potentially useful
XX therapeutically) and for studying protein-DNA interactions.
XX
XX Sequence 3582 BP; 1052 A; 788 C; 679 G; 1063 T; 0 other;
XX
XX Query Match 73.0%; Score 1367; DB 19; Length 3582;
XX Best Local Similarity 99.5%; Pred. No. 0;
XX Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 98 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCGTAATGG 157
Db 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCGTAATGG 344
QY 158 AGATAATTAATCAATCATAGTAAGAAAGCAAGTGCATATTAATGTCATAGTAGACATGT 217
Db 345 AGATAATTAATCAATCATAGTAAGAAAGCAAGTGCATATTAATGTCATAGTAGACATGT 404
QY 218 TTTTGCACATTTCCAGCCCTTTAAATATTCACACACAGAGCAAGCAAAAAGAGACAC 277
Db 405 TTTTGCACATTTCCAGCCCTTTAAATATTCACACACAGAGCAAGCAAAAAGAGACAC 464
QY 278 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTGATGATGAGCCTGCCCTGT 337
Db 465 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTGATGATGAGCCTGCCCTGT 524
QY 338 GCCTGTCCCGCTTGAGAGGAAGGACATTAAGAAATGAATGATGTGTTCCTTAAAGCA 397
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Db 525 GCGTGTCCCGCTGTGGAGGACATAGAAATGATGATGTTCTTAAAGA 584
Oy 398 TGGCGAGAAAACAGATCTGTTGATATTTATTTGACGGGATTCAGATTTGAAT 457
Db 585 TGGCGAGAAAACAGATCTGTTGATATTTATTTGACGGGATTCAGATTTGAAT 644
Oy 458 GAAGTCACAAAGTGAGCTTACCAATGAGAGAAAACGAGAGAAATCTGATGGTT 517
Db 645 GAAGTCACAAAGTGAGCTTACCAATGAGAGAAAACGAGAGAAATCTGATGGTT 704
Oy 518 CACAAGACATGCAACAAACAAATGAGATGATGATGATGATGAGGACCAAGCTGGGG 577
Db 705 CACAAGACATGCAACAAACAAATGAGATGATGATGATGATGAGGACCAAGCTGGGG 764
Oy 578 AGAGATTAACCAAGGGGAGAGGGTCAGATTTGGCCCTGCTGCTTAACCTGTGCTTC 637
Db 765 AGGAGATTAACCAAGGGGAGAGGGTCAGATTTGGCCCTGCTGCTTAACCTGTGCTTC 824
Oy 638 ATAAACCAATGATTCATATTTCTAACCCCAAAACAAAGCTGTGATATCTGATCTC 697
Db 825 ATAAACCAATGATTCATATTTCTAACCCCAAAACAAAGCTGTGATATCTGATCTC 884
Oy 698 TACGGTTCCTCTGGGGCCCAACATTTCTCATATATCCAGCCACACTTTTATATTT 757
Db 885 TACGGTTCCTCTGGGGCCCAACATTTCTCATATATCCAGCCACACTTTTATATTT 944
Oy 758 AGTTCCAGATCTGATCTGATCTCTTCTACAGCTAGATTAACATTAATCTGATTC 817
Db 945 AGTTCCAGATCTGATCTGATCTCTTCTACAGCTAGATTAACATTAATCTGATTC 1004
Oy 818 AAAGACCTTGCTGTGCTGCTAATATATGCTGACGTGTTTCTTAAGGAGTGTCTG 877
Db 1005 AAAGACCTTGCTGTGCTGCTAATATATGCTGACGTGTTTCTTAAGGAGTGTCTG 1064
Oy 878 GCCCAGGGGATCTGTGAACAGGCTGGGAGAGATCTCAAGATCTTCCAGGGTTATCTTA 937
Db 1065 GCCCAGGGGATCTGTGAACAGGCTGGGAGAGATCTCAAGATCTTCCAGGGTTATCTTA 1124
Oy 938 CTAGCACACAGCATGATCATTAACGAGATTAATCTATATCAACATCATCTCAGTGTCT 997
Db 1125 CTAGCACACAGCATGATCATTAACGAGATTAATCTATATCAACATCATCTCAGTGTCT 1184
Oy 998 TTGGCCATATGAAATTCATTTCCCATTTTGTGCCCATTCCTCAAGACCTCAAAATGTCA 1057
Db 1185 TTGGCCATATGAAATTCATTTCCCATTTTGTGCCCATTCCTCAAGACCTCAAAATGTCA 1244
Oy 1058 TTCCATTAATATCAACAGATTAATCTTTTAACTGGAAGATTCATGTTATCATG 1117
Db 1245 TTCCATTAATATCAACAGATTAATCTTTTAACTGGAAGATTCATGTTATCATG 1304
Oy 1118 CAGCTATGGAATTAATTAATCAATATTTGTTTCCAGTGAAGATGATGATGCTCTTAA 1177
Db 1305 CAGCTATGGAATTAATTAATCAATATTTGTTTCCAGTGAAGATGATGATGCTCTTAA 1364
Oy 1178 TCCCTCCCTTGTGTTGATTTTTCAGATATAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1237
Db 1365 TCCCTCCCTTGTGTTGATTTTTCAGATATAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1424
Oy 1238 AGGCTGTATACAGCACAGCTCTGCCCATCTCCAGCTTATCTGATCAGCATCAAC 1297
Db 1425 AGGCTGTATACAGCACAGCTCTGCCCATCTCCAGCTTATCTGATCAGCATCAAC 1484
Oy 1298 CCGTCCCATATNSACCTAAACAAATCTAATCTTGAATCTTGAATCTGAGNCATAC 1357
Db 1485 CCGTCCCATATNSACCTAAACAAATCTAATCTTGAATCTTGAATCTGAGNCATAC 1544
Oy 1358 ATTTTCTCTGCTGCTGAGAGCTCTCTGCTCTTAATNTCTGATGATGATGATGAT 1417
Db 1545 ATTTTCTCTGCTGCTGAGAGCTCTCTGCTCTTAATNTCTGATGATGATGATGATGAT 1604
Oy 1418 TTGATTAAGTACTATCTTACTTCAATGCAAAAGGACATATGATTCATCATCA 1477
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Db 1605 TTGAATTAAGTACTATCTTACTTCATGCAAAAGGACACATATGATTCATCATCA 1664
Oy 1478 CATGACACACAAATCTAATAAGTCTAATTTGATTAATAGAGTTTAGATTAATATGAA 1537
Db 1665 CATGACACACAAATCTAATAAGTCTAATTTGATTAATAGAGTTTAGATTAATATGAA 1724
Oy 1538 ATGCAAGKCCACACAGGGAATGTTATGGGACGTTGTAAGCTGGGATGTAAGA 1597
Db 1725 ATGCAAGKCCACACAGGGAATGTTATGGGACGTTGTAAGCTGGGATGTAAGA 1784
Oy 1598 AAGCAGGGAACCTCATATCTATATTAATATATCTTCAATTTCTATCTATACAA 1657
Db 1785 AAGCAGGGAACCTCATATCTATATTAATATATCTTCAATTTCTATCTATACAA 1844
Oy 1658 TATCCACACAGCTTTCAACAGATTCATGACAGTGAATTCGCCAAAGSTTAACCTTATCC 1717
Db 1845 TATCCACACAGCTTTCAACAGATTCATGACAGTGAATTCGCCAAAGSTTAACCTTATCC 1904
Oy 1718 ATTTGATGCTGAGTGGCTTTAGATTTTGGCAATCATACGTCATCTATCTCAACTT 1777
Db 1905 ATTTGATGCTGAGTGGCTTTAGATTTTGGCAATCATACGTCATCTATCTCAACTT 1964
Oy 1778 TGAGATGCTGTTGCTGCTGATGATTAATGAAGAATAGGGACACTTGTGAGCCACTTT 1837
Db 1965 TGAGATGCTGTTGCTGCTGATGATTAATGAAGAATAGGGACACTTGTGAGCCACTTT 2024
Oy 1838 AGGTTCACTCTGCGCAATTAAGAATTTACAAAGA 1872
Db 2025 AGGTTCACTCTGCGCAATTAAGAATTTACAAAGA 2059
```

RESULT 4
AAS64026
ID AAS64026 standard; cDNA; 3923 BP.

```
AC AAS64026;  
XX  
DT 29-JAN-2002 (first entry)  
DE Human cDNA encoding DD3.  
XX  
KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.  
OS Homo sapiens.  
XX  
PN WO200173032-A2.  
XX  
PD 04-OCT-2001.  
PE 27-MAR-2001; 2001WO-US09919.  
XX  
PR 27-MAR-2000; 2000US-0536857.  
XX  
PR 09-MAY-2000; 2000US-0568100.  
PR 12-MAY-2000; 2000US-0570737.  
PR 13-JUN-2000; 2000US-0593793.  
PR 27-JUN-2000; 2000US-0605783.  
PR 10-AUG-2000; 2000US-0636215.  
PR 29-AUG-2000; 2000US-0651236.  
PR 06-SEP-2000; 2000US-0657279.  
PR 02-OCT-2000; 2000US-0679426.  
PR 10-OCT-2000; 2000US-0685166.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kaios MD;  
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;  
XX WPI: 2001-639232/73.  
XX  
PT New human prostate-specific polypeptides and polynucleotides useful for  
XX the diagnosis and treatment of cancer, especially prostate cancer -
```

PS Claim 1; Page 473-474; 579pp; English.
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;
Query Match 73.08; Score 1367; DB 22; Length 3923;
Best Local Similarly 99.58; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 98 GGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 157
DB 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 344
QY 158 AGATTAATTAACATCACTAGTAAGACAGCAAGATGACATATATGCTAGTAGTACATGT 217
DB 345 AGATTAATTAACATCACTAGTAAGACAGCAAGATGACATATATGCTAGTAGTACATGT 404
QY 218 TTTTGCACATTTCCAGCCCTTTTAATATTCACACACACAGAAAGCAAAAGGAGACAC 277
DB 405 TTTTGCACATTTCCAGCCCTTTTAATATTCACACACAGAAAGCAAAAGGAGACAC 464
QY 278 AGAGATCCCTGGGAGAAATGCCGGCCGATCTGGCTCATGATGATGAGCTGCCCTGT 337
DB 465 AGAGATCCCTGGGAGAAATGCCGGCCGATCTGGCTCATGATGATGAGCTGCCCTGT 524
QY 338 GCGCTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGCTGCTTAAAGA 397
DB 525 GCGCTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGCTGCTTAAAGA 584
QY 398 TGGGCGAGAAACAGATCCCTGCTGTGATTTTATTGAAACGGGATTACAGATTTGAAT 457
DB 585 TGGGCGAGAAACAGATCCCTGCTGTGATTTTATTGAAACGGGATTACAGATTTGAAT 644
QY 458 GAAGTCACAAGTGAGCATTAACCAATGAGAGAAACAGACGAGAAATCTTGATGGCTT 517
DB 645 GAAGTCACAAGTGAGCATTAACCAATGAGAGAAACAGACGAGAAATCTTGATGGCTT 704
QY 518 CACAGACATGCAACAAACAAATGAATACTGTGATGACATGAGCGAGCCAGCTGGG 577
DB 705 CACAGACATGCAACAAACAAATGAATACTGTGATGACATGAGCGAGCCAGCTGGG 764
QY 578 AGAGATTAACAGCGGCGACAGAGGTGAGATTTCTGGCCCTGCTGCTAACTGTGCTTC 637
DB 765 AGAGATTAACAGCGGCGACAGAGGTGAGATTTCTGGCCCTGCTGCTAACTGTGCTTC 824
QY 638 ATAAACCAATCATTTCTATTTCTAAACCTCAAAACAAAGCTGTTGAATATGATCTC 697
DB 825 ATAAACCAATCATTTCTATTTCTAAACCTCAAAACAAAGCTGTTGAATATGATCTC 884
QY 698 TAGGGTCTCTTGGGGCCCAACATTTCCATATATCCAGCCACACTATTTTAATTTT 757
DB 885 TAGGGTCTCTTGGGGCCCAACATTTCCATATATCCAGCCACACTATTTTAATTTT 944
QY 758 AGTTCCAGATCTGCTACTGTGACCTTTCTACACTGTAAGATTAACATTTACTGATTTG 817
DB 945 AGTTCCAGATCTGCTACTGTGACCTTTCTACACTGTAAGATTAACATTTACTGATTTG 1004
QY 818 AAAGACCCCTTGGTGTGCTGCTAATATGAGCGAGCTGTTTTCCTAAGAGGTCTCG 877
DB 1005 AAAGACCCCTTGGTGTGCTGCTAATATGAGCGAGCTGTTTTCCTAAGAGGTCTCG 1064

QY 878 GCCAGGGATCTGTGAACAGAGCGTGGAGACATCTCAAGATCTTCCAGGGTTATACTTA 937
DB 1065 GCCAGGGATCTGTGAACAGAGCGTGGAGACATCTCAAGATCTTCCAGGGTTATACTTA 1124
QY 938 CTAGCACACAGCATGATCATTTAGGAGTAATTTCTAATCAACATCATCTGATGCTT 997
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QY 998 TTGGCCCTACTGAAATTCATTTCCCATTTTGGCCCATTTCTCAAGACCTCAAAATGTCA 1057
DB 1185 TTGGCCCTACTGAAATTCATTTCCCATTTTGGCCCATTTCTCAAGACCTCAAAATGTCA 1244
QY 1058 TTCCATTAATATCAAGATTAACCTTTTAAACCTGGAAGAAATTCATGTTACATG 1117
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DB 1305 CAGCTATGGAATTTAATTAATATTTGTTTCCAGTGCAGAAAGATGACTAGTCTTTA 1364
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DB 1365 TTCCCTCCCTTGTGATTTTTCAGATTAATAGTTAAATGCTTAGCCCTGTACTG 1424
QY 1238 AGGCTGTATACAGACAGCCCTCCCATCCCTCCAGCCCTTATCTGATCACCATCAAC 1297
DB 1425 AGGCTGTATACAGACAGCCCTCCCATCCCTCCAGCCCTTATCTGATCACCATCAAC 1484
QY 1298 CCTCCCATNYSACCTTAACAAATCTAATCTGTAATCTCTTGAACATGTCAGAGNCATAC 1357
DB 1485 CCTCCCATNYSACCTTAACAAATCTAATCTGTAATCTCTTGAACATGTCAGAGNCATAC 1544
QY 1358 ATTATTCCTCTGCTGAGAGAGCTCTCCCTGCTGCTTAATCTAGATGATGTAAGTT 1417
DB 1545 ATTATTCCTCTGCTGAGAGAGCTCTCCCTGCTGCTTAATCTAGATGATGTAAGTT 1604
QY 1418 TTGAATTAAGTTGACTATCTACTTACTATCATGACAAAGAGGACATATGATCATCA 1477
DB 1605 TTGAATTAAGTTGACTATCTACTTACTATCATGACAAAGAGGACATATGATCATCA 1664
QY 1478 CATGACACAGCAATTAATTAAGTTGATTTATAGAGTTTATGATTAATATATGA 1537
DB 1665 CATGACACAGCAATTAATTAAGTTGATTTATAGAGTTTATGATTAATATATGA 1724
QY 1538 ATGCAAGAKCCACAGAGGAGATTTATGAGGAGACGCTTGTAGCCCTGGAGTGAAGMA 1597
DB 1725 ATGCAAGAGCCACAGAGGAGATTTATGAGGAGACGCTTGTAGCCCTGGAGTGAAGMA 1784
QY 1598 AAGGAGGAGAACTCATATGATCTTAATTAATTAATTAATTAATTAATTAATTA 1657
DB 1785 AAGGAGGAGAACTCATATGATCTTAATTAATTAATTAATTAATTAATTAATTA 1844
QY 1658 TATCCAAAGAGCTTTTACAGAAATTCATGAGTGCAGAAATCCCAAGAGTAACTTATGC 1717
DB 1845 TATCCAAAGAGCTTTTACAGAAATTCATGAGTGCAGAAATCCCAAGAGTAACTTATGC 1904
QY 1718 ATTTCATGATGATGAGCTTGAATTTTGAATTTGCAAAATCACTGCTATCTCAACTT 1777
DB 1905 ATTTCATGATGATGAGCTTGAATTTTGAATTTTGAATTTGCAAAATCACTGCTATCTCAACTT 1964
QY 1778 TGAGATGTGTTTGTCTTGTAGTTAATTGAAAGAAATAGGCACTTGTGAGCCACTTT 1837
DB 1965 TGAGATGTGTTTGTCTTGTAGTTAATTGAAAGAAATAGGCACTTGTGAGCCACTTT 2024
QY 1838 AGGGTTCACCTCGGCAATTAAGAAATTTACAAAGA 1872
DB 2025 AGGGTTCACCTCGGCAATTAAGAAATTTACAAAGA 2059
RESULT 5
AAH93861
ID AAH93861 standard; cdna; 3923 BP.

XX AAH93861;
AC 04-OCT-2001 (first entry)
DT
XX
DE Gene DD3 cDNA sequence.
XX
KW Human: prostate cancer; prostate-specific; diagnosis; vaccine;
XX cytosolic; gene therapy; metastasis; ss.
OS Homo sapiens.
XX
XX WO200151633-A2.
XX
XX 19-JUL-2001.
XX
XX 16-JAN-2001; 2001WO-US01574.
XX
XX 14-JAN-2000; 2000US-0483672.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
XX WPI: 2001-425873/45.
XX
XX
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosis, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
XX
XX Claim 1: Page 452-453; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;
SQ

Query Match 73.0%; Score 1367; DB 22; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 525 GCCTGTCGCCGCTGTGAGGGAAGACATTAGAAATGATGATGCTTAAAGCA 584
QY 398 TGGGAGAGAAAAACAGATCCTGTGTGATATTATTGAAGGGATTACAGATTGGAAT 457
Db 585 TGGGAGAGAAAAACAGATCCTGTGTGATATTATTGAAGGGATTACAGATTGGAAT 644
QY 458 GAAAGTCACAAAGTGGAGCATTTACCATGAGAGAAACAGAGAAAAATCTTGATGGCT 517
Db 645 GAAAGTCACAAAGTGGAGCATTTACCATGAGAGAAACAGAGAAAAATCTTGATGGCT 704
QY 518 CACAAGACATGCAACAAACAAATGAAATGATGATGATGATGAGCAGCCAAAGCTGGGG 577
Db 705 CACAAGACATGCAACAAACAAATGAAATGATGATGATGATGAGCAGCCAAAGCTGGGG 764
QY 578 AGGAGATTAACCAAGGGGAGAGAGGATTCGAGATTCTGGCCCTTAACCTGCTTC 637
Db 765 AGGAGATTAACCAAGGGGAGAGAGGATTCGAGATTCTGGCCCTTAACCTGCTTC 824
QY 638 ATTAACCAATGATTTTCATATTCTTAACCTCAAAACAAAGGTTGTAATATCTGATGTC 697
Db 825 ATTAACCAATGATTTTCATATTCTTAACCTCAAAACAAAGGTTGTAATATCTGATGTC 884
QY 698 TACGGTTCCTTGCGGCCCAACATTTCCATATATCCAGCCACACTCATTTTAAATATT 757
Db 885 TACGGTTCCTTGCGGCCCAACATTTCCATATATCCAGCCACACTCATTTTAAATATT 944
QY 758 AGTTCGAGATCTGACTGTGACCTTTCTACACTAGAAATACATTACTATTTTGTTC 817
Db 945 AGTTCGAGATCTGACTGTGACCTTTCTACACTAGAAATACATTACTATTTTGTTC 1004
QY 818 AAAGACCCCTGCTGTGGCTGCTAATATGAGCTGACAGCTGTTTCCAGAGAGCTGCTG 877
Db 1005 AAAGACCCCTGCTGTGGCTGCTAATATGAGCTGACAGCTGTTTCCAGAGAGCTGCTG 1064
QY 878 GCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATACCTTA 937
Db 1065 GCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTATACCTTA 1124
QY 938 CTAGACACAGATGATATCTTACGAGAGGAATATCTATCAACATCTCATCTGCT 997
Db 1125 CTAGACACAGATGATATCTTACGAGAGGAATATCTATCAACATCTCATCTGCT 1184
QY 998 TTGCCATACGTAATATCTTCCACATTTTGGCCATCTTCCAGACCTCAAAATGCA 1057
Db 1185 TTGCCATACGTAATATCTTCCACATTTTGGCCATCTTCCAGACCTCAAAATGCA 1244
QY 1058 TTCCATATATACAGAGATTACTTTTAACTGGAAGAAATTCATGTTACATG 1117
Db 1245 TTCCATATATACAGAGATTACTTTTAACTGGAAGAAATTCATGTTACATG 1304
QY 1118 CAGCTATGGGAATTTAATTACATATTGTTTCCAGTGAAGAAATGACTAAGTCCCTTA 1177
Db 1305 CAGCTATGGGAATTTAATTACATATTGTTTCCAGTGAAGAAATGACTAAGTCCCTTA 1364
QY 1178 TCCCTCCCTTGTGTAATTTTTCAGATTAAGTAAATGCTTAAGCTGTGACG 1237
Db 1365 TCCCTCCCTTGTGTAATTTTTCAGATTAAGTAAATGCTTAAGCTGTGACG 1424
QY 1238 AGGCTGTATACAGACAGCCTCTCCCAATCCCTCAGACTTATCTGTATCCATCAAC 1297
Db 1425 AGGCTGTATACAGACAGCCTCTCCCAATCCCTCAGACTTATCTGTATCCATCAAC 1484
QY 1298 CCCTCCATNTSACCTAAACAAATCTAATCTTGAATCTTGAACATGTGAGNCATAC 1357
Db 1485 CCCTCCATNTSACCTAAACAAATCTAATCTTGAATCTTGAACATGTGAGNCATAC 1544
QY 1358 ATTTTCCTTCCGCTGGAAGACCTCTCCCTGCTTAATCTGATGATGATGATGAT 1417
Db 1545 ATTTTCCTTCCGCTGGAAGACCTCTCCCTGCTTAATCTGATGATGATGATGAT 1604
QY 1418 TTGAATTAAGTGTACTATCTTACTTCAACAAAGAGGACATATGAGATTTCATCATCA 1477
Db 1605 TTGAATTAAGTGTACTATCTTACTTCAACAAAGAGGACATATGAGATTTCATCATCA 1664

QY 818 AAGACCCCTGCTGTTGCTGCTAATATGTAAGTCTGTTTCTTCTAAGAGTCTCTG 877
DB 1005 AAGACCCCTGCTGTTGCTGCTAATATGTAAGTCTGTTTCTTCTAAGAGTCTCTG 1064
QY 878 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTAATCTTA 937
DB 1065 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTAATCTTA 1124
QY 938 CTAGACACAGCATGATCATTAACAGGATTAATCTAATCAATCAATCCAGTCTCT 997
DB 1125 CTAGACACAGCATGATCATTAACAGGATTAATCTAATCAATCAATCCAGTCTCT 1184
QY 998 TTGCCCATACGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1057
DB 1185 TTGCCCATACGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1244
QY 1058 TTCCATTAATATACAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1117
DB 1245 TTCCATTAATATACAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1304
QY 1118 CAGCATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1177
DB 1305 CAGCATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1364
QY 1178 TCCCTCCCTTGTGTTGTTGTTTTCAGTATAAAGTTAAATGCTTAAGCTTGTACTG 1237
DB 1365 TCCCTCCCTTGTGTTGTTTTCAGTATAAAGTTAAATGCTTAAGCTTGTACTG 1424
QY 1238 AGGCTGTATACAGACAGCCTCTCCCATCCCTCAGCCTTAATCTGATCATCATCAAC 1297
DB 1425 AGGCTGTATACAGACAGCCTCTCCCATCCCTCAGCCTTAATCTGATCATCATCAAC 1484
QY 1298 CCCCTCCCATNTSACCTTAACAAATCTAATCTGTAATCTTGAACATGTCAGGCAATAC 1357
DB 1485 CCCCTCCCATNTSACCTTAACAAATCTAATCTGTAATCTTGAACATGTCAGGCAATAC 1544
QY 1358 ATTTTCTCTGCTGAGAAAGCTCTCTCTCTCTTAANTCTAATGATGATTAAGTT 1417
DB 1545 ATTTTCTCTGCTGAGAAAGCTCTCTCTCTCTTAANTCTAATGATGATTAAGTT 1604
QY 1418 TTGAATTAAGTGAATCTTAATCTTAATCAAGAAAGGACATATGATTCATCATCA 1477
DB 1605 TTGAATTAAGTGAATCTTAATCTTAATCAAGAAAGGACATATGATTCATCATCA 1664
QY 1478 CATGACACGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1537
DB 1665 CATGACACGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1724
QY 1538 ATGCAAGACACAGAGGAAATGTTATGGGACAGCTTGTAAAGCTGGGATGTAAGTA 1597
DB 1725 ATGCAAGACACAGAGGAAATGTTATGGGACAGCTTGTAAAGCTGGGATGTAAGTA 1784
QY 1598 AAGCAGGGAACCTCATAGTACTTAATTAATTAATTAATTAATTAATTAATTAATTA 1657
DB 1785 AAGCAGGGAACCTCATAGTACTTAATTAATTAATTAATTAATTAATTAATTAATTA 1844
QY 1658 TATCCAAACAGCTTTTCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1717
DB 1845 TATCCAAACAGCTTTTCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1904
QY 1718 ATTTCATGATGATGCTGTTTGAATTTTGGCAATCAATGCTGCTTAATCAATCT 1777
DB 1905 ATTTCATGATGATGCTGTTTGAATTTTGGCAATCAATGCTGCTTAATCAATCT 1964
QY 1778 TGAGATGTTGTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1837
DB 1965 TGAGATGTTGTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2024
QY 1838 AGGGTCACTCCTGGCAATAAAGAAATTAACAAGA 1872
DB 2025 AGGGTCACTCCTGGCAATAAAGAAATTAACAAGA 2059

RESULT 7
ABL95397
ID ABL95397 standard; cDNA; 3923 BP.
XX
AC ABL95397;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human DD3 cDNA sequence SEQ ID NO 690.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
OS Homo sapiens.
XX
PN US200202248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0570737.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHEM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stoik JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
PI WPI: 2002-255649/30.
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
XX progression of cancer
XX

PS Claim 1; SEQ ID NO 690; 87bp; English.

CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.

XX Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;

Query Match 73.0%; Score 1367; DB 24; Length 3923;

Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
QY 98 GGTGAGAAATTAAGAAAGCTGCTGACCTTTACCATCTAGGCCACACATCTGCTGAATGG 157
DB 285 GGTGAGAAATTAAGAAAGCTGCTGACCTTTACCATCTAGGCCACACATCTGCTGAATGG 344
QY 158 AGATAATTAACATCACTAGAAACAGCAAGATGACAAATATATGCTAAGTAGACATGT 217
DB 345 AGATAATTAACATCACTAGAAACAGCAAGATGACAAATATATGCTAAGTAGACATGT 404
QY 218 TTTTGACATTTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGGAAAGCAC 277
DB 405 TTTTGACATTTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGGAAAGCAC 464
QY 278 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTATGATGAGCCCTGCGCTGT 337
DB 465 AGAGATCCCTGGGAGAAATCCCGGCCCATCTTGGGTATGATGAGCCCTGCGCTGT 524
QY 338 GCCTGGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGTGTCCTTAAGAGGA 397
DB 525 GCCTGGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGTGTCCTTAAGAGGA 584
QY 398 TGGGCGAGAAACAGATCTGTGTGTGATATTTATTTGAACGGGATTACAGATTTGAAT 457
DB 585 TGGGCGAGAAACAGATCTGTGTGTGATATTTATTTGAACGGGATTACAGATTTGAAT 644
QY 458 GAAGTCACAAGTGAGCATTAACCAATGAGAGAAACAGAGCAAAATCTGATGGCTT 517
DB 645 GAAGTCACAAGTGAGCATTAACCAATGAGAGAAACAGAGCAAAATCTGATGGCTT 704
QY 518 CACAGACATGACAAACAAATGGAATCTGTGATGACATGAGCGAGCAAGCTGGGG 577
DB 705 CACAGACATGACAAACAAATGGAATCTGTGATGACATGAGCGAGCAAGCTGGGG 764
QY 578 AGAGATTAACCAAGGGGCAAGAGGTCAAGATTTGCGCCCTGCTAAACTGTGGCTTC 637
DB 765 AGAGATTAACCAAGGGGCAAGAGGTCAAGATTTGCGCCCTGCTAAACTGTGGCTTC 824
QY 638 ATACCAAAATCATTTATATTTCTAACCCTCAAAACAAAGCTGTGTAATATCTGATCTC 697
DB 825 ATACCAAAATCATTTATATTTCTAACCCTCAAAACAAAGCTGTGTAATATCTGATCTC 884
QY 698 TAGGTTCCCTTGTGGGCCCAACATTCCTCATATATCCAGGCACACATCTTTAATATT 757
DB 885 TAGGTTCCCTTGTGGGCCCAACATTCCTCATATATCCAGGCACACATCTTTAATATT 944
QY 758 AGTTCCCAAGATCTGTACTGTGACCTTCTACACTGTAGAAATTAACATTAATCTGTTTC 817
DB 945 AGTTCCCAAGATCTGTACTGTGACCTTCTACACTGTAGAAATTAACATTAATCTGTTTC 1004
QY 818 AAAGACCTTCGTGTGTGCTGCTTAATATAGTACTGCTGTTTCTTAAGAGATGTTCTG 877
DB 1005 AAAGACCTTCGTGTGTGCTGCTTAATATAGTACTGCTGTTTCTTAAGAGATGTTCTG 1064
QY 878 GCCCAGGGATCTGTGAACAGGCTGGAGAGCATCTAAGATCTTTCAGGGTTATACCTTA 937
DB 1065 GCCCAGGGATCTGTGAACAGGCTGGAGAGCATCTAAGATCTTTCAGGGTTATACCTTA 1124
QY 938 CTAGCACACAGCATGATCTTACGGAAGTAATATCTAATCAACATCATCTCCAGTGTCT 997
DB 1125 CTAGCACACAGCATGATCTTACGGAAGTAATATCTAATCAACATCATCTCCAGTGTCT 1184
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QY 998 TTGGCCATCTGAATTCATTTCCACCTTTTGGCCCATCTTCTCAAGACCTCAAAATGTCA 1057
DB 1185 TTGGCCATCTGAATTCATTTCCACCTTTTGGCCCATCTTCTCAAGACCTCAAAATGTCA 1244
QY 1058 TTCCATTAATATCAACAGATTAACCTTTTAACTTGAAGCAATGATGATGATGATGATG 1117
DB 1245 TTCCATTAATATCAACAGATTAACCTTTTAACTTGAAGCAATGATGATGATGATGATG 1304
QY 1118 CAGCTATGGAATTAATTAATTAATTTTGTTCACAGTGCAGAGATGATGATGATGATGATG 1177
DB 1305 CAGCTATGGAATTAATTAATTAATTTTGTTCACAGTGCAGAGATGATGATGATGATGATG 1364
QY 1178 TCCCTCCCTTTTGTGTGATTTTTCACATTAATTAATTTGCTTACCTTGTACTG 1237
DB 1365 TCCCTCCCTTTTGTGTGATTTTTCACATTAATTAATTTGCTTACCTTGTACTG 1424
QY 1238 AGGCTGTATACAGACAGCCTTCCCATCCCTGACAGCCTTATCTGATGATGATGATGATG 1297
DB 1425 AGGCTGTATACAGACAGCCTTCCCATCCCTGACAGCCTTATCTGATGATGATGATGATG 1484
QY 1298 CCCTCCCATNYSACCTTAACCAAAATCTAATCTTGAATTTCTTGAACATGTCAGAGCATAC 1357
DB 1485 CCCTCCCATNYSACCTTAACCAAAATCTAATCTTGAATTTCTTGAACATGTCAGAGCATAC 1544
QY 1358 ATTCTCTCTTCTGCTGAGAGAGCTCTTCTGCTCTTAATCTAGATGATGATGATGATG 1417
DB 1545 ATTCTCTCTTCTGCTGAGAGAGCTCTTCTGCTCTTAATCTAGATGATGATGATGATG 1604
QY 1418 TTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1477
DB 1605 TTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1664
QY 1478 CATGAGACAGCAAAATCTAATTAATTTGATTTAAGAGTTTGAATTAATTAATTAATGAA 1537
DB 1665 CATGAGACAGCAAAATCTAATTAATTTGATTTAAGAGTTTGAATTAATTAATTAATGAA 1724
QY 1538 ATGCAAGACACAGAGAGAGAGATTTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1597
DB 1725 ATGCAAGACACAGAGAGAGAGATTTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1784
QY 1598 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1657
DB 1785 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1844
QY 1658 TATCCAAAGAGCTTTTCAAGAAATTCATGACAGTGCAGAAATCCCAAGAGTAACTTATCC 1717
DB 1845 TATCCAAAGAGCTTTTCAAGAAATTCATGACAGTGCAGAAATCCCAAGAGTAACTTATCC 1904
QY 1718 ATTTCATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1777
DB 1905 ATTTCATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1964
QY 1778 TGAGATGCTGTTTCTGCTGTAGTAAATTTGAAGAAATAGAGGACCTTGTGAGAGCCTTT 1837
DB 1965 TGAGATGCTGTTTCTGCTGTAGTAAATTTGAAGAAATAGAGGACCTTGTGAGAGCCTTT 2024
QY 1838 AGGCTTCACTCTGCAATTAAGAAATTTACAAAGA 1872
DB 2025 AGGCTTCACTCTGCAATTAAGAAATTTACAAAGA 2059
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RESULT 8
ACAS9834
ID ACAS9834 standard; cDNA; 3923 BP.
XX ACAS9834;
AC ACAS9834;
XX 10-JUN-2003 (first entry)
DE Prostate cancer therapy associated cDNA #545.
KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
immunogen; cancer; prostate specific antigen; PSA;


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QY 697 CTAGGTCCTCTGGGCCAACATTCATATATCCAGCCACATCTTTATATAT 756
DB 1170 CTAGGTCCTCTGGGCCAACATTCATATATCCAGCCACATCTTTATATAT 1111
QY 757 TAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGATTAATTAATCTATTTGGT 816
DB 1110 TAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGATTAATTAATCTATTTGGT 1051
QY 817 CAAGACCTTCGTGTGCTGCTTAATATGTAAGTGAAGTGTCT 876
DB 1050 CAAGACCTTCGTGTGCTGCTTAATATGTAAGTGAAGTGTCT 991
QY 877 GGGCCAGGGGATCTGTAAGAGGCTGGGAAGCATCTCAAGATCTTCCAGGTTATCTT 936
DB 990 GGGCCAGGGGATCTGTAAGAGGCTGGGAAGCATCTCAAGATCTTCCAGGTTATCTT 931
QY 937 ACTAGCACAGACATGATCATTCAGAGTGAATTAATCAATCAATCATCTCAGTGTG 996
DB 930 ACTAGCACAGACATGATCATTCAGAGTGAATTAATCAATCAATCATCTCAGTGTG 871
QY 997 TTTGCCATCTAGTAATTCATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTC 1056
DB 870 TTTGCCATCTAGTAATTCATTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTC 811
QY 1057 ATTCATTAATATCAAGATTAATTAATTTTAACTTTTAACTGGAAGATTAATCAATGTTACAT 1116
DB 810 ATTCATTAATATCAAGATTAATTAATTTTAACTTTTAACTGGAAGATTAATCAATGTTACAT 751
QY 1117 GCAGCTATGGAATTAATTAATTAATTTTGTTCAGATGCAAGATGACTAAGTCTTT 1176
DB 750 GCAGCTATGGAATTAATTAATTAATTTTGTTCAGATGCAAGATGACTAAGTCTTT 691
QY 1177 ATCCCTCCCTTTTGTGTATTTTTCAGATTAATTAATGCTTACGCTTGTACT 1236
DB 690 ATCCCTCCCTTTTGTGTATTTTTCAGATTAATTAATGCTTACGCTTGTACT 631
QY 1237 GAGGCTGTATACAG 1251
DB 630 GAGGCTGTATACAG 616
RESULT 10
AAS63898/c
ID AAS63898 standard; cDNA; 2426 BP.
XX
AC AAS63898;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA sequence #432.
XX
KM Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN W0200173032-A2.
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0652729.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
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PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Reiter WM, Stolk JA, Day CH, Vedrick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
DR WPI: 2001-639232/73.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1: Page 386; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
SQ
Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;
Query Match 61.7%; Score 1155; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGCCACACATCTGTAATG 156
DB 1770 AGGTAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGCCACACATCTGTAATG 1711
QY 157 GAGATTAATTAATCACTAGTAAGAAAGCAAGATGACAAATTAATGTTAGTGTGATG 216
DB 1710 GAGATTAATTAATCACTAGTAAGAAAGCAAGATGACAAATTAATGTTAGTGTGATG 1651
QY 217 TTTTTCACATTTCCAGCCCTTTAATATCCACACACACAGAGCAACAAAGAGAGA 276
DB 1650 TTTTTCACATTTCCAGCCCTTTAATATCCACACACACAGAGCAACAAAGAGAGA 1591
QY 277 CAGACATCCCTGGGAGAAATGCGCGCCGCACTTGGGTATGATGATGCTGCCCTG 336
DB 1590 CAGACATCCCTGGGAGAAATGCGCGCCGCACTTGGGTATGATGATGCTGCCCTG 1531
QY 337 TGCCGTGTCGCCCTGTGTGAGGAGACATTTGAATAATGATGATGTTTCTTAAGAG 396
DB 1530 TGCCGTGTCGCCCTGTGTGAGGAGACATTTGAATAATGATGATGTTTCTTAAGAG 1471
QY 397 ATGGCAGAGAAACAGATCCCTGTGTGATTTATTTGAACGGGATTAACAGATTTGAAA 456
DB 1470 ATGGCAGAGAAACAGATCCCTGTGTGATTTATTTGAACGGGATTAACAGATTTGAAA 1411
QY 457 TGAAGTCAACAAAGTAGCATTTACAAATGAGAGAAACAGACAGAAATCTTGTATGCT 516
DB 1410 TGAAGTCAACAAAGTAGCATTTACAAATGAGAGAAACAGACAGAAATCTTGTATGCT 1351
QY 517 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGATGAGGAGGAGCCAACTGGG 576
DB 1350 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGATGAGGAGGAGCCAACTGGG 1291
QY 577 GAGGAGATTAACCAAGGAGGAGGATTCAGGATTCGCGCTGCTCTAACTGTGCGCTT 636
DB 1290 GAGGAGATTAACCAAGGAGGAGGATTCAGGATTCGCGCTGCTCTAACTGTGCGCTT 1231
QY 637 CATTAACCAATCTTTTCAATTTTCAACCTCAAAACAAAGCTGTTGTAATATCTGATCT 696
DB 1230 CATTAACCAATCTTTTCAATTTTCAACCTCAAAACAAAGCTGTTGTAATATCTGATCT 1171
```

QY 697 CTACGGTTCCTCGGGCCCAACAATCTCCATATATCCAGCACACATCTTTTATAT 756
DB 1170 CTACGGTTCCTCGGGCCCAACAATCTCCATATATCCAGCACACATCTTTTATAT 1111
QY 757 TAGTCCAGATCTGTACTGTGACCTTCTACACTGTAGATTAATCATTTTGT 816
DB 1110 TAGTCCAGATCTGTACTGTGACCTTCTACACTGTAGATTAATCATTTTGT 1051
QY 817 CAAGACCCCTTCGTGTGCTGCTTAATATGTAGCTGACTTTTCTTAAGAGTGTCT 876
DB 1050 CAAGACCCCTTCGTGTGCTGCTTAATATGTAGCTGACTTTTCTTAAGAGTGTCT 991
QY 877 GGCCCAAGGATCTGTAAACAGGTGGGAAGCATCTAAGATCTTCCAGGGTATCTT 936
DB 990 GGCCCAAGGATCTGTAAACAGGTGGGAAGCATCTAAGATCTTCCAGGGTATCTT 931
QY 937 ACTAGCACAGCATGTATCTACGAGGTGATATCATCAACATCATCTCAGTGTCT 996
DB 930 ACTAGCACAGCATGTATCTACGAGGTGATATCATCAACATCATCTCAGTGTCT 871
QY 997 TTGGCCCATCTGAATTCATTTCCACTTTGTGCCATCTCCAGACCTCAAAATGTC 1056
DB 870 TTGGCCCATCTGAATTCATTTCCACTTTGTGCCATCTCCAGACCTCAAAATGTC 811
QY 1057 ATTCATTAATATCACAGATTAATCTTTTCTTAACCTGGAAAGATTCATTTTAT 1116
DB 810 ATTCATTAATATCACAGATTAATCTTTTCTTAACCTGGAAAGATTCATTTTAT 751
QY 1117 GCAGCATATGGGAATTAATTAATATTTGTTTCCAGTCAAGATGATAGTCTT 1176
DB 750 GCAGCATATGGGAATTAATTAATATTTGTTTCCAGTCAAGATGATAGTCTT 691
QY 1177 ATCCCTCCCTTGTGTGATTTTCTCCAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1236
DB 690 ATCCCTCCCTTGTGTGATTTTCTCCAGTAAAGTAAAGTAAAGTAAAGTAAAGT 631
QY 1237 GAGGCTGTATACAGC 1251
DB 630 GAGGCTGTATACAGC 616

RESULT 11
AAH93805/c
ID AAH93805 standard; cDNA; 2426 BP.
AC AAH93805;
XX
XX 04-OCT-2001 (first entry)
DE Human prostate-specific cDNA sequence P710P #3.
XX
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosolic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
PN WO200151633-A2.
XX
XX 19-JUL-2001.
PD
XX 16-JAN-2001; 2001MO-US01574.
PF
XX 14-JAN-2000; 2000US-0483672.
PR
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MM, Stolk JA, Skelky YAM;
PI Wang A, Meagher MJ;
XX
XX WPI; 2001-425873/45.
DR
XX
XX New polynucleotide encoding a prostate-specific protein, for

PT diagnosing, monitoring and treating prostate cancer in a patient and
XX for use in vaccines -
PS Claim 1; Page 384-385; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;
XX
Query Match 61.7%; Score 1155; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGAAATTAAGAAAGGCTGCTGACTTATCCATCTGAGCCACATCTGCTGAATG 156
DB 1770 AGGTGAAATTAAGAAAGGCTGCTGACTTATCCATCTGAGCCACATCTGCTGAATG 1711
QY 157 GAGTATATTAACATCACTAGAAACAGCAAGATGACATATATGTCTAATAGTACATG 216
DB 1710 GAGTATATTAACATCACTAGAAACAGCAAGATGACATATATGTCTAATAGTACATG 1651
QY 217 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGAGCA 276
DB 1650 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAGCAAAAGAGCA 1591
QY 277 CAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGGGTCAATGATGAGCCTCGCCCTG 336
DB 1590 CAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGGGTCAATGATGAGCCTCGCCCTG 1531
QY 337 TGGCTGTCCCGCTGTGAGGAGAAAGCAATTAAGAAATGATGATGTCTCTTAAAG 396
DB 1530 TGGCTGTCCCGCTGTGAGGAGAAAGCAATTAAGAAATGATGATGTCTCTTAAAG 1471
QY 397 ATGGCAGAGAAACAGATCTCTGTGTGATATTTATTTGAACGGATACAGATTGAAA 456
DB 1470 ATGGCAGAGAAACAGATCTCTGTGTGATATTTATTTGAACGGATACAGATTGAAA 1411
QY 457 TGAAGTCACAAATGAGCATTTACCAATGAGAGGAAACAGACGAGAAATCTTGATGCT 516
DB 1410 TGAAGTCACAAATGAGCATTTACCAATGAGAGGAAACAGACGAGAAATCTTGATGCT 1351
QY 517 TCACAAGACATGCAACAAACAAATGGAATATCTGTATGACATGAGGAGCCAGGTGGG 576
DB 1350 TCACAAGACATGCAACAAACAAATGGAATATCTGTATGACATGAGGAGCCAGGTGGG 1291
QY 577 GAGGAGATAACACAGGGGAGAGGATCTGGCCCTGCTGCTTAACATGTCGTT 636
DB 1290 GAGGAGATAACACAGGGGAGAGGATCTGGCCCTGCTGCTTAACATGTCGTT 1231
QY 637 CATACCAATATCTATTTCTAACCCTCAAAACAAAGCTGTTGTAATATCTGATCT 696
DB 1230 CATACCAATATCTATTTCTAACCCTCAAAACAAAGCTGTTGTAATATCTGATCT 1171
QY 697 CTACGGTTCCTCGGGCCCAACAATCTCCATATATCCAGCACACATCTTTTATAT 756
DB 1170 CTACGGTTCCTCGGGCCCAACAATCTCCATATATCCAGCACACATCTTTTATAT 1111
QY 757 TAGTCCAGATCTGTACTGTGACCTTCTACACTGTAGATTAATCATTTTGT 816
DB 1110 TAGTCCAGATCTGTACTGTGACCTTCTACACTGTAGATTAATCATTTTGT 1051


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OY 817 CAAGAACCCCTGCTGTGCTGCTAATATAGTAGACGCTTTTTCCTAAGAGAGTCT 876
    |||
Db 1050 CAAAGACCCCTTGCTGTGCTGCTAATATAGTAGACGCTTTTTCCTAAGAGAGTCT 991
OY 877 GGCAGAGGGGATCTGTGAACAGAGCTGGAGCATCTCAAGATCTTCCAGGGTTATCTT 936
    |||
Db 990 GGCAGAGGGGATCTGTGAACAGAGCTGGAGCATCTCAAGATCTTCCAGGGTTATCTT 931
OY 937 ACTACACACAGCATGATCATATACGAGAGATATATCTAATCAATCATCTCTCACTGTC 996
    |||
Db 930 ACTACACACAGCATGATCATATACGAGAGATATATCTAATCAATCATCTCTCACTGTC 871
OY 997 TTTGCCCATCTGAATTCATTTCCACATTTTGTGCCCATCTCTCAAGACCTCAAAATGTC 1056
    |||
Db 870 TTTGCCCATCTGAATTCATTTCCACATTTTGTGCCCATCTCTCAAGACCTCAAAATGTC 811
OY 1057 ATTCATTAATATACACAGATTAACCTTTTAACTTAACTGAGAGATTCATTTATCAT 1116
    |||
Db 810 ATTCATTAATATACACAGATTAACCTTTTAACTTAACTGAGAGATTCATTTATCAT 751
OY 1117 GCAGCTATGGGAATTTAATATATTTTGTTCACAGTGAAGATGACTAGTCCTT 1176
    |||
Db 750 GCAGCTATGGGAATTTAATATATTTTGTTCACAGTGAAGATGACTAGTCCTT 691
OY 1177 ATCCCTCCCTTGTGTGATTTTTCAGATTAAGTTAAATGCTTAGCCTGTACT 1236
    |||
Db 690 ATCCCTCCCTTGTGTGATTTTTCAGATTAAGTTAAATGCTTAGCCTGTACT 631
OY 1237 GAGGCTGTATACAGC 1251
    |||
Db 630 GAGGCTGTATACAGC 616
```

```
RESULT 12
AAH85119/c
ID AAH85119 standard; cDNA; 2426 BP.
XX
AC AAH85119;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence P710P #3.
XX
KM Human: prostate cancer; therapy: diagnosis; cat eye syndrome;
KM chromosome 22q11.2; prostate-specific protein; chromosome 1;
KM prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN WO200134802-A2.
XX
PD 17-MAY-2001.
XX
PE 09-NOV-2000; 2000WO-US30904.
XX
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skelky YAW, Wang A;
DR WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer -
XX
PS Claim 5; Page 284; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
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at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have cytosolic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P5015 was located on chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent CC polynucleotide and polypeptide sequences used in the exemplification of the present invention.

Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;

Query Match 61.7%; Score 1155; DB 22; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACCTTACATCTGAGGCGACACATCTCTGAATG 156
    |||
Db 1770 AGGTGAGAAATTAAGAAAGGCTGCTGACCTTACATCTGAGGCGACACATCTCTGAATG 1711
OY 157 GAGATTAATTAACATCACTAGAAACAGCAAGATGACATTAATTAATGCTTAAGTACATG 216
    |||
Db 1710 GAGATTAATTAACATCACTAGAAACAGCAAGATGACATTAATTAATGCTTAAGTACATG 1651
OY 217 TTTTGGCATTTTCCAGCCCTTTAATATATCCACACACAGAGAACACAAAGAGAGA 276
    |||
Db 1650 TTTTGGCATTTTCCAGCCCTTTAATATATCCACACACAGAGAACACAAAGAGAGA 1591
OY 277 CAGAGATCCCTGGGAAATATGCGCGCGCCATTTGGGTCAATGATGAGCTCCGCCG 336
    |||
Db 1590 CAGAGATCCCTGGGAAATATGCGCGCGCCATTTGGGTCAATGATGAGCTCCGCCG 1531
OY 337 TGCCTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTAAAGG 396
    |||
Db 1530 TGCCTGTCCCGCTTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTAAAGG 1471
OY 397 ATGGGCGAGAAACAGATCTCTGTGGATATTTATTGAACGGGATTAACATTTGAAA 456
    |||
Db 1470 ATGGGCGAGAAACAGATCTCTGTGGATATTTATTGAACGGGATTAACATTTGAAA 1411
OY 457 TGAAGTCACAAGTAGACTTACCAATGAGAGAAACAGAGAAATCTGTAGTGCT 516
    |||
Db 1410 TGAAGTCACAAGTAGACTTACCAATGAGAGAAACAGAGAAATCTGTAGTGCT 1351
OY 517 TCACAAGACATCAACAAATGAATGAAATGATGTGATGACATGAGGACCAACGCTGGG 576
    |||
Db 1350 TCACAAGACATCAACAAATGAATGAAATGATGTGATGACATGAGGACCAACGCTGGG 1291
OY 577 GAGGAGATTAACACAGGGGCGAGAGGTCAGAGATTTGCGCTCTGCTTAACCTGTGCGTT 636
    |||
Db 1290 GAGGAGATTAACACAGGGGCGAGAGGTCAGAGATTTGCGCTCTGCTTAACCTGTGCGTT 1231
OY 637 CATAACCAAAATCATTTCTATATTTCTAACCTCAAAAACAAAGCTGTGTAATTCGATCT 696
    |||
Db 1230 CATAACCAAAATCATTTCTATATTTCTAACCTCAAAAACAAAGCTGTGTAATTCGATCT 1171
OY 697 CTACGGTTCCTTCTGGGCCCAACATTTCTCATATATTCACGCCACACATCTTTTATAT 756
    |||
Db 1170 CTACGGTTCCTTCTGGGCCCAACATTTCTCATATATTCACGCCACACATCTTTTATAT 1111
OY 757 TAGTTCGCCAGATCTGTACGTACCTTTCTACACGTGTAGAAATTAACATTAATTTTGT 816
    |||
Db 1110 TAGTTCGCCAGATCTGTACGTACCTTTCTACACGTGTAGAAATTAACATTAATTTTGT 1051
OY 817 CAAAGACCCCTGCTGTGCTGCTAATATAGTAGACGCTTTTTCCTAAGAGAGTCT 876
    |||
Db 1050 CAAAGACCCCTGCTGTGCTGCTAATATAGTAGACGCTTTTTCCTAAGAGAGTCT 991
OY 877 GGCAGAGGGGATCTGTGAACAGAGCTGGAGCATCTCAAGATCTTCCAGGGTTATCTT 936
    |||
Db 990 GGCAGAGGGGATCTGTGAACAGAGCTGGAGCATCTCAAGATCTTCCAGGGTTATCTT 931
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Db 810 ATTCCATTATATACAGAGATTAACTTTTTTTTAACTGGAGAATTCATGTTACAT 751
OY 1117 GCAGCTATGGGAATTAATTACATATTTTGTTCAGTGCAGAAAGATGACTAGTCTTT 1176
Db 750 GCAGCTATGGGAATTAATTACATATTTTGTTCAGTGCAGAAAGATGACTAGTCTTT 691
OY 1177 ATCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAGTTAAAGTCTAGCCTGTACT 1236
Db 690 ATCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAGTTAAAGTCTAGCCTGTACT 631
OY 1237 GAGGCTGTATACAC 1251
Db 630 GAGGCTGTATACAGC 616

RESULT 14

AAF86948/C

ID AAF86948 standard: cDNA: 2426 BP.

AAF86948:

XX 06-JUL-2001 (first entry)

XX Human P710P Inventive antigen coding sequence SEQ ID NO: 344.

XX Human: mouse; immunotherapy: cancer; leukaemia; WTI; Wilm's tumour gene;
XX chromosome 11p13; zinc finger transcription factor; ss.

XX Homo sapiens.

XX WO200125273-A2.

XX 12-APR-2001.

XX 04-OCT-2000; 2000WO-US27465.

XX 04-OCT-1999; 99US-0157459.

XX (COR-) CORIXA CORP.

XX Skelky YAM, Xu J, Cheever MA, Reed SG;

XX WPI: 2001-328324/34.

XX Polypeptide comprising part of the Wilm's Tumour gene product sequence is
XX used in the diagnosis and treatment of malignant diseases e.g. Leukemia
XX and cancer associated with WTI

XX Disclosure: Page 219-220; 228pp; English.

XX The present invention describes compositions comprising peptides derived
XX from the Wilm's tumour protein WTI and methods for their use in treating
XX malignant diseases. Peptides derived from both the murine and human WTI
XX proteins are provided. The human WTI gene is found on chromosome 11p13,
XX and the protein was shown to be a zinc finger transcription factor. The
XX immunogenic peptides of the invention are particularly useful in the
XX diagnosis and treatment of cancer and leukaemia. The present sequence is
XX a coding sequence used in the exemplification of the invention.

XX Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other;

XX Query Match 61.7%; Score 1155; DB 22; Length 2426;

XX Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

XX Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 AGGTGGAATAAGAAAGCTGCTGACTTTACATCTGAGCCACACATCTGCTGAATG 156
Db 1770 AGGTGGAATAAGAAAGCTGCTGACTTTACATCTGAGCCACACATCTGCTGAATG 1711
OY 157 GAGATTAATTACATCTGAGAAAGCAAGATGACATATTAATGTTAAGTACATG 216
Db 1710 GAGATTAATTACATCTGAGAAAGCAAGATGACATATTAATGTTAAGTACATG 1651

OY 217 TTTTGCATTTTCAGCCCTTTAAATATCCACACACAGAGAACCAAAAGAGCA 276
Db 1650 TTTTGCATTTTCAGCCCTTTAAATATCCACACACAGAGAACCAAAAGAGCA 1591
OY 277 CAGAGATCCCTGGAGAAATGCCCCGCCATCTTGGTTCATCATGAGCTCCGCCG 336
Db 1590 CAGAGATCCCTGGAGAAATGCCCCGCCATCTTGGTTCATCATGAGCTCCGCCG 1531
OY 337 TGCCCTGCTCCCTTTGTGAGGAGAGACATTTAGAAAATGATTTGATGTTCTTTAAAG 396
Db 1530 TGCCCTGCTCCCTTTGTGAGGAGAGACATTTAGAAAATGATTTGATGTTCTTTAAAG 1471
OY 397 ATGGCAGAGAAAACAGATCTCTGTTGAGATTTATTTTACAGGAGATTCAGATTGAA 456
Db 1470 ATGGCAGAGAAAACAGATCTCTGTTGAGATTTATTTTACAGGAGATTCAGATTGAA 1411
OY 457 TGAAGTCAAAAAGTGAGCATTTACAAATGAGAGAAAAACAGAGAAAAATCTTGATGCT 516
Db 1410 TGAAGTCAAAAAGTGAGCATTTACAAATGAGAGAAAAACAGAGAAAAATCTTGATGCT 1351
OY 517 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGATGAGGACCAAGCTGG 576
Db 1350 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGATGAGGACCAAGCTGG 1291
OY 577 GAGGAGATTAACCAAGGAGGAGAGGATTCAGGATTCGCGCTGCTTAACCTGTCGTT 636
Db 1290 GAGGAGATTAACCAAGGAGGAGAGGATTCAGGATTCGCGCTGCTTAACCTGTCGTT 1231
OY 637 CATTAACCAATCATTTATTTCTTAACCTCAAAACAAAGCTGTTGTAATTCGATCT 696
Db 1230 CATTAACCAATCATTTATTTCTTAACCTCAAAACAAAGCTGTTGTAATTCGATCT 1171
OY 697 CTACGCTTCCTTCTGGGCCCAACATTTCTCATATATCCAGCCACTATTTTAATAT 756
Db 1170 CTACGCTTCCTTCTGGGCCCAACATTTCTCATATATCCAGCCACTATTTTAATAT 1111
OY 757 TAGTCCAGATCTGACTGTGACCTTTCTACACCTGATAATATACATTTCTATTTGTT 816
Db 1110 TAGTCCAGATCTGACTGTGACCTTTCTACACCTGATAATATACATTTCTATTTGTT 1051
OY 817 CAAAGACCTTGTGTTGCTGCTTAATATGATGATGATGATGATGATGATGATGATG 876
Db 1050 CAAAGACCTTGTGTTGCTGCTTAATATGATGATGATGATGATGATGATGATGATG 921
OY 877 GGGCCAGGGGATCTGGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGTTATCTT 936
Db 990 GGGCCAGGGGATCTGGAACAGGCTGGGAGACATCTCAAGATCTTCCAGGTTATCTT 931
OY 937 ACTAGACACAGATGATCATTAACGAGAGAAATTAATCAACATCAATCCGAGCTGC 996
Db 930 ACTAGACACAGATGATCATTAACGAGAGAAATTAATCAACATCAATCCGAGCTGC 871
OY 997 TTTGCCATACGAAATTAATTTCCACATTTTGTGCCAATTCAGAGACCTCAAAATGTC 1056
Db 870 TTTGCCATACGAAATTAATTTCCACATTTTGTGCCAATTCAGAGACCTCAAAATGTC 811
OY 1057 ATTCATTAATATACAGAGATTAATTTTAACTGGAAGATTTCAATGTTACAT 1116
Db 810 ATTCATTAATATACAGAGATTAATTTTAACTGGAAGATTTCAATGTTACAT 751
OY 1117 GCAGCTATGGGAATTAATTACATATTTTGTTCAGTGCAGAAAGATGACTAGTCTTT 1176
Db 750 GCAGCTATGGGAATTAATTACATATTTTGTTCAGTGCAGAAAGATGACTAGTCTTT 691
OY 1177 ATCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAGTTAAAGTCTAGCCTGTACT 1236
Db 690 ATCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAGTTAAAGTCTAGCCTGTACT 631
OY 1237 GAGGCTGTATACAC 1251
Db 630 GAGGCTGTATACAGC 616

RESULT: 15
ABL95269/C
ID ABL95269 standard; CDNA: 2426 BP.
XX
AC ABL95269;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P710P cDNA sequence SEQ ID NO 470.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KM gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US202022248-A1.
XX
XX 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FRNG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JT, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stoik JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI: 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
XX PT diseases, in particular prostate cancer, and as markers for the
XX PT progression of cancer
XX
PS Claim 1; SEQ ID NO 470; 87bp; English.

XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 2426 BP; 717 A; 476 C; 548 G; 685 T; 0 other:

Query Match 61.7%; Score 1155; DB 24; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGTGAAGAATAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 156
DB 1770 AGGTGAAGAATAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 1711
QY 157 GAGTAAATTAACATCCTAGAAACAGACAGATGCATATATATGCTAAAGTAGACATG 216
DB 1710 GAGTAAATTAACATCCTAGAAACAGACAGATGCATATATATGCTAAAGTAGACATG 1651
QY 217 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACCAAAAGAGACA 276
DB 1650 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGAGAACCAAAAGAGACA 1591
QY 277 CAGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTATCATGATGACCTCGCCCTG 336
DB 1590 CAGAGATCCCTGGGAGAAATGCCGCCCATCTTGGGTATCATGATGACCTCGCCCTG 1531
QY 337 TGCCTGTCGCCGCTTGAGGAGAAAGACATTAGAAATGAATTGATGTCTCTTAAGG 396
DB 1530 TGCCTGTCGCCGCTTGAGGAGAAAGACATTAGAAATGAATTGATGTCTCTTAAGG 1471
QY 397 ATGGCAGAGAAAACAGATCCCTGTGTGATATTTATTTGAACGGGATTACAGATTTGAAA 456
DB 1470 ATGGCAGAGAAAACAGATCCCTGTGTGATATTTATTTGAACGGGATTACAGATTTGAAA 1411
QY 457 TGAAGTACAAAAGGACATTTACCAATGAGAGAAAACACACGAGAAAATCTGTATGCT 516
DB 1410 TGAAGTACAAAAGGACATTTACCAATGAGAGAAAACACACGAGAAAATCTGTATGCT 1351
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DB 1350 TCACAAAGACATGCACAAACAAATGGAATGACTGTGATGACATGAGCAGCCCAAGCTGGG 1291
QY 577 GAGGAGATTAACACAGGGGCGAGAGGTCAGATTCTGGCCCTGCTTAACCTGTGGCT 636
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QY 637 CATACCAATCATTTATATTTCTTAACCTCAAAACAAAGCTGTGTATATCTATCT 696
DB 1230 CATACCAATCATTTATATTTCTTAACCTCAAAACAAAGCTGTGTATATCTATCT 1171
QY 697 CTACGGTTCCTTGGGGCCCAACATTCCTCATATATCCAGCCACATCTTTTAATAT 756
DB 1170 CTACGGTTCCTTGGGGCCCAACATTCCTCATATATCCAGCCACATCTTTTAATAT 1111
QY 757 TAGTCCACAGATCTGACTGTGACCTTTCTACACTGTAGATAATACATTAATCTAT 816
DB 1110 TAGTCCACAGATCTGACTGTGACCTTTCTACACTGTAGATAATACATTAATCTAT 1051
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QY 877 GGCCCGAGGGATCTGTGAACAGGCTGGGAGCATCTCAAGATCTTCCAGGTTATATCT 936
DB 990 GGCCCGAGGGATCTGTGAACAGGCTGGGAGCATCTCAAGATCTTCCAGGTTATATCT 931
QY 937 ACTAGACACAGATGATCTTAAGAGGATAATTAATTAATCAATCATCTCAGGTGTC 996
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          |||||
Db      810  ATTCATTAAATCCACAGGATTACTTTTTCCTGAGAGAAATTCATGTTACAT 751
QY      1117 GCAGCTATGGGAATTAATTAATTTGTTTCCAGTGCAGAGATGACTAAGTCCTT 1176
          |||||
Db      750  GCAGCTATGGGAATTAATTAATTTGTTTCCAGTGCAGAGATGACTAAGTCCTT 691
QY      1177 ATCCCTCCCTTTGTTGATTTTTCAGATAAAGTTAAATGCTTAGCCTGTACT 1236
          |||||
Db      690  ATCCCTCCCTTTGTTGATTTTTCAGATAAAGTTAAATGCTTAGCCTGTACT 631
QY      1237 GAGGCTGTATACAGC 1251
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Db      630  GAGGCTGTATACAGC 616

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1155	61.7	2426	4	US-09-439-313-470
C 2	1155	61.7	2426	4	US-09-352-616A-470
C 3	1155	61.7	3112	4	US-09-439-313-468
C 4	1155	61.7	3112	4	US-09-352-616A-468
C 5	1034	55.2	2229	4	US-09-439-313-469
C 6	1034	55.2	2229	4	US-09-352-616A-469
C 7	812	43.4	812	4	US-09-439-313-471
C 8	812	43.4	812	4	US-09-352-616A-471
C 9	257	13.7	718	4	US-09-439-313-313
C 10	257	13.7	718	4	US-09-352-616A-313
C 11	257	13.7	718	4	US-09-232-149A-313
C 12	179	9.6	301	4	US-09-439-313-287
C 13	179	9.6	301	4	US-09-352-616A-287
C 14	179	9.6	301	4	US-09-232-149A-287
C 15	26	1.4	1379	4	US-09-620-312D-791
C 16	26	1.4	1462	4	US-09-620-312D-788
C 17	26	1.4	1519	4	US-09-620-312D-789
C 18	20	1.1	1664976	4	US-08-916-421B-1
C 19	19	1.0	161	1	US-08-450-834-3
C 20	19	1.0	98844	4	US-09-791-211-10
C 21	18	1.0	3645	2	US-08-663-112-1
C 22	18	1.0	4527	2	US-08-944-448-8
C 23	18	1.0	4527	4	US-09-353-362-8
C 24	18	1.0	8930	4	US-09-077-096A-1
C 25	18	1.0	17000	4	US-09-679-299A-18
C 26	18	1.0	72604	4	US-09-268-992-7
C 27	18	1.0	72604	4	US-09-657-474-7

C 28	18	1.0	99500	4	US-09-798-096-10	Sequence 10, Appl
C 29	17	0.9	157	1	US-08-392-678-11	Sequence 11, Appl
C 30	17	0.9	157	1	US-08-457-304A-11	Sequence 11, Appl
C 31	17	0.9	157	1	US-08-456-701A-11	Sequence 11, Appl
C 32	17	0.9	157	4	US-08-684-932A-11	Sequence 11, Appl
C 33	17	0.9	426	4	US-09-328-352-2225	Sequence 2225, Ap
C 34	17	0.9	590	4	US-09-364-206-25	Sequence 25, Appl
C 35	17	0.9	659	2	US-08-454-115-1	Sequence 1, Appl
C 36	17	0.9	831	1	US-08-450-834-5	Sequence 5, Appl
C 37	17	0.9	981	4	US-09-134-001C-982	Sequence 982, App
C 38	17	0.9	1017	4	US-09-328-475C-104	Sequence 104, App
C 39	17	0.9	1242	2	US-08-454-115-4	Sequence 4, Appl
C 40	17	0.9	2196	1	US-08-313-274-1	Sequence 1, Appl
C 41	17	0.9	2389	4	US-09-228-986-1	Sequence 1, Appl
C 42	17	0.9	2427	1	US-08-490-099-1	Sequence 1, Appl
C 43	17	0.9	2920	4	US-08-976-259-10	Sequence 10, Appl
C 44	17	0.9	3247	3	US-08-718-388-4	Sequence 4, Appl
C 45	17	0.9	3661	3	US-08-718-388-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1									
US-09-439-313-470/c									
; Sequence 470, Application US/09439313									
; Patent No. 6329505									
; GENERAL INFORMATION:									
; APPLICANT: Xu, Jiangchun									
; APPLICANT: Dillon, David C.									
; APPLICANT: Mitcham, Jennifer L.									
; APPLICANT: Harlocker, Susan Louise									
; APPLICANT: Jiang Yugui									
; APPLICANT: Reed, Steven G.									
; APPLICANT: Kalos, Michael									
; APPLICANT: Fanger, Gary									
; APPLICANT: Retter, Mark									
; APPLICANT: Solk, John									
; APPLICANT: Day, Craig									
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND									
; FILE REFERENCE: 210121.427C9									
; CURRENT APPLICATION NUMBER: US/09/439, 313									
; CURRENT FILING DATE: 1999-11-12									
; NUMBER OF SEQ ID NOS: 575									
; SOFTWARE: FastSeq for Windows Version 3.0									
; SEQ ID NO 470									
; LENGTH: 2426									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
; US-09-439-313-470									
Query Match									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
61.7%; Score 1155; DB 4; Length 2426;									
QY	97	AGGTGGAATTAAGAAAGCGCTGCTGACTTACCATCTGAGCCACACATCTCTGAATG	156						
DB	1770	AGGTGGAATTAAGAAAGCGCTGCTGACTTACCATCTGAGCCACACATCTCTGAATG	1711						
QY	157	GAGATTAATTAACATCACTGAGAAAGCAAGATGACAAATTAATGTTAGTGCATG	216						
DB	1710	GAGATTAATTAACATCACTGAGAAAGCAAGATGACAAATTAATGTTAGTGCATG	1651						
QY	217	TTTTTGCAATTTCCAGCCCTTTAATATCCACACACAGAGAACAAAGAGAGA	276						
DB	1650	TTTTTGCAATTTCCAGCCCTTTAATATCCACACACAGAGAACAAAGAGAGA	1591						
QY	277	CAGAGATCCCTGGAGAAATGCGCGCGCCATCTTGGTCAATGATGACCTCGCCCTG	336						
DB	1590	CAGAGATCCCTGGAGAAATGCGCGCGCCATCTTGGTCAATGATGACCTCGCCCTG	1531						
QY	337	TGCCCTGTCCTGCTGTGAGGAGACATTTGAAATATGATGATGCTTAAAG	396						

|||||
Db 1530 TGCTGGTCCCGCTTGAGGGAAGACATTAGAAATGAATATATGTTCTTAAAGG 1471
QY 397 ATGGGAGAGAAACAGATCCCTGTGTGATATTTATTTGAACGGGATTACAGATTGAAA 456
Db 1470 ATGGGAGAGAAACAGATCCCTGTGTGATATTTATTTGAACGGGATTACAGATTGAAA 1411
QY 457 TGAAGTACAAAGTGAACATTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCT 516
Db 1410 TGAAGTACAAAGTGAACATTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCT 1351
QY 517 TCACAGACATGCAACAAAGAAATGAATATCTGTGATGATAGATAGCCAGCAGCTGGG 576
Db 1350 TCACAGACATGCAACAAAGAAATGAATATCTGTGATGATAGCAGCAGCAGCTGGG 1291
QY 577 GAGGAGATACACAGGGGAGAGGGTACAGATCTGGCCCTGCTCTAAACCTGCTGCTT 636
Db 1290 GAGGAGATACACAGGGGAGAGGGTACAGATCTGGCCCTGCTCTAAACCTGCTGCTT 1231
QY 637 CATACCAAAATCATTTTCAATTTCTAAACCTCAAAACAAAGCTGTGATATCTGATCT 696
Db 1230 CATACCAAAATCATTTTCAATTTCTAAACCTCAAAACAAAGCTGTGATATCTGATCT 1171
QY 697 CTACGGTCTCTGGGCCCCAACATCTCATATATATCCAGCCACATCATTTTAAATAT 756
Db 1170 CTACGGTCTCTGGGCCCCAACATCTCATATATATCCAGCCACATCATTTTAAATAT 1111
QY 757 TAGTCCAGATCTGTACTGTGACCTTTTACACTGAGAAATACATTAATCTATTTGTT 816
Db 1110 TAGTCCAGATCTGTACTGTGACCTTTTACACTGAGAAATACATTAATCTATTTGTT 1051
QY 817 CAAAGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876
Db 1050 CAAAGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
QY 877 GGCCAGGAGATCTGTACAGGCTGGGAGAGCATCTCAAGATCTTTCAGGGTTATCTT 936
Db 990 GGCCAGGAGATCTGTACAGGCTGGGAGAGCATCTCAAGATCTTTCAGGGTTATCTT 931
QY 937 ACTAGACACAGCATGATCATTTACGAGTGAATTTATCTAAATCAATCATCTCAGTGC 996
Db 930 ACTAGACACAGCATGATCATTTACGAGTGAATTTATCTAAATCAATCATCTCAGTGC 871
QY 997 TTTGGCCATCTGAAATTCATTTCCACTTTTGGCCCATCTTCAACACCTCAAAATGTC 1056
Db 870 TTTGGCCATCTGAAATTCATTTCCACTTTTGGCCCATCTTCAACACCTCAAAATGTC 811
QY 1057 ATTCCATTAAATCACAGATTAATTTTAACTTTTAACTGGAAGATTCATGTTTCAAT 1116
Db 810 ATTCCATTAAATCACAGATTAATTTTAACTTTTAACTGGAAGATTCATGTTTCAAT 751
QY 1117 GCAGCTATGGGAATTAATTAATTTTTCAGTSCAAGATGACTAAGTCTTT 1176
Db 750 GCAGCTATGGGAATTAATTAATTTTTCAGTSCAAGATGACTAAGTCTTT 691
QY 1177 ATCCCTCCCTTGTGTTGATTTTTCAGTATTAAGTAAATGTTAGCTGTGACT 1236
Db 690 ATCCCTCCCTTGTGTTGATTTTTCAGTATTAAGTAAATGTTAGCTGTGACT 631
QY 1237 GAGGCTGTATACAGC 1251
Db 630 GAGGCTGTATACAGC 616

RESULT 2
US-09-352-616A-470/c
; Sequence 470, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuyui
; APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352.616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-470
Query Match 61.7%; Score 1155; DB 4; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 156
Db 1770 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 1711
QY 157 GAGATTAATTAACATCTAGAAACAGCAAGATGACATTAATGTTCTAATGATGACATG 216
Db 1710 GAGATTAATTAACATCTAGAAACAGCAAGATGACATTAATGTTCTAATGATGACATG 1651
QY 217 TTTTTCACATTTTCACGCCCCCTTTAATATTCACACACAGAGAGACAAAGAAAGCA 276
Db 1650 TTTTTCACATTTTCACGCCCCCTTTAATATTCACACACACAGAGAGACAAAGAAAGCA 1591
QY 277 CAGAGATCCCTGGAGAAATGCCCCGCCATCTTGGGTATCATGATGACCTTCGCCCTG 336
Db 1590 CAGAGATCCCTGGAGAAATGCCCCGCCATCTTGGGTATCATGATGACCTTCGCCCTG 1531
QY 337 TGCTGGTCCCGCTTGGAGGAGAGACATTAGAAATGAATGATGTTCTCTTAAAG 396
Db 1530 TGCTGGTCCCGCTTGGAGGAGAGACATTAGAAATGAATGATGTTCTCTTAAAG 1471
QY 397 ATGGGAGAGAAACAGATCTGTGTGATATTTATTTGAACGGGATTCAGATTTGAAA 456
Db 1470 ATGGGAGAGAAACAGATCTGTGTGATATTTATTTGAACGGGATTCAGATTTGAAA 1411
QY 457 TGAAGTACAAAGTGAACATTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCT 516
Db 410 TGAAGTACAAAGTGAACATTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCT 1351
QY 517 TCACAGACATGCAACAAAGAAATGAATGATGATGACATGAGGAGCCAAAGCTGGG 576
Db 1350 TCACAGACATGCAACAAAGAAATGAATGATGATGACATGAGGAGCCAAAGCTGGG 1291
QY 577 GAGGAGATACACAGGGGAGAGGGTACAGATCTGGCCCTGCTCTAAACCTGTCGTT 636
Db 1290 GAGGAGATACACAGGGGAGAGGGTACAGATCTGGCCCTGCTCTAAACCTGTCGTT 696
QY 637 CATACCAAAATCATTTTCAATTTCTAACCCTCAAAACAAAGCTGTGATATCTGATCT 1171
Db 1230 CATACCAAAATCATTTTCAATTTCTAACCCTCAAAACAAAGCTGTGATATCTGATCT 1171
QY 697 CTACGGTCTCTGGGCCCCAACATCTCATATATTCAGACGACACATCTTTTAAATAT 756
Db 1170 CTACGGTCTCTGGGCCCCAACATCTCATATATTCAGACGACACATCTTTTAAATAT 1111
QY 757 TAGTCCAGATCTGTACTGTGACCTTTTACACTGAGAAATACATTAATCTCATTTTGT 816
Db 1110 TAGTCCAGATCTGTACTGTGACCTTTTACACTGAGAAATACATTAATCTCATTTTGT 1051
QY 817 CAAAGACCTCTGCTGTTGCTGCTATATGATGATGATGATGATGATGATGATGATGAT 876
Db 1050 CAAAGACCTCTGCTGTTGCTGCTATATGATGATGATGATGATGATGATGATGATGAT 991
QY 877 GGCCAGGAGATCTGGAACAGGCTGGGAGACATCTCAAGATCTTTCAGAGGTTATCTT 936
Db 990 GGCCAGGAGATCTGGAACAGGCTGGGAGACATCTCAAGATCTTTCAGAGGTTATCTT 931

QY	937	ACTAGCACACAGCATGATCATTTAGGAGTGTAATTATCTAATCAACATCATCTAGTGC	996
Db	930	ACTAGCACACAGCATGATCATTTAGGAGTGTAATTATCTAATCAACATCATCTAGTGC	871
QY	997	TTTGCCCATCTCGAAATTCATTTCCCATTTTGGCCCATCTTCACACCCGCAAAATGTC	1056
Db	870	TTTGCCCATCTCGAAATTCATTTCCCATTTTGGCCCATCTTCACACCCGCAAAATGTC	811
QY	1057	ATTCATTAAATATACAGAGATTAACTTTTTTTTTTAACTCGAGAAATTCATGTTACAT	1116
Db	810	ATTCATTAAATATACAGAGATTAACTTTTTTTTTTAACTCGAGAAATTCATGTTACAT	751
QY	1117	GCACGTAATGGGAATTTATATACATATTTGTTCACAGTCGAAGATGACTAACTCCTT	1176
Db	750	GCACGTAATGGGAATTTATATACATATTTGTTCACAGTCGAAGATGACTAACTCCTT	691
QY	1177	ATCCCTCCCTTTTGTGGATTTTTTTCAGATAAAGTTAAATGCTTAGCCTTGACT	1236
Db	690	ATCCCTCCCTTTGTTGGATTTTTTTCAGATAAAGTTAAATGCTTAGCCTTGACT	631
QY	1237	GAGGCTGTATACAGC	1251
Db	630	GAGGCTGTATACAGC	616

```

RESULT 3
US-09-439-313-468
/ Sequence 468, Application US/09439313
/ Patent No. 6329505
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan Louise
/ APPLICANT: Jiang Yugu
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Kalos, Michael
/ APPLICANT: Fanger, Gary
/ APPLICANT: Retter, Mark
/ APPLICANT: Solk, John
/ APPLICANT: Day, Craig
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C9
/ CURRENT APPLICATION NUMBER: US/09/439,313
/ CURRENT FILING DATE: 1999-11-12
/ NUMBER OF SEQ ID NOS: 575
/ SOFTWARE: fastSeq for Windows Version 3.0
/ SEQ ID NO 468
/ LENGTH: 3112
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-439-313-468

```

Query Match	61.7%	Score 1155;	DB 4;	Length 3112;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1155;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	97	AGGTGAGAAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG	156
Db	1312	AGGTGAGAAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG	1371
QY	157	GAGATTAATTAACATCTACCTAGAAACAGCAAGATGCAATATATATGCTTAAGTAGTGACATG	216
Db	1372	GAGATTAATTAACATCTACCTAGAAACAGCAAGATGCAATATATGCTTAAGTAGTGACATG	1431
QY	217	TTTTTGCACATTTCCAGCCCTTTAAATATCCACACACACAGGAGCAAAAGGAAGCA	276
Db	1432	TTTTTGCACATTTCCAGCCCTTTAAATATCCACACACACAGGAGCAAAAGGAAGCA	1491
QY	277	CAGGATTCCTGGGAGAAATGCCCGGCCCATCTTGGGTATGATGAGCCTTGCCCTG	336

Db	1492	CAGAGATCCCTGGGGAGAAATCCCGGCCCATCTTGGGTGATCGATGAGCCTGCGCTG	1551
OY	337	TGCTGTGTCCTGGCTTTGTGAGGGAAGACATTAGAAAAATGAATTGATGTCTTTAAAG	396
Db	1552	TGCTGTGTCCTGGCTTTGTGAGGGAAGACATTAGAAAAATGAATTGATGTCTTTAAAG	1611
OY	397	ATGGGCGAGAAACAGATCCTGTGTGTGATTTTATATTGAACGGGATTTACGATTTGAA	456
Db	1612	ATGGGCGAGAAACAGATCCTGTGTGTGATTTTATATTGAACGGGATTTACGATTTGAA	1671
OY	457	TGAAGTACAAAGTAGACATTACCAATGAGAGAAAAACAGACGAAAAATCTTATGCT	516
Db	1672	TGAGTGCACAAAGTAGACATTACCAATGAGAGAAAAACAGACGAAAAATCTTATGCT	1731
OY	517	TCACAGACATGCACAAACAAAATGGATATCTGTGATGACATGAGCGACCAAGCTGG	576
Db	1732	TCACAGACATGCACAAACAAAATGGATATCTGTGATGACATGAGCGACCAAGCTGG	1791
OY	577	GAGAGATTAACACAGGGGACAGAGGTACAGATTGTGGGCCCTGCTGCTAAACTGTGGT	636
Db	1792	GAGAGATTAACACAGGGGACAGAGGTACAGATTGTGGGCCCTGCTGCTAAACTGTGGT	1851
OY	637	CATTAACCAATCATTTTCATATTTCTAAACCTCAAAACAAAAGCTGTGTAATATCTGAT	696
Db	1852	CATTAACCAATCATTTTCATATTTCTAAACCTCAAAACAAAAGCTGTGTAATATCTGAT	1911
OY	697	CTACGGTTCCTCTTGGGGCCCAACATTTGCCATATATCCAGCCACATCATTTTAAAT	756
Db	1912	CTACGGTTCCTCTTGGGGCCCAACATTTGCCATATATCCAGCCACATCATTTTAAAT	1971
OY	757	TAGTTCACAGATCTGTACTGTGACCTTCTCTACACTGTAAGTAATACATTACATTTGTT	816
Db	1972	TAGTTCACAGATCTGTACTGTGACCTTCTCTACACTGTAAGTAATACATTACATTTGTT	2031
OY	817	CAAAAGACCTTCTGTGTGCTGCCCTAATATGATGCTGACTGTTTTTCTTAAGAGACTGTCT	876
Db	2032	CAAAAGACCTTCTGTGTGCTGCCCTAATATGATGCTGACTGTTTTTCTTAAGAGACTGTCT	2091
OY	877	GGCCACAGGGATCTGTGTAACAGGCTGGGAGACATCTCAAGATCTTTCCAGGGTATACT	936
Db	2092	GGCCACAGGGATCTGTGTAACAGGCTGGGAGACATCTCAAGATCTTTCCAGGGTATACT	2151
OY	937	ACTAGCACACAGCATGATCTTAGCGAGTGAAATATCTAAATCAATCATCTCAGAGTC	996
Db	2152	ACTAGCACACAGCATGATCTTAGCGAGTGAAATATCTAAATCAATCATCTCAGAGTC	2211
OY	997	TTTTGCCATACGTAATTCATTTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTC	1056
Db	2212	TTTTGCCATACGTAATTCATTTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTC	2271
OY	1057	ATTTCATTTAATATCACAGATTTAACTTTTTTTTAACTCGGAAGAAATTCATGTTACAT	1116
Db	2272	ATTTCATTTAATATCACAGATTTAACTTTTTTTTAACTCGGAAGAAATTCATGTTACAT	2331
OY	1117	GCACCTAATGGGAATTTAATATTCATATTTTGTTCACAGTCGAAGAATGACATAAGCTCT	1176
Db	2332	GCACCTAATGGGAATTTAATATTCATATTTTGTTCACAGTCGAAGAATGACATAAGCTCT	2391
OY	1177	ATCCCTCCCTCTTCTTGTGATTTTCTTCCACTATAAAGTTAAATGCTGTAGCCTGTACT	1236
Db	2392	ATCCCTCCCTCTTCTTGTGATTTTCTTCCACTATAAAGTTAAATGCTGTAGCCTGTACT	2451
OY	1237	GAGCTGTATACAGC 1251	
Db	2452	GAGCTGTATACAGC 2466	

RESULT 4
US-09-352-616A-468
: Sequence 468, Application US/09352616A
: Patent No. 6395278
: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.

APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352.616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616A-468

Query Match 61.7%; Score 1155; DB 4; Length 3112;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATTAAGAAGCGCTGACTTACATCTGAGGCCACACATCTGCGTAATG 156
DB 1312 AGGTGAGAAATTAAGAAGCGCTGACTTACATCTGAGGCCACACATCTGCGTAATG 1371
QY 157 GAGATAATTAACATCACTAGAAACAGACAGATGCAATTAATGCTAAGTAGACATG 216
DB 1372 GAGATAATTAACATCACTAGAAACAGACAGATGCAATTAATGCTAAGTAGACATG 1431
QY 217 TTTTGGACATTTCCAGCCCTTAAATATCCACACACAGAGCAACAAAGAGCA 276
DB 1432 TTTTGGACATTTCCAGCCCTTAAATATCCACACACAGAGCAACAAAGAGCA 1491
QY 277 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCTGCGCTG 336
DB 1492 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCTGCGCTG 1551
QY 337 TGCTGGTCCCGCTGTGTGAGGAAAGACATTAAGAAATGAATGTGTCTTAAAG 396
DB 1552 TGCTGGTCCCGCTGTGTGAGGAAAGACATTAAGAAATGAATGTGTCTTAAAG 1611
QY 397 ATGGGCGAGAAACAGATCCCTGTGTGATATTTATTTGAACGGGATTAAGATTGAAA 456
DB 1612 ATGGGCGAGAAACAGATCCCTGTGTGATATTTATTTGAACGGGATTAAGATTGAAA 1671
QY 457 TGAAGTCACAAAGTAGACATTAACATGAGAGGAAACAGACGAAATCTTGATGCT 516
DB 1672 TGAAGTCACAAAGTAGACATTAACATGAGAGGAAACAGACGAAATCTTGATGCT 1731
QY 517 TCACAGACATGCAACAAACAAATGGAATGATGTGATGACATGAGCAGCCAAAGCTGG 576
DB 1732 TCACAGACATGCAACAAACAAATGGAATGATGTGATGACATGAGCAGCCAAAGCTGG 1791
QY 577 GAGGAGATACACAGCGGGGAGAGGATCTGAGATCTGCGCTGCTTAAAGCTGGCT 636
DB 1792 GAGGAGATACACAGCGGGGAGAGGATCTGAGATCTGCGCTGCTTAAAGCTGGCT 1851
QY 637 CATACCAAAATCATTTTCAATTTCTAACCCTCAAAACAAAGCTGTTTAAATCTGATCT 696
DB 1852 CATACCAAAATCATTTTCAATTTCTAACCCTCAAAACAAAGCTGTTTAAATCTGATCT 1911
QY 697 CTACGGTCTCTGCGGCCCAACATTTCTCATATATCCAGCCACATCTTTTAAATAT 756
DB 1912 CTACGGTCTCTGCGGCCCAACATTTCTCATATATCCAGCCACATCTTTTAAATAT 1971
QY 757 TAATTCACAGATCTGATCTGACCTTTCTACACTGAGATAACATTAACATTTTGT 816
DB 1972 TAATTCACAGATCTGATCTGACCTTTCTACACTGAGATAACATTAACATTTTGT 2031
QY 817 CAAGAGCCCTTCTGTGCTGCTTAATATATGATGATGATGATGATGATGATGATGAT 876
DB 2032 CAAGAGCCCTTCTGTGCTGCTTAATATATGATGATGATGATGATGATGATGATGAT 2091

QY 877 GCGCCAGGGATCTGTGACAGCGCTGGGAACATCTCAGATCTTCCAGGTTACTT 936
DB 2092 GCGCCAGGGATCTGTGACAGCGCTGGGAACATCTCAGATCTTCCAGGTTACTT 2151
QY 937 ACTAGCACACAGCATGATCATTTACGAGTGAATATATCAACATCATCTCAGTGC 996
DB 2152 ACTAGCACACAGCATGATCATTTACGAGTGAATATATCAACATCATCTCAGTGC 2211
QY 997 TTTGCCCATCTGAAATTCATTTTCCACTTTTGGCCATTTCTCAAGCTCAAAATGTC 1056
DB 2212 TTTGCCCATCTGAAATTCATTTTCCACTTTTGGCCATTTCTCAAGCTCAAAATGTC 2271
QY 1057 ATTCATTAATATACAGAGATTAACCTTTTAACTTTTAACTGGAAGATTAATGTTACAT 1116
DB 2272 ATTCATTAATATACAGAGATTAACCTTTTAACTTTTAACTGGAAGATTAATGTTACAT 2331
QY 1117 GCAGCTATGGAAATTTAATACATTTTGTTCAGTGCAGAGATGACATACTCTT 1176
DB 2332 GCAGCTATGGAAATTTAATACATTTTGTTCAGTGCAGAGATGACATACTCTT 2391
QY 1177 ATCCCTCCCTTTGATTTTTCAGATATTAAGTTAAATGCTTAGCCTTACT 1236
DB 2392 ATCCCTCCCTTTGATTTTTCAGATATTAAGTTAAATGCTTAGCCTTACT 2451
QY 1237 GAGGCTGTATACAGC 1251
DB 2452 GAGGCTGTATACAGC 2466

RESULT 5

US-09-439-313-469/c
Sequence 469; Application US/09439313
Patent No. 6329505

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439, 313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 469
LENGTH: 2229
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-469

Query Match 55.2%; Score 1034; DB 4; Length 2229;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 97 AGGTGAGAAATTAAGAAGCGCTGCTGACTTACATCTGAGGCCACACATCTGCGTAATG 156
DB 1776 AGGTGAGAAATTAAGAAGCGCTGCTGACTTACATCTGAGGCCACACATCTGCGTAATG 1717
QY 157 GAGATAATTAACATCACTAGAAACAGACAGATGCAATTAATGCTAAGTAGACATG 216
DB 1716 GAGATAATTAACATCACTAGAAACAGACAGATGCAATTAATGCTAAGTAGACATG 1657
QY 217 TTTTGGACATTTCCAGCCCTTAAATATCCACACACAGAGAGCAACAAAGAGCA 276
DB 1656 TTTTGGACATTTCCAGCCCTTAAATATCCACACACAGAGAGCAACAAAGAGCA 1597

QY 277 CAGAGATCCCTGGAGAAATGCCCGCCCATCTTGGTCAATCGATGAGCCCTGCCCTG 336
1596 CAGAGATCCCTGGAGAAATGCCCGCCCATCTTGGTCAATCGATGAGCCCTGCCCTG 1537
QY 337 TCCCTGGTCCCTGTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAGG 396
1536 TCCCTGGTCCCTGTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAGG 1477
QY 397 ATGGGAGGAGAAACAGATCTGTGTGATATTTATTTGAGGGATTTACAGTTTGAAA 456
1476 ATGGGAGGAGAAACAGATCTGTGTGATATTTATTTGAGGGATTTACAGTTTGAAA 1417
QY 457 TGAAGTCAAAAGTGAAGTATTAACATGAGAGAAAACAGAGAAAATCTTGATGCT 516
1416 TGAAGTCAAAAGTGAAGTATTAACATGAGAGAAAACAGAGAAAATCTTGATGCT 1357
QY 517 TCACAGACATGCAACAAACAAATGAATGAAATGATGATGATGAGGAGCCAAAGCTGG 576
1356 TCACAGACATGCAACAAACAAATGAATGATGATGATGATGAGGAGCCAAAGCTGG 1297
QY 577 GAGGAGATTAACACGGGGGAGAGAGGTCAGAGATTTCTGGCCCTGCTTAACGTCTG 636
1296 GAGGAGATTAACACGGGGGAGAGAGGTCAGAGATTTCTGGCCCTGCTTAACGTCTG 1237
QY 637 CATTAACCAATATTTTCAATATTTCTTAACCTCAAAACAAAGGCTGTGATATCTGATCT 696
1236 CATTAACCAATATTTTCAATATTTCTTAACCTCAAAACAAAGGCTGTGATATCTGATCT 1177
QY 697 CTACGGTTCCTTCTGGGCCCAACATTTCTCATATATTCAGCCACATCAATTTTAATAT 756
1176 CTACGGTTCCTTCTGGGCCCAACATTTCTCATATATTCAGCCACATCAATTTTAATAT 1117
QY 757 TAGTCCCGAGATCTGTACGTGACCTTTCTACACTAGAAATTAACATTTCTCTATTTGTT 816
1116 TAGTCCCGAGATCTGTACGTGACCTTTCTACACTAGAAATTAACATTTCTCTATTTGTT 1057
QY 817 CAAAGACCTTGTGTGCTGCTAATATGATGATGATGATGATGATGATGATGATGATG 876
1056 CAAAGACCTTGTGTGCTGCTAATATGATGATGATGATGATGATGATGATGATGATG 997
QY 877 GGCACAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGCTTATCTT 936
996 GGCACAGGGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGCTTATCTT 937
QY 937 ACTAGACACAGCATGATCATTAACGAGTGAATTAATCATCAATCTCTCACTGCTC 996
936 ACTAGACACAGCATGATCATTAACGAGTGAATTAATCATCAATCTCTCACTGCTC 877
QY 997 TTTGCCCATGAGAAATTAATTTCCACTTTTGTGCCAATTCAGAGACCTCAAAATGTC 1056
876 TTTGCCCATGAGAAATTAATTTCCACTTTTGTGCCAATTCAGAGACCTCAAAATGTC 817
QY 1057 ATTCATTAATATCAACAGATTAACATTTTAACTTGAAGTGAAGTGAAGTGAAGTGAAG 1116
816 ATTCATTAATATCAACAGATTAAC - TTTTATTTTAACTTGAAGTGAAGTGAAGTGAAG 758
QY 1117 GCAGCATGGAATTAATTAACATATTTTGTTCAGTGAAGTGAAGTGAAGTGAAGTGAAG 1176
757 GCAGCATGGAATTAATTAACATATTTTGTTCAGTGAAGTGAAGTGAAGTGAAGTGAAG 698
QY 1177 ATCCCTCCCTTGTGTGATTTTTCAGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1236
697 ATCCCTCCCTTGTGTGATTTTTCAGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 638
QY 1237 GAGGCTGTATACAGC 1251
637 GAGGCTGTATACAGC 623
Db

RESULT 6
US-09-352-616A-469/c
; Sequence 469, Application US/09352616A

; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352, 616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-469
Query Match 55.2%; Score 1034; DB 4; Length 2229;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 97 AGGTGAGAAATAGAAAGGCTGCTGACTTACATCTGAGGCGCACACATCTGCTGAATG 156
Db 1776 AGGTGAGAAATAGAAAGGCTGCTGACTTACATCTGAGGCGCACACATCTGCTGAATG 1717
QY 157 GAGATTAATTAACATCTAGAAACAGCAAGATGACAAATATATGCTTAAGTACTGACATG 216
Db 1716 GAGATTAATTAACATCTAGAAACAGCAAGATGACAAATATATGCTTAAGTACTGACATG 1657
QY 217 TTTTTCGACATTTCCAGCCCTTTAATATCCACACACAGAGAACACAAAGGAAGCA 276
Db 1656 TTTTTCGACATTTCCAGCCCTTTAATATCCACACACAGAGAACACAAAGGAAGCA 1597
QY 277 CAGAGATCCCTGGGAGAAATGCGCGCCCATCTTGGGTCATCATGAGCCCGCCCTG 336
Db 1596 CAGAGATCCCTGGGAGAAATGCGCGCCCATCTTGGGTCATCATGAGCCCGCCCTG 1537
QY 337 TGCCTGGTCCCTGTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAGG 396
Db 1536 TGCCTGGTCCCTGTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAAGG 1477
QY 397 ATGGGAGGAGAAACAGATCTGTGTGATATTTATTTGAGGGATTTACAGTTTGAAA 456
Db 1476 ATGGGAGGAGAAACAGATCTGTGTGATATTTATTTGAGGGATTTACAGTTTGAAA 1417
QY 457 TGAAGTCAAAAGTGAAGTATTAACATGAGAGAAAACAGAGAAAATCTTGATGCT 516
Db 1416 TGAAGTCAAAAGTGAAGTATTAACATGAGAGAAAACAGAGAAAATCTTGATGCT 1357
QY 517 TCACAGACATGCAACAAACAAATGAATGAAATGATGATGATGATGATGATGATGATG 576
Db 1356 TCACAGACATGCAACAAACAAATGAATGAAATGATGATGATGATGATGATGATGATG 1297
QY 577 GAGGAGATTAACACGGGGGAGAGAGGTCAGAGATTTCTGGCCCTGCTTAACGTCTG 636
Db 1296 GAGGAGATTAACACGGGGGAGAGAGGTCAGAGATTTCTGGCCCTGCTTAACGTCTG 1237
QY 637 CATTAACCAATATTTTCAATATTTCTTAACCTCAAAACAAAGGCTGTGATATCTGATCT 696
Db 1236 CATTAACCAATATTTTCAATATTTCTTAACCTCAAAACAAAGGCTGTGATATCTGATCT 1177
QY 697 CTACGGTTCCTTCTGGGCCCAACATTTCTCATATATTCAGCCACATCAATTTTAATAT 756
Db 1176 CTACGGTTCCTTCTGGGCCCAACATTTCTCATATATTCAGCCACATCAATTTTAATAT 1117
QY 757 TAGTCCCGAGATCTGTACGTGACCTTTCTACACTAGAAATTAACATTTCTCTATTTGTT 816
Db 1116 TAGTCCCGAGATCTGTACGTGACCTTTCTACACTAGAAATTAACATTTCTCTATTTGTT 1057
QY 817 CAAAGACCTTGTGTGCTGCTAATATGATGATGATGATGATGATGATGATGATGATG 876

Db	1056	CAAGACCCCTTCGCTGCTTCCTTAATATGTAAGCTGACTGTTTTCCTTAAGGAGTGTCT	997
QY	877	GGCCAGGGGATCTGTGTGACAGGCTGGGAACATCTCAAGATCTTTCAGGGTTATACTT	936
Db	996	GGCCAGGGGATCTGTGACAGGCTGGGAACATCTCAAGATCTTTCAGGGTTATACTT	937
QY	937	ACTAGCACACGCAATGATCATTACGAGGTGAATTAATCAACATCATCCTCAGTGTG	996
Db	936	ACTAGCACACAGCATGATCATTACGAGGTGAATTAATCAACATCATCCTCAGTGTG	877
QY	997	TTTCCCATACTGAAATTCATTTCGCCACTTTTGCCCATCTCAAGACCTCAAAATGTC	1056
Db	876	TTTCCCATACTGAAATTCATTTCGCCACTTTTGCCCATCTCAAGACCTCAAAATGTC	817
QY	1057	ATTCCATTAAATATACAGAGATTAACCTTTTTTAAACCTGAGAGAAATCAATGTATAT	1116
Db	816	ATTCCATTAAATATACAGAGATTAAC-TTTTTTTTTAACCTGAGAGAAATCAATGTATAT	758
QY	1117	GCACCTAATGGGAATTAATTAATCAATATTTTGTTCACAGTGCAGAGATGACTAAGCTCTT	1176
Db	757	GCACCTAATGGGAATTAATTAATCAATATTTTGTTCACAGTGCAGAGATGACTAAGCTCTT	698
QY	1177	ATCCCTCCCTTTGTGTGATTTTTTTTCCAGATATAAAGTTAAAAATGCTTAGCCTGTACT	1236
Db	697	ATCCCTCCCTTTGTGTGATTTTTTTTCCAGATATAAAGTTAAAAATGCTTAGCCTGTACT	638
QY	1237	GAGGCTGTATACAGC 1251.	
Db	637	GAGGCTGTATACAGC 623	

```

; RESULT 7
; US-09-439-313-471/C
; Sequence 471, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuguí
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Reltter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-439-313-471

```

Query Match	43.4%	Score 812	DB 4	Length 812
Best Local Similarity	100.0%	Pred. NO.	0	
Matches 812	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 6 CTGGCATCAGAAAAACAGAGGGGAGCAATTGTGTGGCTGTACCCGAGGAGACCAAGAGA 65

Db 812 CTGGCATCAGAAAAACAGAGGGGAGCAATTGTGTGGCTGTACCCGAGGAGACCAAGAGA 753

QY 66 TCTGCATGTGGGAAGACCTGTGATATACAGAGGTGAGAAATAAGAAAGCGTGTGACTT 125

Db 752 TCTGCATGTGGGAAGACCTGTGATATACAGAGGTGAGAAATAAGAAAGCGTGTGACTT 693

QY	126	TACCATCTGAGGCGCACACATCTGCTGCGTAATGAGACATTAATTAACTCACTAGAAAACAGCA	185
Db	692	TACCATCTGAGGCGCACACATCTGCTGCGTAATGAGACATTAATTAACTCACTAGAAAACAGCA	633
QY	186	GATGACAAATATAATGTCTAAGTAGTACATGTTTTGACATTTCCAGGCCCTTTAAATA	245
Db	632	GATGACAAATATAATGTCTAAGTAGTACATGTTTTGACATTTCCAGGCCCTTTAAATA	573
QY	246	TCCACACACACAGGAAGCAGAAAGGAACACAGATTCCTGGGAGAAATGCCGGCCG	305
Db	572	TCCACACACACAGGAAGCAGAAAGGAACACAGATTCCTGGGAGAAATGCCGGCCG	513
QY	306	CCATCTTGGGTATCATGATGAGCCTGCACCCTGGCTCCCGCTTGAGAGGAAGACA	365
Db	512	CCATCTTGGGTATCATGATGAGCCTGCACCCTGGCTCCCGCTTGAGAGGAAGACA	453
QY	366	TTAGAAAATGAAATGATGTGTTCTTTAAAGATGGGCGAGAAAACAGATCCTGTGTGA	425
Db	452	TTAGAAAATGAAATGATGTGTTCTTTAAAGATGGGCGAGAAAACAGATCCTGTGTGA	393
QY	426	TATTTATTTGAACGGGATTCAGATTTGAAATGAAAGTCACAAAGTGAACATTTCCAAATGA	485
Db	392	TATTTATTTGAACGGGATTCAGATTTGAAATGAAAGTCACAAAGTGAACATTTCCAAATGA	353
QY	486	GAGGAAAACAGACAGAAAATCTTGATGGCTTCACAAAGATGCACAAACAAAATATGAA	545
Db	332	GAGGAAAACAGACAGAAAATCTTGATGGCTTCACAAAGATGCACAAACAAAATATGAA	273
QY	546	TACTGTGATGACATGAGGCGCAGGCAAGCTGGGGAGAGATTAACCAAGGGGCGAGAGGTCAG	605
Db	272	TACTGTGATGACATGAGGCGCAGGCAAGCTGGGGAGAGATTAACCAAGGGGCGAGAGGTCAG	213
QY	606	GATTCGTGGCCCTGCTGCCCTTAAACTGTGGCTCATTAACCAAAATCATATTTCTTAAC	665
Db	212	GATTCGTGGCCCTGCTGCCCTTAAACTGTGGCTCATTAACCAAAATCATATTTCTTAAC	153
QY	666	CTCAAAACAAAGCTGTGTTGAATATCTGATCTGATACAGTTCTCTTGGGGCCCAACATCTC	725
Db	152	CTCAAAACAAAGCTGTGTTGAATATCTGATCTGATACAGTTCTCTTGGGGCCCAACATCTC	93
QY	726	CATATATCCAGCCACACTCATTTTAAATATTTAGTTCCCAAGATCTGACTGTGACCTTC	785
Db	92	CATATATCCAGCCACACTCATTTTAAATATTTAGTTCCCAAGATCTGACTGTGACCTTC	33
QY	786	TACACTGTAGATTAACATTAATCTCATTTTGTTC	817
Db	32	TACACTGTAGATTAACATTAATCTCATTTTGTTC	1

```

US-09-352-616A-471/c
Sequence 471, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.42708
CURRENT APPLICATION NUMBER: US/09/352.616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 471
LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616A-471

```

Query Match	43.48;	Score 812;	DB 4;	Length 812;
-------------	--------	------------	-------	-------------

Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGGCATCAGAAAAACAGAGGGAGATTTGTGCTGCTGACCCGAGGGAGACAGAGAA 65
DB 812 CTGGCATCAGAAAAACAGAGGGAGATTTGTGCTGCTGACCCGAGGGAGACAGAGAA 753
QY 66 TCTGATGTTGGGAGGACCTGATGATACAGAGTGAGAGAAATAAAGAGGCTGCATCT 125
DB 752 TCTGATGTTGGGAGGACCTGATGATACAGAGTGAGAGAAATAAAGAGGCTGCATCT 693
QY 126 TACCATCTGAGGCCACACATCTGCTGAATAGAGATTAATTAACATCAGTAAGACGCA 185
DB 692 TACCATCTGAGGCCACACATCTGCTGAATAGAGATTAATTAACATCAGTAAGACGCA 633
QY 186 GATGACAAATTAATGCTTAAGTAGTACATGTTTTTGCACATTTCCAGCCCTTTAAATA 245
DB 632 GATGACAAATTAATGCTTAAGTAGTACATGTTTTTGCACATTTCCAGCCCTTTAAATA 573
QY 246 TCCACACACAGAGAAAGCAAAAGAGACAGATCCCTGGGAGAAATCCCGGCG 305
DB 572 TCCACACACAGAGAAAGCAAAAGAGACAGATCCCTGGGAGAAATCCCGGCG 513
QY 306 CCATCTTGGTCATGATGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 365
DB 512 CCATCTTGGTCATGATGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
QY 366 TTGCAAAATGAATGATGCTGCTTAAAGATGGGACAGAAACAGATCCTGTTGTGGA 425
DB 452 TTGCAAAATGAATGATGCTGCTTAAAGATGGGACAGAAACAGATCCTGTTGTGGA 393
QY 426 TATTAATTTGAAGGGATTTACAGATTTGAATGAATGACACAAAGAGATTTACCAATGA 485
DB 332 TATTAATTTGAAGGGATTTACAGATTTGAATGAATGACACAAAGAGATTTACCAATGA 333
QY 486 GAGGAAAAACAGACGAGAAATCTTGATGCTTACACAGACATGCAACAAACAAATGGA 545
DB 332 GAGGAAAAACAGACGAGAAATCTTGATGCTTACACAGACATGCAACAAACAAATGGA 273
QY 546 TACTGTGATGACATGAGCAGCAGCTGGGGAGAGATTAACACAGGGGACAGAGCTCAG 605
DB 272 TACTGTGATGACATGAGCAGCAGCTGGGGAGAGATTAACACAGGGGACAGAGCTCAG 213
QY 606 GATTCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665
DB 212 GATTCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 153
QY 666 CTCAAAACAAAGCTGTTGTAATCTGATCTCTACGTTCTCTGCGGCCCAACATCTTC 725
DB 152 CTCAAAACAAAGCTGTTGTAATCTGATCTCTACGTTCTCTGCGGCCCAACATCTTC 93
QY 726 CATATATCCAGCCACATCTTAAATATTTAGTCCAGATCTGTAAGCTGACCTTTC 785
DB 92 CATATATCCAGCCACATCTTAAATATTTAGTCCAGATCTGTAAGCTGTAAGCTTTC 33
QY 786 TACACTGAGATTAACATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 817
DB 32 TACACTGAGATTAACATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1

RESULT 9
US-09-439-313-313
; Sequence 313, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuyui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary

APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 313
LENGTH: 718
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(718)
OTHER INFORMATION: n = A,T,C or G

US-09-439-313-313

Query Match 13.7%; Score 257; DB 4; Length 718;
Best Local Similarity 99.4%; Pred. No. 1,1e-114;
Matches 357; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 42 TGCAGCCGAGGAGACAGGAAGATCTGCATGCTGGGAGACCTGATGATACAGAGTG 101
DB 17 TGCAGCCGAGGAGACAGGAAGATCTGCATGCTGGGAGACCTGATGATACAGAGTG 76
QY 102 AGAAATTAAGAAAGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATGAGAT 161
DB 77 AGAAATTAAGAAAGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATGAGAT 136
QY 162 AATTAACATCACTAAGAACAGACATGACATTAATATGCTTAAGTAGACATGTTT 221
DB 137 AATTAACATCACTAAGAACAGACATGACATTAATATGCTTAAGTAGACATGTTT 196
QY 222 GCACATTCGAGCCCTTTAATATCCACACACAGAGAGCAAAAGAGACAGAG 281
DB 197 GCACATTCGAGCCCTTTAATATCCACACACAGAGAGCAAAAGAGACAGAG 256
QY 282 ATCCCTGGAGAAATGCCCCGCCCATCTTGATCATGATGAGCCTGCGCTGCT 341
DB 257 ATCCCTGGAGAAATGCCCCGCCCATCTTGATCATGATGAGCCTGCGCTGCT 316
QY 342 GGTCCCGCTTGAGAGGAGAGCATTAAGAAATGAATGATGTTCTTAAGATG 400
DB 317 GNTCCCGCTTGAGAGGAGAGCATTAAGAAATGAATGATGTTCTTAAGATG 375

RESULT 10
US-09-352-616A-313
; Sequence 313, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuyui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(718)


```

? TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
? TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
? FILE REFERENCE: 210121.427C08
? CURRENT APPLICATION NUMBER: US/09/352,616A
? CURRENT FILING DATE: 1999-07-13
? NUMBER OF SEQ ID NOS: 472
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 287
? LENGTH: 301
? TYPE: DNA
? ORGANISM: Homo sapien
? US-09-352-616A-287

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Query Match	9.68;	Score 179;	DB 4;	Length 301;
Best Local Similarity	99.68;	Pred. No. 6.2e-77;		
Matches 229; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	477	AGCATTTACCAATGAGGAGGAAAACACACAGAAAATCTTGATGGCTTCACAAGACATCCAA	531
Db	301	AGCATTTACCAATGAGGAGGAAAACACACAGAAAATCTTGATGGCTTCACAAGACATCCAA	242
QY	532	CAACCAAAATGSAATACTGTGTGATGCATGAGGACGACCAAGCTGGGGAGGAGATPAACACG	591
Db	241	CAACCAAAATGSAATACTGTGTGATTAACATGAGGACGACCAAGCTGGGGAGGAGATPAACACG	182
QY	592	GGGCGAGAGGGTACAGATTCTGGCCCTGCTGCTTAACCTGTGCTTCAATTAACCAATATT	651
Db	181	GGGCGAGAGGGTACAGATTCTGGCCCTGCTGCTTAACCTGTGCTTCAATTAACCAATATT	122
QY	652	TCATATTTTAAACCCCAAAACAAAGCGTTGTATATATCATATCTACAG	701
Db	121	TCATATTTTAAACCCCAAAACAAAGCGTTGTATATATCATATCTACAG	72

```

RESULT 14
US-09-232-149A-287/c
: Sequence 287, Application US/09232149A
: Patient No. 6465611
:
: GENERAL INFORMATION:
:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
: TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
: FILE REFERENCE: 210121.427C6
: CURRENT APPLICATION NUMBER: US/09/232,149A
: CURRENT FILING DATE: 1999-01-15
: NUMBER OF SEQ ID NOS: 338
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 287
:
: LENGTH: 301
:
: TYPE: DNA
:
: ORGANISM: Homo sapien
:
: US-09-232-149A-287

```

Query Match	9.6%	Score 179;	DB 4;	Length 301;
Best Local Similarity	99.6%	Pred. No. 6	2e-77;	
Matches	229;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	472	AGCATTTACCAATGAGAGGAAAACAGACGAGAAAATCTTGATGGCTTCACAAAGACATGCAA	531	
Db	301	AGCATTTACCAATGAGAGGAAAACAGACGAGAAAATCTTGATGGCTTCACAAAGACATGCAA	242	
QY	532	CAAAACAATGGAATGACTGTGTATACATGAGGAGCCAAAGCTGGGGAGAGATTAACCAAG	591	
Db	241	CAAAACAATGGAATGACTGTGTATACATGAGGAGCCAAAGCTGGGGAGAGATTAACCAAG	182	
QY	592	GGGGAGAGGGGACGAGATTCTGGCCCTGTGGCTAAACTGTGGTTCATTAACCAATCAAT	651	
Db	181	GGGGAGAGGGGACGAGATTCTGGCCCTGTGGCTAAACTGTGGTTCATTAACCAATCAAT	122	
QY	652	TCATATTTCTAACCTCAAAACAAGCTGTTGTAAATATCTGATCTCTACG	701	

Db 121 TCATATTTCTAACCTCAAACAAAGCTGTTGTAATATCTGATCTCTAG 72

```

RESULT 15
US-09-620-312D-791
Sequence 791, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunxui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radote R.
TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: 09/488,725
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt-FL-genes Version 1.0
SEQ ID NO 791
LENGTH: 1379
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (109)..(789)
US-09-620-312D-791

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Query Match	1.4%	Score 26	DB 4	Length 1379
Best Local Similarity	100.0%	Pred. No. 0.0066		
Matches 26	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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Search completed: September 27, 2003, 11:43:52
Job time : 110.441 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:44:18 : Search time 433.819 Seconds
(without alignments)
10742.554 Million cell updates/sec

Title: US-09-402-713A-3

Perfect score: 1872

Sequence: 1 agaagctgcgtcagcaaaaa.....caataagaattaccaga 1872

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1678620 seqs, 1244745471 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1367	73.0	3923	US-09-759-143-690	Sequence 690, App
2	1367	73.0	3923	US-09-780-669-690	Sequence 690, App
3	1367	73.0	3923	US-09-822-827-690	Sequence 690, App
4	1367	73.0	3923	US-09-895-793-690	Sequence 690, App
5	1367	73.0	3923	US-09-895-814-690	Sequence 690, App
6	1367	73.0	3923	US-10-144-678A-690	Sequence 690, App
7	1367	73.0	3923	US-10-012-896-690	Sequence 690, App
8	1367	73.0	3923	US-10-205-823-316	Sequence 316, App
9	1367	73.0	3923	US-09-759-143-470	Sequence 470, App
10	1155	61.7	2426	US-09-780-669-470	Sequence 470, App
11	1155	61.7	2426	US-09-822-827-470	Sequence 470, App
12	1155	61.7	2426	US-09-895-793-470	Sequence 470, App
13	1155	61.7	2426	US-09-895-814-470	Sequence 470, App
14	1155	61.7	2426	US-10-144-678A-470	Sequence 470, App
15	1155	61.7	2426	US-10-012-896-470	Sequence 470, App
16	1155	61.7	2426	US-10-010-940-470	Sequence 470, App

C 17	1155	61.7	2426	14	US-10-205-823-448	Sequence 448, App
18	1155	61.7	3112	9	US-09-759-143-468	Sequence 468, App
19	1155	61.7	3112	9	US-09-780-669-468	Sequence 468, App
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34	835	44.6	876	11	US-09-957-708-3	Sequence 3, Appl1
35	812	43.4	812	9	US-09-759-143-471	Sequence 471, App
36	812	43.4	812	9	US-09-780-669-471	Sequence 471, App
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38	812	43.4	812	10	US-09-895-793-471	Sequence 471, App
39	812	43.4	812	10	US-09-895-814-471	Sequence 471, App
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41	812	43.4	812	13	US-10-012-896-471	Sequence 471, App
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44	467	24.9	1102	14	US-10-198-846-11000	Sequence 11000, A
45	465	24.8	1036	14	US-10-198-846-13213	Sequence 13213, A

ALIGNMENTS

RESULT 1
US-09-759-143-690

Sequence 690, Application US/09759143

Patent No. US2002002248A1

GENERAL INFORMATION:

APPLICANT: Xu, Jlangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqun

APPLICANT: Henderson, Robert A.

APPLICANT: Katos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retler, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Veddyck, Thomas S.

APPLICANT: Carter, Darriek

APPLICANT: Wang, Aljun

APPLICANT: Li, Samuel

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C23

CURRENT APPLICATION NUMBER: US/09/759,143

NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 690

LENGTH: 3923

TYPE: DNA

ORGANISM: Homo sapien

US-09-759-143-690

Query Match 73.0%; Score 1367; DB 9; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	98	GGTGAAGAAATAAGAGCTGCTGACTTTTACCATCTGAGGCCACACATCTGCTGAATAGG	157
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QY	158	AGATTAATTAACATCACTAGAAACAGCAGATGACAAATTAATGTCTAAGTAGTGATCATGT	217
Dd	345	AGATTAATTAACATCACTAGAAACAGCAGATGACAAATTAATGTCTAAGTAGTGATCATGT	404
QY	218	TTTTCACATTTTCCAGCCCCCTTTTAATTTCCACACACACAGAGACACAAANAGAGCAC	277
Dd	405	TTTTCACATTTTCCAGCCCCCTTTTAATTTCCACACACACAGAGAACACAAANAGAGCAC	464
QY	278	AGAGATCCCTGGGAGAAATGCGCGGCCCATCTTGGGTCATCGATGAGCCGCGCCGTG	337
Dd	465	AGAGATCCCTGGGAGAAATGCGCGGCCCATCTTGGGTCATCGATGAGCCGCGCCGTG	524
QY	338	GCCCTGTCCTCCGCTGTGTGAGGAGAGACATTAAGAAAATGAATGTGTCTCTTAAAGGA	397
Dd	525	GCCCTGTCCTCCGCTGTGTGAGGAGAGACATTAAGAAAATGAATGTGTCTCTTAAAGGA	584
QY	398	TGGGAGAGAAAACAGATCTGTGTGAGATTTATTTGAGGGGTTCTCAGATTGGAAT	457
Dd	585	TGGGAGAGAAAACAGATCTGTGTGAGATTTATTTATTTAGGGGATTCAGATTGGAAT	644
QY	458	GAAGTACAAAGTGAGACTTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCTT	517
Dd	645	GAAGTACAAAGTGAGACTTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCTT	704
QY	518	CACAAGACATCAACAAACAAATGGATACCTGTGATACATACATGAGGCGCAAGCTGGGG	577
Dd	705	CACAAGACATCAACAAACAAATGGATACTGTGTATACATGAGGCGCAAGCTGGGG	764
QY	578	AGAGATTAACACGCGGGGACAGGGTCAGGATTTGCGCCCTGCGCTAACTGTGCTTC	637
Dd	765	AGGAGATTAACACGCGGGGACAGGGTCAGGATTTGCGCCCTGCGCTAACTGTGCTTC	824
QY	638	ATTAACCAATCATTTTCAATATTCTTAACCTCAAAAACAAGCTGTGTATATTCGATCTC	697
Dd	825	ATTAACCAATCATTTTCAATATTCTTAACCTCAAAAACAAGCTGTGTATATTCGATCTC	884
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Dd	885	TACGGTTCCTTCTGGGGCCCAATTTCTCATATATCCAGCCACTCATTTTATATTT	944
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QY	818	AAAGACCCCTTGCTGTGCTGCTAATATGATAGCTGACGTTTTTCCTAAGAGAGTCTG	877
Dd	1005	AAAGACCCCTTGCTGTGCTGCTAATATGATAGCTGACGTTTTTCCTAAGAGAGTCTG	1066
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Dd	1065	GCCCAAGGGGATCTGTGAACAGGCTGGGAGAGCATCTCAAGATCTTCCAGGGTTATCTTA	1124
QY	938	CTAGACACACACATGATCATTAAGGAGGATTTTCTTAATCAATCAATCTCTGCTGCT	997
Dd	1125	CTAGACACACACATGATCATTAAGGAGGATTTATCTTAATCAATCAATCTCTGCTGCT	1184
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QY	1058	TTCCATTAATTAATCACAGATTAACCTTTTATTTTAACTGGAAGCAATTTGTAATG	1117
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FILE REFERENCE: 210121.534C1
 CURRENT APPLICATION NUMBER: US/09/822.827
 CURRENT FILING DATE: 2001-03-28
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 690
 LENGTH: 3923
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-822-827-690

Query Match 73.0%; Score 1367; DB 9; Length 3923;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 GGTGAGAAATAGAAAGCTGTGACTTACATCTGAGGCCACATCTGCTGAATGG 157
 DB 285 GGTGAGAAATAGAAAGCTGTGACTTACATCTGAGGCCACATCTGCTGAATGG 344
 QY 158 AGATTAATTAACATCAGTAAGAACAGATGACATATTAATGCTAAGTAGTGCATGT 217
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 DB 465 AGAGATCCCTGGGAGAAATCCCGCCGATCTTGGGTCATGATGAGCCCTGCTGT 524
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 DB 525 GCTGTGCTCCGCTTTGTGAGGAGAGACATTAGAAATGAATGTGTTCTTAAAGA 584
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 DB 765 AGGAGATTAACGAGGGGAGAGGGTCAAGATCTGGGCCCTGCTAAACCTGCGCTTC 824
 QY 638 ATACCAAAATCATTTTCTATTTCTAAACCTCAAAACAAAGCTGTGTAATCTGATCTC 697
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DB 1125 CTAGCACAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1184
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 DB 1425 AGGCTGATACAGACAGCTTCCTCCATCCCTCAGCCTTATGTCATCACCATCAAC 1484
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 QY 1418 TTGAATTAAGTGTGATCTTCTTCTGATGCAAAAGAGGACATATGATGATGATGATG 1477
 DB 1605 TTGAATTAAGTGTGATCTTCTTCTGATGCAAAAGAGGACATATGATGATGATGATG 1664
 QY 1478 CATGAGACAGCAATTAATTAAGTGTGATGATGATGATGATGATGATGATGATGATG 1537
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 DB 1725 ATGCAAGAMKACAGAGGGAATGTTATGAGGACGTTGTATGAGCTGGGATGGAAGA 1784
 QY 1598 AAGGACAGGACCTCATAGTATCTTATATATATATATATATATATATATATATATAT 1657
 DB 1785 AAGGACAGGACCTCATAGTATCTTATATATATATATATATATATATATATATATAT 1844
 QY 1658 TATCCAAACAAGCTTTTACAGAAATTCATGAGAGCAAAATCCCAAGATTAACCTTATCC 1717
 DB 1845 TATCCAAACAAGCTTTTACAGAAATTCATGAGAGCAAAATCCCAAGATTAACCTTATCC 1904
 QY 1718 ATTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1777
 DB 1905 ATTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1964
 QY 1778 TGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1837
 DB 1965 TGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2024
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 DB 2025 AGGGTTCACCTCCGCAATTAAGATTTTCAAGA 2059

RESULT 4
 US-09-895-793-690
 Sequence 690, Application US/09895793
 Publication No. US20020192763A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yugu

```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedicik, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 690
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo saplen
; US-09-895-793-690

Query Match      73.0%: Score 1367; DB 10; Length 3923;
Best Local Similarity 99.5%: Pred No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 GGTGGAATAAGAAAGCGTGTGACTTACATCTGAGCCACACATCTGCTGAATG 157
DB 285 GGTGGAATAAGAAAGCGTGTGACTTACATCTGAGCCACACATCTGCTGAATG 344
QY 158 AGATATTTAATCTACTGAAACACAGAAATGACATATATAGTCTAGTATGACATG 217
DB 345 AGATATTTAATCTACTGAAACACAGAAATGACATATATAGTCTAGTATGACATG 404
QY 218 TTTTCACATTTCCAGCCCTTTAATATCCACACACAGAGAGACACAAAAGAACAC 277
DB 405 TTTTCACATTTCCAGCCCTTTAATATCCACACACAGAGAGACACAAAAGAACAC 464
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QY 398 TGGGAGAGAAACAGATCCTGTTGTGATATTTATTTGAACGGATTAAGATTTGAAT 457
DB 585 TGGGAGAGAAACAGATCCTGTTGTGATATTTATTTGAACGGATTAAGATTTGAAT 644
QY 458 GAAGTCACAAAGTAGCATTTACCAATGAGAGAGAAACAGACGAGAAATCTTGATGCTT 517
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DB 705 CACAAGACATGCAACAAACAAATGAAATACGTGATGATGACAGAGCCCAAGCTGGGG 764
QY 578 AGAGATTAACCAAGGGGAGAGAGGTGAGATTTGGCCCTGCTGCTTAACGTGCTTC 637
DB 765 AGAGATTAACCAAGGGGAGAGAGGTGAGATTTGGCCCTGCTGCTTAACGTGCTTC 824
QY 638 ATACCAAAATCATTTTCATATTTCTAACCCTCAAAACAAAGCTGTTGTAATATCTGATCTC 697
DB 825 ATACCAAAATCATTTTCATATTTCTAACCCTCAAAACAAAGCTGTTGTAATATCTGATCTC 884
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QY 698 TACGGTCCCTCTGGGGCCCAACATCTCCATATATCCAGCACACATTTTAAATTT 757
DB 885 TACGGTCCCTCTGGGGCCCAACATCTCCATATATCCAGCACACATTTTAAATTT 944
QY 758 AGTTCCACAGATCTGACTGTGACCTTTACACTGTAGAAATTAACATTTACTCATTTGCTTC 817
DB 945 AGTTCCACAGATCTGACTGTGACCTTTTACACTGTAGAAATTAACATTTACTCATTTGCTTC 1004
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DB 1065 GCCCAGGGGATCTGTGAAACAGGCTGGGAAGCAATCCATCTTCCAGGTTATACCTA 1124
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DB 1425 AGGCTGTATACAGACAGCCCTCCGCCATCCCTCCAGCTTATCTGTCATCCACATCAC 1484
QY 1298 CCTCCCATATNSACCTAAACAAATCTAATCTGTATTTCTTGAACATGTCAAGNCATAC 1357
DB 1485 CCTCCCATATNSACCTAAACAAATCTAATCTGTATTTCTTGAACATGTCAAGNCATAC 1544
QY 1358 ATTTTCTCTTGCTGAGAGCTCTCTCTTCTTAATCTGAATGATGTAAGTT 1417
DB 1545 ATTTTCTCTTGCTGAGAGCTCTCTCTTCTTAATCTGAATGATGTAAGTT 1604
QY 1418 TTGAATTAAGTGAATCTTACTTCAATGCAAGAAAGGGACATATGATTCATCATCA 1477
DB 1605 TTGAATTAAGTGAATCTTACTTCAATGCAAGAAAGGGACATATGATTCATCATCA 1664
QY 1478 CATGAGACAGCAAAATCTAAAGTGAATTTATTAAGATTTAGATTAATATATGA 1537
DB 1665 CATGAGACAGCAAAATCTAAAGTGAATTTATTAAGATTTAGATTAATATATATGA 1724
QY 1538 ATGCAAGACCAACAGAGGAATGTTATGGGACGTTTGTAAGCTGGGATGTGAAGA 1597
DB 1725 ATGCAAGACCAACAGAGGAATGTTATGGGACGTTTGTAAGCTGGGATGTGAAGA 1784
QY 1598 AAGGCAAGGAACTCATATGATTTATATATATATATATATATATATATATATATAT 1657
DB 1785 AAGGCAAGGAACTCATATGATTTATATATATATATATATATATATATATATATATAT 1844
QY 1658 TATCCAAACAGCTTTTACAGATTCATGACAGTGAAGAAATCCCAAGGTAACCTTTATCC 1717
DB 1845 TATCCAAACAGCTTTTACAGATTCATGACAGTGAAGAAATCCCAAGGTAACCTTTATCC 1904
QY 1718 ATTTATGAGTGTGCTGCTTTGATTTTGGCAATCATCTGCTGCTATCTCAACT 1777
DB 1905 ATTTATGAGTGTGCTGCTTTGATTTTGGCAATCATCTGCTGCTATCTCAACT 1964
```

Qy	1778	GAAGATGTTGGTTTGGCTTGTGTGTAATTTGGAAGAAATRGGGCACTCTTGTGAGCAGCTT	1837
Db	1965	TGAATGTGTTTGTCTCTTGTAGTTAATTTGAAGAAGAAATRGGGCACTCTTGTGAGCAGCTT	2024
Qy	1838	AGGTTCACTCTCTGGCATAAAGAAATTTCACAAGA	1872
Db	2025	AGGGTTCACTCTCTGGCATAAAGAAATTTCACAAGA	2059

RESULT 5

US-09-895-814-690

; Sequence 690, Application US/09895814

; Publication No. US20020193296A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Kalos, Michael D.
APPLICANT: Rettor Marc W

APPLICANT: Ketter, Marc W.
APPLICANT: Stolk, John A

APPLICANT: Day, Craig H

APPLICANT: Vedwick, Thomas

APPLICANT: Carter, Darrick

APPLICANT: HJ, Samuel X
AFFILIANT: CALCEL, DALLICK

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Heppler, William T

APPLICANT: Henderson, Robert

APPLICANT: Hural, John

APPLICANT: McNeill, Patricia

APPLICANT: Houghton, Raymond

APPLICANT: Vinàls de Bassols

; APPLICANT: Foy, Teresa

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITION

TITLE OF INVENTION: DIAGNOSIS

FILE REFERENCE: 210121.427C26

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; CURRENT APPLICATION NUMBER: U
; CURRENT FITTING DATE: 2001-06

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; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEC ID NOS: 990

```

NUMBER OF SEQ ID NOS: 990
SOFTWARE: FASTSEQ FOR WINDOWS

```

; SOFTWARE: FASTSEQ IOT WINDOWS
; SEQ ID NO 690

```

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; SEQ ID NO 690
LENGTH: 3923

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```

; LENGTH: 3923
; TYPE: DNA

```

ORGANISM: Homo sapien

US-09-895-814-690

6
 5
 4
 3
 2
 1

Query Match 73.08%

Model	Best Local Similarity
Model 1	99.58%

Matches 1767; Conservative

QY	98	GGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGGCCACACATCTGCTGAAATGG	157
Db	285	GGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGGCCACACATCTGCTGAAATGG	344
QY	158	AGATAATTAACATCACTAGAAACGCAAGATGACAAATATATGTTCTAAGTAGTACATGT	217
Db	345	AGATAATTAACATCACTAGAAACGCAAGATGACAAATATATGTTCTAAGTAGTACATGT	404
QY	218	TTTTGGCAATTTCCAGCCCTTTTAATATATCCACACACACAGGAAGCACAAAAGGAGACAC	277
Db	405	TTTTGGCAATTTCCAGCCCTTTTAATATATCCACACACAGGAAGCACAAAAGGAGACAC	464
QY	278	AGAGATCCCTGGGGAATGCCCCGGCCGCACTCTGGGTATCGATGAGGCTGGCCCTGT	337
Db	465	AGAGATCCCTGGGGAATGCCCCGGCCGCACTCTGGGTATCGATGAGGCTGGCCCTGT	524
QY	338	GCCCTGGTCCGCTTGTGAGGGAGGACATTAGAAAATGAATTGATGTGTTCTTTAAAGA	397
Db	525	GCCCTGGTCCGCTTGTGAGGGAGGACATTAGAAAATGAATTGATGTGTTCTTTAAAGA	584

OY	398	TGGCGAGAAAACGATCTCTTGGATATTATTTTGAACGGGATTACAGATTTGAAAT	457
Db	585	TGGCGAGGAAAAAGATCTCTGTTGGATATTATTTTGAACGGGATTACAGATTTGAAAT	644
OY	458	GAGTCACAAAGTAGAGCATTTACAAATGAGGAGAAACAGACGAGAAAATCTGTGGCTT	517
Db	645	GAACTCACAAAGTAGAGCATTTACAAATGAGGAGAAACAGACGAGAAAATCTGTGGCTT	704
OY	518	CACAAGACATGCACAAACAAATGGAATACTGTGATGACATGAGGACGCAAGCTTGGG	577
Db	705	CACAAGACATGCACAAACAAATGGAATACTGTGATGACATGAGGACGCAAGCTTGGG	764
OY	578	AGGAGATTAACACAGGGGAGACAGGGCTCAGAGATTCTGGCCCTGTGCTCTTAACTGTGGTCTG	637
Db	765	AGGAGATTAACACAGGGGAGAGGGCTCAGAGATTCTGGCCCTGTGCTCTTAACTGTGGTCTG	824
OY	638	ATAACCAAAATCATTTCAATTTCTAACCCTCAAAACAAAGCTGTGTAATATCGATCTGC	697
Db	825	ATAACCAAAATCATTTCAATTTCTAACCCTCAAAACAAAGCTGTGTAATATCGATCTGC	884
OY	698	TACGGTTCCTTCTGGGGCCCAACATTTCTCATATATCCAGCACACTATTTTAAATATTT	757
Db	885	TACGGTTCCTTCTGGGGCCCAACATTTCTCATATATCCAGCACACTATTTTAAATATTT	944
OY	758	AGTTCCACAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTAATCTATTTGGTTC	817
Db	945	AGTTCCACAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTAATCTATTTGGTTC	1004
OY	818	AAAACACCTTGSTGTGCTGCTCAATATATGATGCTGACTGTTTTTCCTAAGSAGTGTCTG	877
Db	1005	AAAACACCTTGSTGTGCTGCTCAATATATGATGCTGACTGTTTTTCCTAAGSAGTGTCTG	1064
OY	878	GCCCCAGGGGATCTGTGAACAGGCGTGGGAGAGCATCTCAAGATCTTTCCAGGGTAACTCTTA	937
Db	1065	GCCCCAGGGGATCTGTGAACAGGCGTGGGAGAGCATCTCAAGATCTTTCCAGGGTAACTCTTA	1124
OY	938	CTACACACACAGCATGATCATTTACGAGTGAATTTCTAATCAACATCATCTCAGTGTCT	997
Db	1125	CTACACACACAGCATGATCATTTACGAGTGAATTTCTAATCAACATCATCTCAGTGTCT	1184
OY	998	TTGGCCCATACTGAAATTCATTTTCCCACTTTTGTGCCATTTCTCAAGCTTCAAAATGTCA	1057
Db	1185	TTGGCCCATACTGAAATTCATTTTCCCACTTTTGTGCCATTTCTCAAGCTTCAAAATGTCA	1244
OY	1058	TTTCATTAAATTCACAGAGTAACTTTTTTTTAACTGGAAGAAATCTCAATGTTACATG	1117
Db	1245	TTTCATTAAATTCACAGAGTAACTTTTTTTTAACTGGAAGAAATCTCAATGTTACATG	1304
OY	1118	CAGCTATGGGAATTTAATACATATTTTGTGTTTCCAGTGCAGAAAGATGACTAAGTCCTTAA	1177
Db	1305	CAGCTATGGGAATTTAATACATATTTTGTGTTTCCAGTGCAGAAAGATGACTAAGTCCTTAA	1364
OY	1178	TCCCTCCCCCTTGTGTTGATTTTTTTTCCAGTATATAAGTTAAATGCTTACGCTTGTACTG	1237
Db	1365	TCCCTCCCCCTTGTGTTGATTTTTTTTCCAGTATATAAGTTAAATGCTTACGCTTGTACTG	1424
OY	1238	AGGCTGTAATACAGACAGCGCTCCGCCATCCCTCAGCCTTAATCTGTCATCACACATTAAC	1297
Db	1425	AGGCTGTAATACAGACAGCGCTCCGCCATCCCTCAGCCTTAATCTGTCATCACACATTAAC	1484
OY	1358	ATTATTTCCTTCTGCTGAGAGGCTCTTCTGTTGCTCTTAANTCTAGATATGTAAGTTT	1417
Db	1545	ATTATTTCCTTCTGCTGAGAGGCTCTTCTGTTGCTCTTAANTCTAGATATGTAAGTTT	1604
OY	1418	TTGGAATAGTTGATATCTTACTTCAATGCAGAAAGGAGACACATATGAGATTCATCATCA	1477
Db	1605	TTGGAATAGTTGATATCTTACTTCAATGCAGAAAGGAGACACATATGAGATTCATCATCA	1664
OY	1478	CATGAGACAGCAAAATACTTAAAGAGTATTAATTTGATTTATTAACAGTTTATGATTAATATGAA	1537

Db 1665 CATGAGACGCAAACTAAAGTGTATTTGATATATAAGTTAGTATTAATATATGCA 1724
Qy 1358 ATGCAAGKCCACAGAGGAAATGTTATGCGGCACGTTTGAAGCTGGATGTGAAGA 1597
Db 1725 ATGCAAGKCCACAGAGGAAATGTTATGCGGCACGTTTGAAGCTGGATGTGAAGA 1784
Qy 1598 AAGGAGGGAACCCATAGTATCTATATATATATCTTCTATCTTATCTATACACA 1657
Db 1785 AAGGAGGGAACCCATAGTATCTATATATATCTTCTATCTTATCTATACACA 1844
Qy 1658 TATCCAAACAGCTTTTCACAGAAATCATGAGTGAATCCCAAGGTAACCTTATCC 1717
Db 1845 TATCCAAACAGCTTTTCACAGAAATCATGAGTGAATCCCAAGGTAACCTTATCC 1904
Qy 1718 ATTTGATGAGTGCAGTCCGCTTGAATTTTGGCAATCATCTGCTATCTCACTT 1777
Db 1905 ATTTGATGAGTGCAGTCCGCTTGAATTTTGGCAATCATCTGCTATCTCACTT 1964
Qy 1778 TGAGATGTTGTGCTTGTATGTTAATGAAGAATAGGCACTCTGTGAGCCACTT 1837
Db 1965 TGAGATGTTGTGCTTGTATGTTAATGAAGAATAGGCACTCTGTGAGCCACTT 2024
Qy 1838 AGGCTTCACTCCTGGCAATTAAGAATTTTCAAGA 1872
Db 2025 AGGCTTCACTCCTGGCAATTAAGAATTTTCAAGA 2059

RESULT 6

US-10-144-678A-690
; Sequence 690, Application US/10144678A
; Publication No. US20030157089A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42YC28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapiens
US-10-144-678A-690

Query Match 73.0%; Score 1367; DB 12; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 98 GGTGAAATTAAGAAAGGCTGCTGACTTTACCATCTAGAGCCACACATCTGCTGAATGG 157
Db 285 GGTGAAATTAAGAAAGGCTGCTGACTTTACCATCTAGAGCCACACATCTGCTGAATGG 344
Qy 158 AGATATATTAACATCACTAGAAACACCAAGATGACATATTAATGCTTAAGTAGTACATGT 217
Db 345 AGATATATTAACATCACTAGAAACACCAAGATGACATATTAATGCTTAAGTAGTACATGT 404
Qy 218 TTTTGACATTTTCCAGCCCTTTAAATATCCACACACACAGAGAACACAAAAGAAAGAC 277
Db 405 TTTTGACATTTTCCAGCCCTTTAAATATCCACACACACAGAGAACACAAAAGAAAGAC 464
Qy 278 AGAGATCCCTGGGAAATATGCCCGCCCATCTTGGGTGATCATGAGCCCTGCCCTGT 337
Db 465 AGAGATCCCTGGGAAATATGCCCGCCCATCTTGGGTGATCATGAGCCCTGCCCTGT 524
Qy 338 GCCGTGCTCCGCTTGAAGGAAAGACATTAAGAAATGATGATGCTTCTTAAAGGA 397
Db 525 GCCGTGCTCCGCTTGAAGGAAAGACATTAAGAAATGATGATGCTTCTTAAAGGA 584
Qy 398 TGGCAGAAAACAGATCCTGTTGTGATATTTATTTGAACGGATTAACAGATTTGAAT 457
Db 585 TGGCAGAAAACAGATCCTGTTGTGATATTTATTTGAACGGATTAACAGATTTGAAT 644
Qy 458 GAAGTCACAAAGTGAAGCATTTACCATTTGAGAGAAAACAGACAGAAATCTTGATGGCTT 517
Db 645 GAAGTCACAAAGTGAAGCATTTACCAATGAGAGAAAACAGACAGAAATCTTGATGGCTT 704
Qy 518 CACAAGACATGCACAAACAAATGAATGATGATGATGATGATGATGATGATGATGATG 577
Db 705 CACAAGACATGCACAAACAAATGAATGATGATGATGATGATGATGATGATGATGATG 764
Qy 578 AGGAGATACCAACGGGGCAGAGGGTTCAGAGATTTGCGCCCTGCTTAACCTGCGTTTC 637
Db 765 AGGAGATACCAACGGGGCAGAGGGTTCAGAGATTTGCGCCCTGCTTAACCTGCGTTTC 824
Qy 638 ATTAACCAATGATTTTCAATATTTTCAACCTCAACCAACCAAGGTTGATATTCGATCTC 697
Db 825 ATTAACCAATGATTTTCAATATTTTCAACCTCAACCAACCAAGGTTGATATTCGATCTC 884
Qy 825 TACGTTCTCTTGCGGCCAACATCTTCCATATTCACGCCACACTATTTTAAATTT 757
Db 885 TACGTTCTCTTGCGGCCAACATCTTCCATATTCACGCCACACTATTTTAAATTT 944
Qy 758 AGTCCAGATCTGATGCTGACCTTTCTACACTGATGAATTAACATTAATCTCAATTTGTTTC 817
Db 945 AGTCCAGATCTGATGCTGACCTTTCTACACTGATGAATTAACATTAATCTCAATTTGTTTC 1004
Qy 818 AAAGACCTTGTGCTGCTGCTTATATGATGATGATGATGATGATGATGATGATGATG 877
Db 1005 AAAGACCTTGTGCTGCTGCTTATATGATGATGATGATGATGATGATGATGATGATG 1064
Qy 878 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTAACTTA 937
Db 1065 GCCCAGGGGATCTGGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTTAACTTA 1124
Qy 938 CTAGCAGACAGCATGATTAAGGATGATTAATCTAATCAACATCAATCTCACTGCTT 997
Db 1125 CTAGCAGACAGCATGATTAAGGATGATTAATCTAATCAACATCAATCTCACTGCTT 1184
Qy 998 TTGCCCATACGAAATGATTTCCCACTTTTGGCCCATCTCAAGACCTCAAAATGTTCA 1057
Db 1185 TTGCCCATACGAAATGATTTCCCACTTTTGGCCCATCTCAAGACCTCAAAATGTTCA 1244
Qy 1058 TTCCATTAATACAGAGATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1117
Db 1245 TTCCATTAATACAGAGATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1304
Qy 1118 CAGCTATGGAATTAATTAATTAATTTTGTTCAGTGAAGAAAGTGAAGTCTTGA 1177
Db 1305 CAGCTATGGAATTAATTAATTAATTTTGTTCAGTGAAGAAAGTGAAGTCTTGA 1364

1178 TCCCTCCCTGTTGGATTTTTCAGATTAAGTTAAATGCTTACCTGTACTG 1237
1365 TCCCTCCCTGTTGGATTTTTCAGATTAAGTTAAATGCTTACCTGTACTG 1424
1238 AGGCTGATACAGACAGCCTTCCCATGCTTACCTGTACTG 1237
1425 AGGCTGATACAGACAGCCTTCCCATGCTTACCTGTACTG 1484
1298 CCGTCCCATATACAGACAGCCTTCCCATGCTTACCTGTACTG 1357
1485 CCGTCCCATATACAGACAGCCTTCCCATGCTTACCTGTACTG 1544
1358 ATTTTCCTTCTGCTGAGAGCTCTTCTCTTAATCTAGATGATGAAGTT 1417
1545 ATTTTCCTTCTGCTGAGAGCTCTTCTCTTAATCTAGATGATGAAGTT 1604
1418 TTGATATAGTACTATCTTACTTATGAGAGGAGACATATGATGATGATG 1477
1605 TTGATATAGTACTATCTTACTTATGAGAGGAGACATATGATGATGATG 1664
1478 CATGAGACAGCAATATCTTAAAGTGTATTTGATTTATAGAGTTTATGAT 1537
1665 CATGAGACAGCAATATCTTAAAGTGTATTTGATTTATAGAGTTTATGAT 1724
1538 ATGCAAGACAGCAATATCTTAAAGTGTATTTGATTTATAGAGTTTATGAT 1597
1725 ATGCAAGACAGCAATATCTTAAAGTGTATTTGATTTATAGAGTTTATGAT 1784
1598 AAGGACAGGAGCAATATCTTAAAGTGTATTTGATTTATAGAGTTTATGAT 1657
1785 AAGGACAGGAGCAATATCTTAAAGTGTATTTGATTTATAGAGTTTATGAT 1844
1658 TATCCAAAGAGCTTTTTCAGAGATTCATGAGTGCATATCCCAAGAGTATTC 1717
1845 TATCCAAAGAGCTTTTTCAGAGATTCATGAGTGCATATCCCAAGAGTATTC 1904
1718 ATTTCATGATGATGCTTATGATTTTGGCAATATCTGCTATCTTATCTCA 1777
1905 ATTTCATGATGATGCTTATGATTTTGGCAATATCTGCTATCTTATCTCA 1964
1778 TGAGATGATGATGCTTATGATTTTGGCAATATCTGCTATCTTATCTCA 1837
1965 TGAGATGATGATGCTTATGATTTTGGCAATATCTGCTATCTTATCTCA 2024
1838 AGGCTTACTCTGAGCAATTAAGATTTTCAAGA 1872
2025 AGGCTTACTCTGAGCAATTAAGATTTTCAAGA 2059

RESULT 7

US-10-012-896-690
Sequence 690, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.

APPLICANT: Vinals de Basols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012.896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-690

Query Match 73.0%; Score 1367; DB 13; Length 3923;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

98 GGTGAGAAATTAAGAAAGGCTGCTGATTTTACATCTGAGGCCACATCTGCTGAATGG 157
285 GGTGAGAAATTAAGAAAGGCTGCTGATTTTACATCTGAGGCCACATCTGCTGAATGG 344
158 AGATTAATTAATCATCATGAGAGAGAGCAAGATGACATATATATGCTTAAGTACATGT 217
345 AGATTAATTAATCATCATGAGAGAGAGCAAGATGACATATATATGCTTAAGTACATGT 404
218 TTTTGCATATTTCCAGCCCTTTAATATATCCACACACAGAGAGAGCAAGAGAGAGAG 277
405 TTTTGCATATTTCCAGCCCTTTAATATATCCACACACAGAGAGAGAGAGAGAGAGAG 464
278 AGAGATCCCTGAG 337
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338 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 397
525 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
398 TGGGAG 457
585 TGGGAG 644
458 GAAGTCAAG 517
645 GAAGTCAAG 704
518 CACAG 577
705 CACAG 764
578 AGAGAGATTAACAG 637
765 AGAGAGATTAACAG 824
638 ATTAACCAAT 697
825 ATTAACCAAT 884
698 TACGATGCTTCTGAGGAG 757
885 TACGATGCTTCTGAGGAG 944
758 AGTTCCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 817
945 AGTTCCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1004
818 AAG 877
1005 AAG 1064

QY 878 GCCCAGGGGATCTGGAAGGCTGGAGCATCTCAAGATCTTCCAGGGTTACTTAA 937
DB 1065 GCCCAGGGGATCTGGAAGGCTGGAGCATCTCAAGATCTTCCAGGGTTACTTAA 1124
QY 938 CTAGACACACAGCATGATCTTACGAGATGAAATCTATCAATCAATCATCTCTAGTGTCT 997
DB 1125 CTAGACACACAGCATGATCTTACGAGATGAAATCTATCAATCAATCATCTCTAGTGTCT 1184
QY 998 TTGCCCATCTGAAATTTATTTCCACTTTTGTGCCCCATCTCAGAGACTTCAAAATGTCA 1057
DB 1185 TTGCCCATCTGAAATTTATTTCCACTTTTGTGCCCCATCTCAGAGACTTCAAAATGTCA 1244
QY 1058 TTCCATTAATATCAAGATTAATCTTTTAACTGGAGAAATCAATGTTACATG 1117
DB 1245 TTCCATTAATATCAAGATTAATCTTTTAACTGGAGAAATCAATGTTACATG 1304
QY 1118 CAGCTATGGAATTTAATTAATATTTTGTTCAGTGCAGAAAGATGACTAAGTCTTTA 1177
DB 1305 CAGCTATGGAATTTAATTAATATTTTGTTCAGTGCAGAAAGATGACTAAGTCTTTA 1364
QY 1178 TCCCTCCCTTGTGTTGATTTTTCAGATATAAGTTAAATGCTTACCTTGTACTG 1237
DB 1365 TCCCTCCCTTGTGTTGATTTTTCAGATATAAGTTAAATGCTTACCTTGTACTG 1424
QY 1238 AGGCTGTATACAGACACCTCTCCCATCCCTCAGCCTTATCTGATCAGCATCAAC 1297
DB 1425 AGGCTGTATACAGACACCTCTCCCATCCCTCAGCCTTATCTGATCAGCATCAAC 1484
QY 1298 CCGTCCCATATYACCTTAACAAATCTAATCTTGAATCTTGAACATGTCAGNCATAC 1357
DB 1485 CCGTCCCATATYACCTTAACAAATCTAATCTTGAATCTTGAACATGTCAGNCATAC 1544
QY 1358 ATTTCTCTTCTGCTGGAAGCTTCTCTGCTCTTAATCTGAATGATGTAAGTT 1417
DB 1545 ATTTCTCTTCTGCTGGAAGCTTCTCTGCTCTTAATCTGAATGATGTAAGTT 1604
QY 1418 TTGAATTAAGTACTATCTTACTTATGCAAAAGAGGAGACATATGATTCATCATCA 1477
DB 1605 TTGAATTAAGTACTATCTTACTTATGCAAAAGAGGAGACATATGATTCATCATCA 1664
QY 1478 CATGAGACAGCAAAATCTAATAAGTGTATTTGATTTAAGAGTTAGATAATATATGAA 1537
DB 1665 CATGAGACAGCAAAATCTAATAAGTGTATTTGATTTAAGAGTTAGATAATATATGAA 1724
QY 1538 ATGCAAGACACAGAGGGAATGTTATGAGGACAGCTTGTAGAGCTGGAGTGAAGAA 1597
DB 1725 ATGCAAGACACAGAGGGAATGTTATGAGGACAGCTTGTAGAGCTGGAGTGAAGAA 1784
QY 1598 AAGGAGGGAACCTATAGTATCTATATATATATCTTCTATCTCTATCTATCACA 1657
DB 1785 AAGGAGGGAACCTATAGTATCTATATATATATCTTCTATCTCTATCTATCACA 1844
QY 1658 TATCCAAACAGCTTTTACAGAAATCATGAGTGAAGAAATCCCAAGAGTAACTTATCC 1717
DB 1845 TATCCAAACAGCTTTTACAGAAATCATGAGTGAAGAAATCCCAAGAGTAACTTATCC 1904
QY 1718 ATTTATGAGTGAAGCTGTTAGAAATTTTGGCAAAATCACTGCTACTTATCTCACTT 1777
DB 1905 ATTTATGAGTGAAGCTGTTAGAAATTTTGGCAAAATCACTGCTACTTATCTCACTT 1964
QY 1778 TGAGATGAGTGTGCTGTTGATTTAATGAAAGAAATAGGGGACCTGTGAGCCACATTT 1837
DB 1965 TGAGATGAGTGTGCTGTTGATTTAATGAAAGAAATAGGGGACCTGTGAGCCACATTT 2024
QY 1838 AGGCTTACTCTCTGCAATTAAGAATTTACAAAGA 1872
DB 2025 AGGCTTACTCTCTGCAATTAAGAATTTACAAAGA 2059

RESULT 8
US-10-205-823-316
; Sequence 316, Application US/10205823

/ Publication No. US20030108963A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Monahan, John E.
/ APPLICANT: Endege, Wilson O.
/ APPLICANT: Gannavarapu, Manjula
/ APPLICANT: Gorbacheva, Bella
/ APPLICANT: Hoersch, Sebastian
/ APPLICANT: Kamatkar, Shubhangi
/ APPLICANT: Monsey, Angela M.
/ APPLICANT: Gialt, Karen
/ APPLICANT: Zhao, Xumel
/ APPLICANT: Anderson, Dustin
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
/ METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ THERAPY OF PROSTATE CANCER
/ TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
/ FILE REFERENCE: MRI-044
/ CURRENT APPLICATION NUMBER: US/10/205.823
/ CURRENT FILING DATE: 2002-07-25
/ PRIOR APPLICATION NUMBER: 60/307,982
/ PRIOR FILING DATE: 2001-07-25
/ PRIOR APPLICATION NUMBER: 60/314,356
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/325,020
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 60/341,746
/ PRIOR FILING DATE: 2001-12-12
/ PRIOR APPLICATION NUMBER: 60/362,158
/ PRIOR FILING DATE: 2002-03-05
/ NUMBER OF SEQ ID NOS: 455
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 316
/ LENGTH: 3923
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-205-823-316

Query Match 73.0% Score 1367; DB 14; Length 3923;
Best Local Similarity 99.5% Pred. No. 0;
Matches 1167; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 GGTGGAATTAAGAAGCTGCTGACTTATACATCTGAGGCCACATCTGCTGAATGG 157
DB 285 GGTGGAATTAAGAAGCTGCTGACTTATACATCTGAGGCCACATCTGCTGAATGG 344
QY 158 AGATATTAACATCTAGAAAACAGCAAGATGACATATATGCTCTAAGTATGACATGT 217
DB 345 AGATATTAACATCTAGAAAACAGCAAGATGACATATATGCTCTAAGTATGACATGT 404
QY 218 TTTTGCACATTTCCAGCCCTTTAATATCCACACACAGGAAGCAACAAAAGAAAGCAG 277
DB 405 TTTTGCACATTTCCAGCCCTTTAATATCCACACACAGGAAGCAACAAAAGAAAGCAG 464
QY 278 AGAGATCCCTGGAGAAATAGCCCGCCCATCTTGGGTCATGATGAGAGCTCGCCCTGT 337
DB 465 AGAGATCCCTGGAGAAATAGCCCGCCCATCTTGGGTCATGATGAGAGCTCGCCCTGT 524
QY 338 GCGTGTCCCGCTTGAAGGGAAGACATTTAGAAATGAATGATGTCTTCTTAAAGGA 397
DB 525 GCGTGTCCCGCTTGAAGGGAAGACATTTAGAAATGAATGATGTCTTCTTAAAGGA 584
QY 398 TGGGAGAGAAAACAGATCTGTGTGATATTTATTAAGCGGATTTACAGATTTGAAT 457
DB 585 TGGGAGAGAAAACAGATCTGTGTGATATTTATTAAGCGGATTTACAGATTTGAAT 644
QY 458 GAAGTCACAAAGTGAAGTATACCATGAGAGAAACAGAGAAATCTTGATGAGCTT 517
DB 645 GAAGTCACAAAGTGAAGTATACCATGAGAGAAACAGAGAAATCTTGATGAGCTT 704
QY 518 CACAAGACATGCAACAAACAAATGGAATCTGTGATGATGATGAGGAGCCAGCTGGGG 577
DB 705 CACAAGACATGCAACAAACAAATGGAATCTGTGATGATGATGAGGAGCCAGCTGGGG 764

Db 1530 TGCCTGCTCCGCTTGTGAGGAGGACATTAGAAAATGATTTGATGCTTCTTAAGG 1471
QY 397 ATGGCAGGAAACAGATCTGTTGGATTTATTTTGAACGGGATTCAGATTGGAA 456
Db 1470 ATGGCAGGAAACAGATCTGTTGGATTTATTTTGAACGGGATTCAGATTGGAA 1411
QY 457 TGAAGTCACAAAGTACATTTACCAATGAGAGGAAACAGACAGAAATCTTGATGCT 516
Db 1410 TGAAGTCACAAAGTACATTTACCAATGAGAGGAAACAGACAGAAATCTTGATGCT 1351
QY 517 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGAGGACCAAGCTGGG 576
Db 1350 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGAGGACCAAGCTGGG 1291
QY 577 GAGGAGATTAACACGGGGGAGAGGATTCAGAGATTCGGCCCTGCTTAAGCTGGCT 636
Db 1290 GAGGAGATTAACACGGGGGAGAGGATTCAGAGATTCGGCCCTGCTTAAGCTGGCT 1231
QY 637 CATTAACCAATCTTCAATTTCTTAACCTCAAAACAAAGCTGTTGTAATCTGATCT 696
Db 1230 CATTAACCAATCTTCAATTTCTTAACCTCAAAACAAAGCTGTTGTAATCTGATCT 1171
QY 697 CTACGGTCTCTCTGGGCCCAACATTTCTCATATATCCAGCCACACTATTTTAATAT 756
Db 1170 CTACGGTCTCTCTGGGCCCAACATTTCTCATATATCCAGCCACACTATTTTAATAT 1111
QY 757 TGTGTCACGATCTCTGATGATCTTCTTACCTGTAGATTAATTAATTAATTTGTT 816
Db 1110 TGTGTCACGATCTCTGATGATCTTCTTACCTGTAGATTAATTAATTAATTTGTT 1051
QY 817 CAAGAACCCTTCTGCTGCTGCTAATATGATGATGATGATTTTCTTAAGAGTGTCT 876
Db 1050 CAAGAACCCTTCTGCTGCTGCTAATATGATGATGATGATTTTCTTAAGAGTGTCT 991
QY 877 GGCCAGGAGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGTTATATCT 936
Db 991 GGCCAGGAGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGTTATATCT 931
QY 931 ACTACACACAGCATGATCATTTACGAGAGTATTTATCTAATCAATCATCTCTCACTGTC 996
Db 930 ACTACACACAGCATGATCATTTACGAGAGTATTTATCTAATCAATCATCTCTCACTGTC 871
QY 997 TTTGGCCATCTGAAATTCATTTCCACTTTTGTGCCCATCTCTCAAGACCTCAAAATGTC 1056
Db 870 TTTGGCCATCTGAAATTCATTTCCACTTTTGTGCCCATCTCTCAAGACCTCAAAATGTC 811
QY 1057 ATTCATTAATATATCAAGAGATTAATCTTTTATTAACCTGGAAGATTCATTTGATCAT 1116
Db 810 ATTCATTAATATATCAAGAGATTAATCTTTTATTAACCTGGAAGATTCATTTGATCAT 751
QY 1117 GAGGCTATGGAATTAATTAATTAATTTGTTTCCAGTGAAGATGACTAAGCTCTT 1176
Db 750 GAGGCTATGGAATTAATTAATTAATTTGTTTCCAGTGAAGATGACTAAGCTCTT 691
QY 1177 ATCCCTCCCTTGTGTTGATTTTTCAGTATAAAGTTAAAGTCTTAAGCTTGATCT 1236
Db 690 ATCCCTCCCTTGTGTTGATTTTTCAGTATAAAGTTAAAGTCTTAAGCTTGATCT 631
QY 1237 GAGGCTATTAACGC 1251
Db 630 GAGGCTATTAACGC 616

RESULT 10

US-09-780-669-470/c

; Sequence 470, Application US/09780669

; Patent No. US2002005197A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, David C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yugu

QY 97 AGGTAGAATTAAGAAAGCTGCTGACTTACCATCTGAGGCCACACATCTCTGAATG 156
Db 1770 AGGTAGAATTAAGAAAGCTGCTGACTTACCATCTGAGGCCACACATCTCTGAATG 1711
QY 157 GAGATTAATTAACATCTGCTGAACACAGATGACAAATTAATGTTAGTATGATGATG 216
Db 1710 GAGATTAATTAACATCTGCTGAACACAGATGACAAATTAATGTTAGTATGATGATG 1651
QY 217 TTTTGGACATTTCCAGCCCTTTTAATATTCACACACACAGAGAACACAAAGAGCA 276
Db 1650 TTTTGGACATTTCCAGCCCTTTTAATATTCACACACACAGAGAACACAAAGAGCA 1591
QY 277 CAGAGATCCCTGGGAAATAGCCCGGCCCATCTGGGTCAATGATGAGCTCGCCCTG 336
Db 1590 CAGAGATCCCTGGGAAATAGCCCGGCCCATCTGGGTCAATGATGAGCTCGCCCTG 1531
QY 337 TGCCTGCTCCGCTTGTGAGGAGAGACATTTAGAAATGAATGATGATGTTCTTAAAG 396
Db 1530 TGCCTGCTCCGCTTGTGAGGAGAGACATTTAGAAATGAATGATGATGTTCTTAAAG 1471
QY 397 ATGGCAGGAAACAGATCTGTTGATTTATTTGAACGGATTCACAGATTGGAAT 456
Db 1470 ATGGCAGGAAACAGATCTGTTGATTTATTTGAACGGATTCACAGATTGGAAT 1411
QY 457 TGAAGTCACAAAGTACATTTACCAATGAGAGGAAACAGACAGAAATCTTGATGCT 516
Db 1410 TGAAGTCACAAAGTACATTTACCAATGAGAGGAAACAGACAGAAATCTTGATGCT 1351
QY 517 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGAGGACCAAGCTGGG 576
Db 1350 TCACAAGACATGCAACAAACAAATGGAATGATGATGATGAGGACCAAGCTGGG 1291
QY 577 GAGGAGATTAACACGGGGGAGAGGATTCAGAGATTCGGCCCTGCTTAAGCTGGCT 636
Db 1290 GAGGAGATTAACACGGGGGAGAGGATTCAGAGATTCGGCCCTGCTTAAGCTGGCT 1231
QY 637 CATTAACCAATCTTCAATTTCTTAACCTCAAAACAAAGCTGTTGTAATCTGATCT 696
Db 1230 CATTAACCAATCTTCAATTTCTTAACCTCAAAACAAAGCTGTTGTAATCTGATCT 1171
QY 697 CTACGGTCTCTCTGGGCCCAACATTTCTCATATATCCAGCCACACTATTTTAATAT 756

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Db      1170 CTAGCGTTCCTTGGGCCCCACATCTCCATATATCCAGCCACACATCTTAAATAT 1111
QY      757 TAGTCCAGATCTGCTGCTGACCTTTTACACTGAGATATACATCTACTATTGT 816
Db      1110 TAGTCCAGATCTGCTGCTGACCTTTTACACTGAGATATACATCTACTATTGT 1051
QY      817 CAAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876
Db      1050 CAAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
QY      877 GGGCCAGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 936
Db      990 GGGCCAGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
QY      937 ACTAGCACAGCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
Db      930 ACTAGCACAGCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
QY      997 TTGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1056
Db      870 TTGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
QY      1057 ATTCCATTAATATCAGAGATTAATCTTTTAACTGGAAGATTAATCTTACAT 1116
Db      810 ATTCCATTAATATCAGAGATTAATCTTTTAACTGGAAGATTAATCTTACAT 751
QY      1117 GCAGCTATGGAATTAATTAATTAATTTTTCAGATTAAGATTAAGATTAAGATTAAGATTA 1176
Db      750 GCAGCTATGGAATTAATTAATTAATTTTTCAGATTAAGATTAAGATTAAGATTAAGATTA 691
QY      1177 ATCCCTCCCTTGTGTTGATTTTTCAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1236
Db      690 ATCCCTCCCTTGTGTTGATTTTTCAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 631
QY      1237 GAGGCTGTATACAGC 1251
Db      630 GAGGCTGTATACAGC 616

RESULT 11
US-09-822-470/c
; Sequence 470, Application US/09822827
; Patent No. US2002081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822, 827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-822-470

Query Match      61.7%; Score 1155; DB 9; length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      97 AGGTGAATTAAGAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 156
Db      1770 AGGTGAATTAAGAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1711
QY      157 GAGATTAATTAACATCTAGTAAACAGCAGATGACATATATATGCTTAAGTAGATG 216
Db      1710 GAGATTAATTAACATCTAGTAAACAGCAGATGACATATATATGCTTAAGTAGATG 1651
QY      217 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAGGACAAAGGAAGCA 276
Db      1111 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAGGACAAAGGAAGCA 1111

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Db      1650 TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGGAGGACAAAGGAAGCA 1591
QY      277 CAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGGTGCATGATGAGCTCGCCCTG 336
Db      1590 CAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGGTGCATGATGAGCTCGCCCTG 1531
QY      337 TGCCGTGCTCCGCTTGTGAGGGAAGGACATTAAGAAATGAATGATGTCTTAAAG 396
Db      1530 TGCCGTGCTCCGCTTGTGAGGGAAGGACATTAAGAAATGAATGATGTCTTAAAG 1471
QY      397 ATGGGCGAGAAACAGATCCCTGTTGATATATTAATGAAGGATTAAGATTTGAAA 456
Db      1470 ATGGGCGAGAAACAGATCCCTGTTGATATATTAATGAAGGATTAAGATTTGAAA 1411
QY      457 TGAAGTCACAAAGTACATTTACCAATGAGAGGAAACAGACAGAAATCTTGATGCT 516
Db      1410 TGAAGTCACAAAGTACATTTACCAATGAGAGGAAACAGACAGAAATCTTGATGCT 1351
QY      517 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGGACCAAGCTGGG 576
Db      1350 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGGACCAAGCTGGG 1291
QY      577 GAGGAGTAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 636
Db      1290 GAGGAGTAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1231
QY      637 CATTAACCAATATCTGATATTTCTAACCCTCAAAACAGCTGTTAATATCTGATCT 696
Db      1230 CATTAACCAATATCTGATATTTCTAACCCTCAAAACAGCTGTTAATATCTGATCT 1171
QY      697 CTACGGTCTCTTGGGCCCCAACATTTCTCAATATATCAGGACACATCTTTTAATAT 756
Db      1170 CTACGGTCTCTTGGGCCCCAACATTTCTCAATATATCAGGACACATCTTTTAATAT 1111
QY      757 TAGTCCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816
Db      1110 TAGTCCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
QY      817 CAAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876
Db      1050 CAAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
QY      877 GGGCCAGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 936
Db      990 GGGCCAGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
QY      937 ACTAGCACAGCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
Db      930 ACTAGCACAGCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
QY      997 TTGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1056
Db      870 TTGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
QY      1057 ATTCCATTAATATCAGAGATTAATCTTTTAACTGGAAGATTAATCTTACAT 1116
Db      810 ATTCCATTAATATCAGAGATTAATCTTTTAACTGGAAGATTAATCTTACAT 751
QY      1117 GCAGCTATGGAATTAATTAATTAATTTTTCAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1176
Db      750 GCAGCTATGGAATTAATTAATTAATTTTTCAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 691
QY      1177 ATCCCTCCCTTGTGTTGATTTTTCAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1236
Db      690 ATCCCTCCCTTGTGTTGATTTTTCAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 631
QY      1237 GAGGCTGTATACAGC 1251
Db      630 GAGGCTGTATACAGC 616

RESULT 12
US-09-895-793-470/c

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; Sequence 470, Application US/09895793
; GENERAL INFORMATION:
; Publication No. US20020192763A1
;
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
;
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
;
; SEQ ID NO: 470
; LENGTH: 2426
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-895-793-470

Query Match          61.7%; Score 1155; DB 10; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATAGAAAGGTGCTGACTTTTACATCTGAGCCACACATCTGCTGAATG 156
DB 1770 AGGTGAGAAATAGAAAGGTGCTGACTTTTACATCTGAGCCACACATCTGCTGAATG 1711
QY 157 GAGATATTAATACATCTAGAAACAGCAAGATGACATATTAATGCTTAAGTAGACATG 216
DB 1710 GAGATATTAATACATCTAGAAACAGCAAGATGACATATTAATGCTTAAGTAGACATG 1651
QY 217 TTTTGGACATTTCCAGCCCTTTAATATCCACACACAGCAAGCAACAAAGAGCA 276
DB 1650 TTTTGGACATTTCCAGCCCTTTAATATCCACACACAGCAAGCAACAAAGAGCA 1591
QY 277 CAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGGTATCGATGAGCCTCGCCCTG 336
DB 1590 CAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGGTATCGATGAGCCTCGCCCTG 1531
QY 337 TGCGTGTCCGCTTGTGAGGAGGACATTAAGAAATGAATGATGCTGCTTAAAGG 396
DB 1530 TGCGTGTCCGCTTGTGAGGAGGACATTAAGAAATGAATGATGCTGCTTAAAGG 1471
QY 397 ATGGGACAGAAAGCATCTGTTGTGATATTTTGAACGGGATTAACAGATTGAAA 456
DB 1470 ATGGGACAGAAAGCATCTGTTGTGATATTTTGAACGGGATTAACAGATTGAAA 1411
QY 457 TGAAGTCAAAAGTGAGCATTAACATAGAGAGAAAGCAAGAGAAATCTTGTATGCT 516
DB 1410 TGAAGTCAAAAGTGAGCATTAACATAGAGAGAAAGCAAGAGAAATCTTGTATGCT 1351
QY 517 TCACAGCATGCAACAAACAAATGAAATGATCTGTGATGACATGAGGACCCAGCTGGG 576
DB 1350 TCACAGCATGCAACAAACAAATGAAATGATCTGTGATGACATGAGGACCCAGCTGGG 1291
```

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QY 577 GAGGATTAACACAGGGGAGAGGGGTACAGGATTTCGGCCCTGCTCAAACTGNGCCT 636
DB 1290 GAGGATTAACACAGGGGAGAGGGGTACAGGATTTCGGCCCTGCTCAAACTGNGCCT 1231
QY 637 CATTAACCAATTCATTTATTTCTTAACCTCAAAACAAAGCTGTTGAATATGACAT 696
DB 1230 CATTAACCAATTCATTTATTTCTTAACCTCAAAACAAAGCTGTTGAATATGACAT 1171
QY 697 CTAGGTTCTCTTGGGCCCCAATTCATCAATATTCACAGCCACATCTATTTTAATAT 756
DB 1170 CTAGGTTCTCTTGGGCCCCAATTCATCAATATTCACAGCCACATCTATTTTAATAT 1111
QY 757 TAGTCCAGATCTGATGAGACCTTTCTACAGTGAATATCAATATCAATATTTGTT 816
DB 1110 TAGTCCAGATCTGATGAGACCTTTCTACAGTGAATATCAATATCAATATTTGTT 1051
QY 817 CAAGACCTTCCTGTTGCTGCTTAATATGATGAGTGAATTTCTTAAGAGTGTCT 876
DB 1050 CAAGACCTTCCTGTTGCTGCTTAATATGATGAGTGAATTTCTTAAGAGTGTCT 991
QY 877 GGCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGTTATCTT 936
DB 990 GGCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGTTATCTT 931
QY 937 ACTAGCACACAGCATCATTAAGAGGATTTATCAATCAATCATCTCACTGATGTC 996
DB 930 ACTAGCACACAGCATCATTAAGAGGATTTATCAATCAATCATCTCACTGATGTC 871
QY 997 TTTGCCATATGCAATTCATTTCCACTTTTGTGCTCCCATCTCAAGACCTCAAAATGTC 1056
DB 870 TTTGCCATATGCAATTCATTTCCACTTTTGTGCTCCCATCTCAAGACCTCAAAATGTC 811
QY 1057 ATTCATTAATATCAACAGGATTAACCTTTTAACTGGAAGATTAATCAATGTTTAC 1116
DB 810 ATTCATTAATATCAACAGGATTAACCTTTTAACTGGAAGATTAATCAATGTTTAC 751
QY 1117 GCAGCTATGGGAATTAATTAATTTTGTTCACAGTGAAGATGACTAAGCTT 1176
DB 750 GCAGCTATGGGAATTAATTAATTTTGTTCACAGTGAAGATGACTAAGCTT 691
QY 1177 ATCCCTCCCTTTGTTGATTTTTCAGATATAAGTTAAATGCTTAGCCTGTACT 1236
DB 690 ATCCCTCCCTTTGTTGATTTTTCAGATATAAGTTAAATGCTTAGCCTGTACT 631
QY 1237 GAGGCTGTATACAGC 1251
DB 630 GAGGCTGTATACAGC 616

RESULT 13
US-09-895-814-470/c
; Sequence 470, Application US/09895814
; GENERAL INFORMATION:
; Publication No. US20020193296A1
;
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
```

APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 470
LENGTH: 2426
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-814-470

Query Match 61.7%; Score 1155; DB 10; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

97 AGGTGAGAAATTAAGAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 156
1770 AGGTGAGAAATTAAGAGGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 1711
157 GAGATAATTAACATCTAGTAAGACAGAGATGACATATATATCTTAAGTATGATG 216
1710 GAGATAATTAACATCTAGTAAGACAGAGATGACATATATATCTTAAGTATGATG 1651
217 TTTTTCGACATTTCCACCCCTTTAAATTCACACACACAGAGACAAAGAAAGCA 276
1650 TTTTTCGACATTTCCACCCCTTTAAATTCACACACAGAGACAAAGAAAGCA 1591
277 CAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGGTTCATGATGAGCTGGCCCTG 336
1590 CAGAGATCCCTGGGAGAAATGCCGGCCCATCTTGGTTCATGATGAGCTGGCCCTG 1531
337 TGCCTGTCCTGCTGTGTGAGGAGAGACATTAAGAAATGATGTGCTTTAAAG 396
1530 TGCCTGTCCTGCTGTGTGAGGAGAGACATTAAGAAATGATGTGCTTTAAAG 1471
397 ATGGGCGAGAAACAGATCCTGTTGTGATATTTATTTGAACGGGATTAAGATTGAAA 456
1470 ATGGGCGAGAAACAGATCCTGTTGTGATATTTATTTGAACGGGATTAAGATTGAAA 1411
457 TGAAGTCACAAAGTACATTTACCAATGAGAGAAACAGACGAGAAATCTTGATGCT 516
1410 TGAAGTCACAAAGTACATTTACCAATGAGAGAAACAGACGAGAAATCTTGATGCT 1351
517 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGCCAGACGCTGG 576
1350 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGCCAGACGCTGG 1291
577 GAGGAGATACACAGGGGAGAGGAGTGTGATGCTGCTGCTTAACCTGTGCTT 636
1290 GAGGAGATACACAGGGGAGAGGAGTGTGATGCTGCTGCTTAACCTGTGCTT 1231
637 CATACCAATCAATTTCAATTTCTAACCTCAAAACAAAGCTGTGTATATATGATCT 696
1230 CATACCAATCAATTTCAATTTCTAACCTCAAAACAAAGCTGTGTATATGATCT 1171
697 CTACGCTCTCTTGGGCCCAACATCTTCATATATCCACGACCAACATCTTTTAATAT 756
1170 CTACGCTCTCTTGGGCCCAACATCTTCATATATCCACGACCAACATCTTTTAATAT 1111
757 TACTTCCCAATCTGTACTGTGACCTTTTACACCTGTAGAAATACATTAATCTATTTT 816
1110 TACTTCCCAATCTGTACTGTGACCTTTTACACCTGTAGAAATACATTAATCTATTTT 1051
817 CAAGAAGCCCTGCTGTGCTGCTTAATATATGATGCTGCTTTTCTTAAGAGATGCTCT 876
1050 CAAGAAGCCCTGCTGTGCTGCTTAATATATGATGCTGCTTTTCTTAAGAGATGCTCT 991

877 GGCCAGGAGATCTGTGAACAGGCTGGGAAAGCATCTCAAGATCTTCCAGGGTATACTT 936
990 GGCCAGGAGATCTGTGAACAGGCTGGGAAAGCATCTCAAGATCTTCCAGGGTATACTT 931
937 ACTAGCACAGCATGTATCATTAAGGAGTGAATATATATCAACATCAATCCAGGCTC 996
930 ACTAGCACAGCATGTATCATTAAGGAGTGAATATATCAACATCAATCAATCCAGGCTC 871
997 TTTGCCCATCTGTAATTCATTTTCCACTTTTGGCCCATTTCAAGACCTCAAAAGTGC 1056
870 TTTGCCCATCTGTAATTCATTTTCCACTTTTGGCCCATTTCAAGACCTCAAAAGTGC 811
1057 ATTCCATTAATATACAGAGATTAATCTTTTAACTGGAAGAAATCAATGTTACAT 1116
810 ATTCCATTAATATACAGAGATTAATCTTTTAACTGGAAGAAATCAATGTTACAT 751
1117 GCACATATGGAATTTATTAATTTTGTTCACAGTGCAGAAAGATGACTAAGTCTTT 1176
750 GCACATATGGAATTTATTAATTTTGTTCACAGTGCAGAAAGATGACTAAGTCTTT 691
1177 ATCCCTCCCTTTGTTGATTTTTCAGATATTAAGTTAAATGCTTAGCCTTACT 1236
690 ATCCCTCCCTTTGTTGATTTTTCAGATATTAAGTTAAATGCTTAGCCTTACT 631
1237 GAGGCTGTATACAGC 1251
630 GAGGCTGTATACAGC 616

RESULT 14
US-10-144-678A-470/c
Sequence 470, Application US/10144678A
Publication No. US20030157089A1
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick L.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: Hurst, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 470
LENGTH: 2426
TYPE: DNA
ORGANISM: Homo sapiens
US-10-144-678A-470

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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QY	157	GAGATAATTAATCATCTAGAAACAGCAAGATGACATATATATGTCTAAGTAGACATG	216	
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DB	1650	TTTTTGCAATTTCCAGCCCTTTAAATATCCACACACAGAAAGACCAAAAGAGAGCA	1591	
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QY	457	TGAAGTCACAAGAGGAGCATTAACATAGAGGAAACAGAGAAATCTGTATGCT	516	
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RESULT 15				
US-10-012-896-470/c				
; Sequence 470, Application US/10012896				
; Publication No. US20020183251A1				
; GENERAL INFORMATION:				
; APPLICANT: Xu, Jiaqun				
; APPLICANT: Dillon, David C.				
; APPLICANT: Mitcham, Jennifer L.				
; APPLICANT: Harlocker, Susan L.				
; APPLICANT: Jiang, Yugu				
; APPLICANT: Kalos, Michael D.				
; APPLICANT: Retter, Marc W.				
; APPLICANT: Stolk, John A.				
; APPLICANT: Day, Craig H.				
; APPLICANT: Vedvick, Thomas S.				
; APPLICANT: Carter, Darlick				
; APPLICANT: Li, Samuel X.				
; APPLICANT: Wang, Aijun				
; APPLICANT: Skeiky, Yasir A.W.				
; APPLICANT: Hepler, William T.				
; APPLICANT: Henderson, Robert A.				
; APPLICANT: Hural, John				
; APPLICANT: McNeill, Patricia D.				
; APPLICANT: Houghton, Raymond L.				
; APPLICANT: Vinals de Bassols, Carlota				
; APPLICANT: Foy, Teresa				
; APPLICANT: Fanger, Gary R.				
; APPLICANT: Mantabe, Yoshinro				
; APPLICANT: Meagher, Madeleine Joy				
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND				
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER				
; FILE REFERENCE: 210121.42/C27				
; CURRENT APPLICATION NUMBER: US/10/012,896				
; CURRENT FILING DATE: 2001-12-10				
; NUMBER OF SEQ ID NOS: 1011				
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; SEQ ID NO 470				
; LENGTH: 2426				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-10-012-896-470				
Query Match				
Best Local Similarity 100.0%; Pred. No. 0;				
Matches 1155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	97	AGGTGAGAAATTAAGAAAGCGTGTGCTACTTTACATCTAGAGCCACACATCTGTCTAAATG	156	
DB	1770	AGGTGAGAAATTAAGAAAGCGTGTGCTACTTTACATCTAGAGCCACACATCTGTCTAAATG	1711	
QY	157	GAGATAATTAATCATCTAGAAACAGCAAGATGACATATATATGTCTAAGTAGACATG	216	
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QY	217	TTTTTGCAATTTCCAGCCCTTTAAATATCCACACACAGAAAGACCAAAAGAGAGCA	276	
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QY	277	CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTGTGGTCAATGATAGCTGCCCTG	336	
DB	1590	CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTGTGGTCAATGATAGCTGCCCTG	1531	
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Db      990 GGGCCAGGGGATCTGTGACAGAGCTGGGAAGCATCTCAGATCTTCCAGGGTTATACCT 931
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QY      997 TTGGCCATACGAAATTCATTTCCACTTTGTGCCATCTCAGACCTCAAAATGTC 1056
Db      870 TTGGCCATACGAAATTCATTTCCACTTTGTGCCATCTCAGACCTCAAAATGTC 811
QY      1057 ATTCCATTAATATCACAGATTAATCTTTTAACTGGAAGATTCATGTTACAT 1116
Db      810 ATTCCATTAATATCACAGATTAATCTTTTAACTGGAAGATTCATGTTACAT 751
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 Job time : 436.819 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:39:38 : Search time 3928.47 seconds
(without alignments)
11581.589 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
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2: em_esthum:*
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6: em_estpl:*
7: em_estro:*
8: em_hic:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	367	19.6	402	9	AA578773
2	238	12.7	290	10	BF373619
3	222	11.9	654	28	AQ319247
4	214	11.4	226	10	BF858371

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7	198	10.6	282	10	BF373581
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9	147	7.9	856	9	A1557225
10	124	6.6	441	10	BF858890
11	100	5.3	572	13	BQ292550
12	86	4.6	657	9	A1557495
13	43	2.3	451	28	AQ246715
14	26	1.4	305	14	RQ1974
15	26	1.4	371	14	T79384
16	26	1.4	438	14	R24922
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33	26	1.4	943	9	AL540648
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35	26	1.4	961	13	B0174024
36	26	1.4	984	12	B1517827
37	26	1.4	1021	12	BM924430
38	26	1.4	1043	12	BM919376
39	26	1.4	1059	12	BM546894
40	26	1.4	1201	9	AL517341
41	26	1.4	1201	9	AL530467
42	26	1.4	1201	13	BX361048
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ALIGNMENTS

RESULT 1
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ACCESSION
AA578773
VERSION
AA578773.1
KEYWORDS
GI:2356957
SOURCE
EST.
ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 402)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished
CONTACT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html

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High quality sequence stop: 373.
Location/Qualifiers

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BASE COUNT 128 a 86 c 84 g 104 t
ORIGIN

Query Match 19.6%; Score 367; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.3e-146;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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BF373619

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DEFINITION MKO-FT0175-310800-106-h09 FT0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF373619
VERSION BF373619.1 GI:11335644

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 290)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
MEDLINE
PUBMED
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ftl-MR0&ct2-MR0-FT0175-
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Location/Qualifiers

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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
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Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION RCI11-108L4.JV RPCI-11 Homo sapiens genomic clone RPCI-11-108L4,
genomic survey sequence.
ACCESSION AQ319247
VERSION AQ319247.1 GI:4052212

KEYWORDS

GSS.

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 654)
AUTHORS Adams M.D., Rounsley S.D., Zhao S., Bass S., Linher K., Golden K., Berry K., Granger D., Suh E., Wible C., de Jong P. and Venter J.C.
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetlgr.org

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DB 654 TGGCCATTCTCAAGACCTCAAAATGTCATTTCATTAAATCAAGATTACCTTTT 595
QY 1090 TTAACCTGGAGAAATTCATGTACATGACGATAGGGAATTAATTCATATTTTGT 1149
DB 594 TTAACCTGGAGAAATTCATGTACATGACGATAGGGAATTAATTCATATTTTGT 535
QY 1150 TCCAGTGCAGAGATGACTAAGCTTATCCCTCCCTTTGTTGATTTTTCACGTA 1209
DB 534 TCCAGTGCAGAGATGACTAAGCTTATCCCTCCCTTTGTTGATTTTTCACGTA 475
QY 1210 TAAAGTAAATGCTTACCTGTACTAGAGCTGTATACAGC 1251
DB 474 TAAAGTAAATGCTTACCTGTACTAGAGCTGTATACAGC 433

RESULT 4
BF858371/c 226 bp mRNA linear EST 16-JAN-2001
LOCUS BF858371
DEFINITION RC5-FT0193-211100-012-E11 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF858371
VERSION BF858371.1 GI:12246115
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 226)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

REFERENCE
AUTHORS

TITLE 'M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
JOURNAL Shotgun sequencing of the human transcriptome with ORF expressed
MEDLINE sequence tags
PUBMED Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC5&cl2=RC5-FT0193-
211100-012-E11&cl3=2000-11-21&cl4=1)
Seq primer: puc 18 forward
High quality sequence stop: 226.

FEATURES
source
1. .226
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0193"
/note="Organ: prostate-tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT
79 a 29 c 59 g 59 t

ORIGIN

Query Match 11.4%; Score 214; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.1e-80;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 622 CCTAAGTGGGTCATATACCAATTCATATTTCTATACCCCAAAAGAGCTG 681
DB 226 CCTAAGTGGGTCATATACCAATTCATATTTCTATACCCCAAAAGAGCTG 167
QY 682 TGTAAATGATCTCTACGCTTCTCTGGGCCCAACATTCATATATCCAGCACA 741
DB 166 TGTAAATGATCTCTACGCTTCTCTGGGCCCAACATTCATATATCCAGCACA 107
QY 742 CTCATTTTAAATTTAGTTCCTCCAGATCTGACCTTTTCTACACTGTAGAAATAC 801
DB 106 CTCATTTTAAATTTAGTTCCTCCAGATCTGACCTTTTCTACACTGTAGAAATAC 47
QY 802 ATTACTCAATTTGTCAAAGACCTTCGTTGTC 835
DB 46 ATTACTCAATTTGTCAAAGACCTTCGTTGTC 13

RESULT 5
AQ206972/c 394 bp DNA linear GSS 17-SEP-1998
LOCUS AQ206972
DEFINITION HS_3238_B1_G11_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3238 Col=21 Row=N, genomic survey
sequence.
ACCESSION AQ206972
VERSION AQ206972.1 GI:3617542
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 394)

REFERENCE

AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	Proc. Natl. Acad. Sci. U.S.A.	96 (17), 9739-9744 (1999)	99380589	
	Contact: Mahairas GG, Wallace JC, Hood L			10449764	
	High Throughput Sequencing Center				
	University of Washington				
	401 Queen Anne Avenue North, Seattle, WA 98109, USA				
	Tel: (206) 616-3618				
	Fax: (206) 616-3887				
	Email: jwallace@u.washington.edu				
	Sequence Tagged Connector				
	Plate: 3238 row: N column: 21				
	Class: BAC ends				
	High quality sequence stop: 394.				
	Location/Qualifiers				
	1..394				
	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
	/clone="Plate=3238 COL=21 Row=N"				
	/sex="male"				
	/clone_lib="CIT Approved Human Genomic Sperm Library D"				
	/note="Organ: Sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"				
BASE COUNT	134 a	62 c	93 g	103 t	2 others
ORIGIN					
Query Match	11.4%	Score 214;	DB 28;	Length 394;	
Best Local Similarity	99.4%;	Pred. No. 1e-80;			
Matches 314:	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
OY	718	ACATTCCTCATATATCCAGCCACATCTATTTTATATTTAGTTGCCAGATCTGACGT	777		
DB	361	ACATTCTCATATATCCAGCCACATCTATTTTATATTTAGTTGCCAGATCTGACGT	322		
OY	778	GACCTTCTACACGTAGATAATACATTTACTGATTTTGTCAAAAGACCTTGCTGCTG	837		
DB	321	GACCTTCTACACGTAGATAATACATTTACTGATTTTGTCAAAAGACCTTGCTGCTG	262		
OY	838	CCTAATATGTAAGCTGACTGTTTTCCTAAGAGTGTTCGGCCAGGGGATCTGAGACA	897		
DB	261	CCTAATATGTAAGCTGACTGTTTTCCTAAGAGTGTTCGGCCAGGGGATCTGAGACA	202		
OY	898	GGCGGGGAGATCTCAAGATCTTCCAGGGTTATTTACTTACTAGACACAGCATGATCAT	957		
DB	201	GGCGGGGAGATCTCAAGATCTTCCAGGGTTATTTACTTACTAGACACAGCATGATCAT	142		
OY	958	TACGAGAGTAATTTCTATACATCAATCAATCTCAAGTGTCTTGGCCATCTGGAATTCAT	1017		
DB	141	TACGAGAGTAATTTCTATACATCAATCAATCTCAAGTGTCTTGGCCATCTGGAATTCAT	82		
OY	1018	TTCCCACTTTTGTGCC 1033			
DB	81	TTCCCACTTTTGTGCC 66			
RESULT 6					
LOCUS	BF858286	332 bp	mRNA	linear	EST 16-JAN-2001
DEFINITION	RC5-FT0193-201100-012-D06 FT0193				
ACCESSION	BF858286				
VERSION	BF858286.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 332)				

AUTHORS	Dias Neto, E., Garcia Correa, R., Veijovskij-Almeida, S., Bionesi, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldmann, G. H., Carvalho, A. F., Matsukuma, A., Bata, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
MEDLINE	20202663			
PUBMED	10737800			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-FT0193-201100-012-D06&t3=2000-11-20&t4=1) Seq primer: puc 18 forward High quality sequence stop: 332.			
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Source	1..332			
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	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/dex_stg="adult"			
	/clone_lib="FT0193"			
	/note="Organ: prostate_tumor; Vector: puc18; Site_1: Smal; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
BASE COUNT	90 a 84 c 64 g 94 t			
ORIGIN				
Query Match	11.4% Score 213; DB 10; Length 332:			
Best Local Similarity	100.0%; Pred. No. 2.7e-80;			
Matches 213; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
OY	576 GGAGGAATACACCGGGGAGAGGAGGATCTGGCCCTGCTGAACGTGTCGT 635			
Db	61 GGAGGAATACACCGGGGAGAGGAGGATCTGGCCCTGCTGAACGTGTCGT 120			
OY	636 TCATACCAATCATTTTCATATTTCTCAACCTCAAAACAAGCTGTTGTAATATCGATC 695			
Db	121 TCATACCAATCATTTTCATATTTCTCAACCTCAAAACAAGCTGTTGTAATATCGATC 180			
OY	696 TCTAGGCTCTCTTGGGCCCAACATTTCTCCATATATCCAGCCACACTCATTTTAAATAT 755			
Db	181 TCTAGGCTCTCTTGGGCCCAACATTTCTCCATATATCCAGCCACACTCATTTTAAATAT 240			
OY	756 TTATGTCACGATCTGACTGTGACCTTTCAC 788			
Db	241 TTATGTCACGATCTGACTGTGACCTTTCAC 273			
RESULT 7	BF373581/c			
LOCUS	BF373581 282 bp mRNA linear EST 24-NOV-2000			
DEFINITION	MR0-FT0175-210800-101-d05 FT0175 Homo sapiens cDNA, mRNA sequence.			
ACCESSION	BF373581			
VERSION	BF373581.1 GI:11335606			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

REFERENCE 1 (bases 1 to 282)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=MR0&t2=MR0-FT0175-210800-101-d05&t3=2000-08-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 35
High quality sequence stop: 282.
Location/Qualifiers
1..282
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0175"
/note="Organ: prostate_tumor; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 85 a 51 c 70 g 76 t
ORIGIN
Query Match 10.6%; Score 198; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.6e-74;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 588 CACGGGCGAGAGGCTGAGATTCGGCCCTGCTCAACGTCGCTCAACCAAT 647
Db 262 CACGGGCGAGAGGCTGAGATTCGGCCCTGCTCAACGTCGCTCAACCAAT 203
Oy 648 CATTCAATATTTCTAACCCCAAAAGAGCTGTGTAATATCGATCTACGGTCT 707
Db 202 CATTCAATATTTCTAACCCCAAAAGAGCTGTGTAATATCGATCTACGGTCT 143
Oy 708 TCTGGGCCAATTTCTCAATATATCCAGCACTATTTTAAATTTAGTCCAGA 767
Db 142 TCTGGGCCAATTTCTCAATATATCCAGCACTATTTTAAATTTAGTCCAGA 83
Oy 768 TCTGTAATGTGATGCTTTC 785
Db 82 TCTGTAATGTGATGCTTTC 65
RESULT 8
BF373406 167 bp mRNA linear EST 24-NOV-2000
LOCUS BF373406
DEFINITION IL2-FT0159-070800-120-H01 FT0159 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF373406
VERSION BF373406.1 GI:11335431
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 167)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=IL2&t2=IL2-FT0159-070800-120-H01&t3=2000-08-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 167.
Location/Qualifiers
1..167
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0159"
/note="Organ: prostate_tumor; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 47 a 38 c 49 g 33 t
ORIGIN
Query Match 8.9%; Score 167; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.6e-60;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 254 CACAGGAACACAAAGAGAGACAGATTCCTGGAGAAATGCCGCGCCATCTTG 313
Db 1 CACAGGAACACAAAGAGAGACAGATTCCTGGAGAAATGCCGCGCCATCTTG 60
Oy 314 GGTCAATGATAGAGCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 373
Db 61 GGTCAATGATAGAGCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Oy 374 TGAATTTGATGTTCTTAAAGATGGCAGAGAAACAGATCTT 420
Db 121 TGAATTTGATGTTCTTAAAGATGGCAGAGAAACAGATCTT 167
RESULT 9
A1557225 856 bp mRNA linear EST 09-AUG-1999
LOCUS A1557225
DEFINITION PT2.1.15_B05.r tumor2 Homo sapiens cDNA 3', mRNA sequence.
ACCESSION A1557225
VERSION A1557225.1 GI:4489588
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 856)
Huang,G.M., Ng,W.L., Farkas,J., He,L., Liang,H.A., Gordon,D., Yu,J. and Hood,L.
Prostate cancer expression profiling by cDNA sequencing analysis
Genomics 59 (2), 178-186 (1999)
99333982
JOURNAL MEDLINE
PUBMED 10409429
Contact: Guyang Matthew Huang
Leroy Hood
University of Washington
Department of Molecular Biotechnology, Box 357730, University of Washington, Seattle, WA 98195
Tel: 5106280100
Fax: 5106280108
Email: huanggm@yahoo.com.
Location/Qualifiers
1. 856
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_idb="tumor2"
/note="Organ: Prostate; Vector: pBluescript; Directional cDNA library was constructed using lambda ZP II kit (Stratagene). mRNA was extracted from a frozen prostate tumor tissue (Mayo Clinics)."
BASE COUNT 237 a 191 c 180 g 214 t 34 others
ORIGIN

Query Match 7.9%; Score 147; DB 9; Length 856;
Best Local Similarity 100.0%; Pred. No. 4.9e-52;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 TCTAGATGATGTAAGTTTGAATAGTGTACTACTTCTCATGCAAGAAGGACA 1458
|||||
Db 251 TCTAGATGATGTAAGTTTGAATAGTGTACTACTTCTCATGCAAGAAGGACA 310
QY 1459 CATATGAGATTCATCATCATGAGACAGCAAACTAAAGTAAATTGATTATAGA 1518
|||||
Db 311 CATATGAGATTCATCATCATGAGACAGCAAACTAAAGTAAATTGATTATAGA 370
QY 1519 GTTTAGATTAATATATGAATGCAAGA 1545
|||||
Db 371 GTTTAGATTAATATATGAATGCAAGA 397

RESULT 10
BF858890 441 bp mRNA linear EST 16-JAN-2001
LOCUS BF858890
DEFINITION RC5-FT0194-071200-023-G11 FT0194 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF858890
VERSION BF858890.1 GI:12246634
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 441)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., de Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL MEDLINE
PUBMED 10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC5&ct=RC5-FT0194-071200-023-G11&t3=2000-12-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 3
High quality sequence stop: 416.
Location/Qualifiers
1. 441
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_idb="FT0194"
/note="Organ: prostate_tumor; Vector: puc18; Site-1: SmaI; Site-2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 142 a 67 c 97 g 135 t
ORIGIN

Query Match 6.6%; Score 124; DB 10; Length 441;
Best Local Similarity 100.0%; Pred. No. 4e-42;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1128 AATTAATTCATATTTTGTTCACAGTGAAGATGACTAAAGCTTTATCCCTCCCT 1187
|||||
Db 441 AATTAATTCATATTTTGTTCACAGTGAAGATGACTAAAGCTTTATCCCTCCCT 392
QY 1188 TTGTTGATTTTTCACATTAATTAAGTAAAGTCTTACCTTGACTGAGCCTGTATA 1247
|||||
Db 381 TTGTTGATTTTTCACATTAATTAAGTAAAGTCTTACCTTGACTGAGCCTGTATA 322
QY 1248 CAGC 1251
|||||
Db 321 CAGC 318

RESULT 11
BQ292550 572 bp mRNA linear EST 15-MAY-2002
LOCUS BQ292550
DEFINITION PM0-AN0087-240501-019-a06 AN0087 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ292550
VERSION BQ292550.1 GI:20801500
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 572)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., de Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL MEDLINE
PUBMED 10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=PM0&l2=PM0-AN0087-240501-019-a06&l3=2001-05-24&l4=1)
Seq primer: puc 18 forward
High quality sequence stop: 572.

FEATURES

Location/Qualifiers

1..572

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="AN0087"

/note="Organ: amnion_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT

150 a 90 c 169 g 163 t

ORIGIN

Query Match 5.3%; Score 100; DB 13; Length 572;

Best Local Similarity 100.0%; Pred. No. 7.6e-32;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

1 AGAAGCTGGCATCGAAGAAACAGAGGAGATTTGTGGTCGACGCCGAGGAGACACAG 60

116 AGAAGCTGGCATCGAAGAAACAGAGGAGATTTGTGGTCGACGCCGAGGAGACACAG 175

Db

61 GAAGATCTGCATGCTGGGAGACCTGATGATACAGAGT 100

176 GAAGATCTGCATGCTGGGAGACCTGATGATACAGAGT 215

RESULT 12

LOCUS

AI557495 657 bp mRNA linear EST 09-AUG-1999

PT2.1.7.H12.r tumor2 Homo sapiens CDNA 3', mRNA sequence.

AI557495 AI557495.1 GI:4489858

KEYWORDS

EST.

SOURCE

Homo sapiens

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 657)

Huang,G.M., Ng,W.L., Fairkas,J., He,L., Liang,H.A., Gordon,D., Yu,J.

and Hood,L.

Prostate cancer expression profiling by cDNA sequencing analysis

Genomics 59 (2), 178-186 (1999)

99339982

10409429

Contact: Guyang Matthew Huang

Leroy Hood

Department of Washington

Biotechnology, Box 357730, University of

Washington, Seattle, WA 98195

Tel: 5106280100

Fax: 5106280108

Email: huanggm@yahoo.com.

Location/Qualifiers

1..657

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="tumor2"

/note="Organ: Prostate; Vector: pbluescript; Directional

CDNA library was constructed using Lambda ZP II kit (Stratagene). mRNA was extracted from a frozen prostate tumor tissue (Mayo Clinics)."

Query Match 4.6%; Score 86; DB 9; Length 657;

Best Local Similarity 100.0%; Pred. No. 7.6e-26;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

BASE COUNT

179 a 112 c 153 g 166 t 47 others

ORIGIN

13 CAGAAACAGAGGAGATTTGTGGTCGACGCCGAGGAGACAGAGATCTGCAT 72

14 CAGAAACAGAGGAGATTTGTGGTCGACGCCGAGGAGACAGAGATCTGCAT 73

73 GGTGGAGAGACCTGATGATACAGAG 98

74 GGTGGAGAGACCTGATGATACAGAG 99

RESULT 13

LOCUS

AO246715 451 bp DNA linear GSS 06-OCT-1998

HS_2059_B2_E08_T7 CIT Approved Human Genomic Sperm Library D Homo

sapiens genomic clone plate=2059 Col=16 Row=J, genomic survey

sequence.

AO246715 AO246715.1 GI:3696897

KEYWORDS

SOURCE

Homo sapiens

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 451)

Mahalras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

10449764

99380589

10449764

Contact: Mahalras GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3687

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 2059 row: J column: 16

Class: BAC ends

High quality sequence stop: 451.

Location/Qualifiers

1..451

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone_plate=2059 Col=16 Row=J"

/sex="male"

/note="Organ: sperm; Vector: pellobAC11; BAC Clones in

E-Coli DH10B"

BASE COUNT 133 a 101 c 86 g 130 t 1 others

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Best Local Similarity 100.0%; Pred. No. 2.2e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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26 TTGGCAATCACTACTGTCACCTATCTCAACTTTGAGATGCT 68

RESULT	14
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DEFINITION	R01974 305 bp mRNA linear EST 31-MAR-1995 ye8f01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:124537 5', mRNA sequence.
ACCESSION	R01974
VERSION	R01974.1 GI:751710
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 305) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman, M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rittin,L., Roelliging,T., Soares,M., Tan,F., Treviskis,E., Waterston, R., Williamson,A., Woldmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished
TITLE	Contact: Wilson RK
JOURNAL	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
COMMENT	Insert Size: 864 High quality sequence stops: 200 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 864 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 200. Location/Qualifiers 1..305 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:477082" /db_xref="taxon:9606" /clone="IMAGE:124537" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares fetal liver spleen INFLS" /note="Organ: Liver and Spleen. Vector: PT73D (Pharmacia) with a modified polylinker. Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACTGCAGAAATTATTAAGAATCTTTTCTTTTCTT 3'] , double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	76 a 68 c 69 g 86 t 6 others
ORIGIN	
Query Match	1.4%; Score 26; DB 14; Length 305;
Best Local Similarity	100.0%; Pred. No. 4.7;
Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	977 TCACATCATCCTCAGTCGTCTTGCC 1002
Db	20 TCACATCATCCTCAGTCGTCTTGCC 45
RESULT	15
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DEFINITION	T79384 371 bp mRNA linear EST 15-MAR-1995 ydt4g09.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:114016 5', mRNA sequence.
ACCESSION	T79384
VERSION	T79384.1 GI:697893
KEYWORDS	EST.

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Mammalia; Euteheria; Chordata; Craniata; Vertebrata; Eumleostomi;
AUTHORS     Eukaryota; Metazoa; Primates; Carnivora; Homnina; Hominidae; Homo.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished
COMMENT     Other ESTs: yd74g09.s1
            Contact: Wilson RK
            Washington University School of Medicine
            444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel.: 314 286 1800
            Fax: 314 286 1810
            Email: est@watsun.wustl.edu
            Insert Size: 1236
            High quality sequence stops: 275 Source: IMAGE Consortium, LNL
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.jnl.gov) for further information.
            Insert Length: 1236 Std Error: 0.00
            Seq primer: MI3RPI
            High quality sequence stop: 275.
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                /db_xref="taxon:9606"
                /clone="IMAGE:II40I6"
                /sex="male"
                /dev_stage="20 week-post conception fetus"
                /lab_host="DH10B (ampicillin resistant)"
                /note="Organ: Liver and Spleen; Vector: pTZ19 (Pharmacia)
                    with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                    1st strand cDNA was primed with a Pac I - oligo(dT) primer
                    15' AACGTGAAGAATTAATTAAACATCTTTTTTTTTCCTTGCC 3';
                    double-stranded cDNA was ligated to Eco RI adaptors
                    (Pharmacia), digested with Pac I and cloned into the Pac I
                    and Eco RI sites of the modified pTZ19 vector. Library
                    went through one round of normalization. Library
                    constructed by Bento Soares and W.Fatima Bonaldo."
BASE COUNT  105 a          81 c          70 g          113 t          2 others
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Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY              977 TCACATCATCCTCAGTGTCTTTGCC 1002
                  |||||||
Db               127 TCACATCATCTCGTAGTCTTTGCC 152
Search completed: September 27, 2003, 11:35:44
Job time : 3929.47 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:01:08 ; Search time 2984.11 Seconds
(without alignments)
11241.524 Million cell updates/sec

Title: US-09-402-713A-4

Perfect score: 820

Sequence: 1 agaagctgcacgcagaaaaa.....cattactcatttgcacaa 820

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_cm:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_din:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
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40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	820	100.0	820	6 BD082484	BD082484 PCA3, PCA
2	820	100.0	1872	6 BD082483	BD082483 PCA3, PCA
3	812	99.0	812	6 AR261039	AR261039 Sequence
4	812	99.0	812	6 AR278570	AR278570 Sequence
5	812	99.0	812	6 AX106207	AX106207 Sequence
6	812	99.0	812	6 AX106690	AX106690 Sequence
7	812	99.0	812	6 AX140981	AX140981 Sequence
8	812	99.0	812	6 AX200841	AX200841 Sequence
9	812	99.0	812	6 AX267497	AX267497 Sequence
10	812	99.0	812	6 AR261037	AR261037 Sequence
11	812	99.0	812	6 AR278568	AR278568 Sequence
12	812	99.0	812	6 AX106205	AX106205 Sequence
13	812	99.0	812	6 AX106688	AX106688 Sequence
14	812	99.0	812	6 AX140979	AX140979 Sequence
15	812	99.0	812	6 AX200839	AX200839 Sequence
16	812	99.0	812	6 AX267495	AX267495 Sequence
17	812	99.0	812	6 AR261038	AR261038 Sequence
18	812	99.0	812	6 AR278569	AR278569 Sequence
19	812	99.0	812	6 AX106206	AX106206 Sequence
20	812	99.0	812	6 AX106689	AX106689 Sequence
21	812	99.0	812	6 AX140980	AX140980 Sequence
22	812	99.0	812	6 AX200840	AX200840 Sequence
23	812	99.0	812	6 AX267496	AX267496 Sequence
24	812	99.0	812	6 AR261036	AR261036 Sequence
25	812	99.0	812	6 AR278567	AR278567 Sequence
26	812	99.0	812	6 AX106204	AX106204 Sequence
27	812	99.0	812	6 AX106687	AX106687 Sequence
28	812	99.0	812	6 AX140978	AX140978 Sequence
29	812	99.0	812	6 AX200838	AX200838 Sequence
30	812	99.0	812	6 AX267494	AX267494 Sequence
31	812	99.0	812	6 BD082482	BD082482 PCA3, PCA
32	812	99.0	812	6 BD082485	BD082485 PCA3, PCA
33	812	99.0	812	6 AR261166	AR261166 Sequence
34	812	99.0	812	6 AR278697	AR278697 Sequence
35	812	99.0	812	6 AX200988	AX200988 Sequence
36	812	99.0	812	6 AX267716	AX267716 Sequence
37	812	99.0	812	6 AF103907	AF103907 Sequence
38	812	99.0	812	6 AF103908	AF103908 Homo sapi
39	812	99.0	812	6 AL359314	AL359314 Human DNA
40	812	99.0	812	6 BD078456	BD078456 101 human
41	812	99.0	812	6 AX018075	AX018075 Sequence
42	812	99.0	812	6 BD134961	BD134961 Human nuc
43	812	99.0	812	6 BD030513	BD030513 Sequence
44	812	99.0	812	6 AR237401	AR237401 Sequence
45	812	99.0	812	6 AR260894	AR260894 Sequence

ALIGNMENTS

RESULT 1
LOCUS BD082484 820 bp DNA
DEFINITION PCA3, PCA3 genes, and methods of use.
ACCESSION BD082484
VERSION BD082484.1 GI:22628094
KEYWORDS JP 2001522240-A/3.
SOURCE JP 2001522240-A/3.
ORGANISM Mastadenovirus
Mastadenovirus
Virus; dsDNA viruses, no RNA stage; Adenoviridae.
1 (bases 1 to 820)
REFERENCE Bussemakers, M.J.G.
TITLE PCA3, PCA3 genes, and methods of use
Patent: JP 2001522240-A 3 13-NOV-2001;
JOURNAL DIAGNOSTIC INC

COMMENT PN JP 2001522240-A/3
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC
C1201/68,
PC G01N33/577, A61K39/395, A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.

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source 1..820
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"

BASE COUNT 262 a 169 c 191 g 198 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCGAAAAACAGAGGGAGATTGTTGCTGCTGCAGCCGAGGAGACCAG 60
DB 1 AGAAGCTGGCATCGAAAAACAGAGGGAGATTGTTGCTGCTGCAGCCGAGGAGACCAG 60
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DB 61 GAAGATCTGATGGTGGGAAGGAGCCTGATGATACAGAGGTGAGAAATAGAAAGGCTGCT 120
QY 121 GACTTTACCATCTGAGGCCACACATCTGCTGAAATGGAGATTAATTAACATCATAAGAAC 180
DB 121 GACTTTACCATCTGAGGCCACACATCTGCTGAAATGGAGATTAATTAACATCATAAGAAC 180
QY 181 AGCAAGATGACAAATATATGCTTAAGTAGAGACATGTTTGGCATTTCAGCCCTTT 240
DB 181 AGCAAGATGACAAATATATGCTTAAGTAGAGACATGTTTGGCATTTCAGCCCTTT 240
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DB 421 GTGATATTTATTTGAAGGGGATTAAGATTTGAAGTCAACAAAGTGAAGCATTAAC 480
QY 481 AATGAGAGGAAAAACAGACGAAAAATCTTGATGGCTTCAACAAGCATGCAACAAACAAA 540
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Db 781 CTTTCTACACCTGTAGAAATACATTAATGATTTTGTTCAAA 820

RESULT 2
LOCUS BD082483 1872 bp DNA linear PAT 27-AUG-2002
DEFINITION PC3, PC3 genes, and methods of use.
ACCESSION BD082483
VERSION BD082483.1 GI:22628093
KEYWORDS JP 2001522240-A/2.
SOURCE Mastadenovirus
ORGANISM Mastadenovirus
VIRUSES dsDNA viruses, no RNA stage: Adenoviridae.
REFERENCE 1 (bases 1 to 1872)
AUTHORS Bussemakers, M.J.G.
TITLE PC3, PC3 genes, and methods of use
JOURNAL Patent: JP 2001522240-A 2 13-NOV-2001;
DIAGNOCURE INC

COMMENT PN JP 2001522240-A/2
PD 13-NOV-2001
PF 09-APR-1998 JP 1998542194
PR 10-APR-1997 US 60/041836
PI MARION J G BUSSEMAKERS
PC C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC
C1201/68,
PC G01N33/577, A61K39/395, A01K67/027
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.

FEATURES
source 1..1872
/organism="Mastadenovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10509"

BASE COUNT 567 a 389 c 369 g 539 t 8 others

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGCATCGAAAAACAGAGGGAGATTGTTGCTGCTGCAGCCGAGGAGACCAG 60
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DB 61 GAAGATCTGATGGTGGGAAGGAGCCTGATGATACAGAGGTGAGAAATAGAAAGGCTGCT 120
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QY 361 GGACATTAGAAAAATGATGATGCTCTTAAGGATGGGCAAGAAACAGATCCTGTT 420
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OY	421	TTGATATATTTTGAACGGGATTCAGATTTGSAATGAACGCAAAAGTGACATTAC	480
Db	421	GTGATATATTTTGAACGGGATTCACATTTTGAATGAATGCAAAAGTGACATTAC	480
OY	481	AATGAGAGGAACAAGACGAGAAAATCTTGATGGCTTCACAAGACATCAACAACAAA	540
Db	481	AATGAGAGGAACAAGACGAGAAAATCTTGATGGCTTCACAAGACATCAACAACAAA	540
OY	541	TGGAATACTGTGATGACATGAGGACGCCAAGCTGGGGAGGAGATTAACACAGGGGACAGG	600
Db	541	TGGAATACTGTGATGACATGAGGACGCCAAGCTGGGGAGGAGATTAACACAGGGGACAGG	600
OY	601	GTCAGGATTCGGGCCCTCTGCCCTTAACATGTGCGCTTCATAACCAAAATATTTCATATTC	660
Db	601	GTCAGGATTCGGGCCCTCTGCCCTTAACATGTGCGCTTCATAACCAAAATATTTCATATTC	660
OY	661	TAACCCCTAAACAAGCTGTTGTAATTCGATCTCAAGGTTCTCTGAGGCCACACA	720
Db	661	TAACCCCTAAACAAGCTGTTGTAATTCGATCTCTGAGGTTCTCTGAGGCCACACA	720
OY	721	TTCTCCATATATCCAGCCACACTATTTTAAATATTTAGTTCCAGATCTGTACTGTGAC	780
Db	721	TTCTCCATATATCCAGCCACACTATTTTAAATATTTAGTTCCAGATCTGTACTGTGAC	780
OY	781	CTTCTCAGCTGTGAATTAACATTAATCTATTTTGTTCAAA	820
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[illegible]

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				0:	Indels
				0:	Gaps
QY	6	CTGCATCAGAAAAACAGAGGGAGATTGTGTGGCTCAGCCGAGGAGACAGAGA	65		
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QY	66	TCTGCATGTTGGGAAGCACTGATGATTCACAGGGTGAATAATTAAGAAAGCTGCTGACTT	125		
Db	752	TCTGCATGTTGGGAAGCACTGATGATTCACAGGGTGAATAATTAAGAAAGCTGCTGACTT	693		
QY	126	TACCATCTGAGGCCACACATCTGCTGAATGAGAGTAATTAACATCACTAGAAACAGAA	185		
Db	692	TACCATCTGAGGCCACACATCTGCTGAATGAGAGTAATTAACATCACTAGAAACAGAA	633		
QY	186	GATGACAAATTAATGTTCTTAAGTAGAGCATGTTTTCACAAATTCACCCCTTTAAATA	245		
Db	632	GATGACAAATTAATGTTCTTAAGTAGAGCATGTTTTCACAAATTCACCCCTTTAAATA	573		
QY	246	TTCCACACACAGAGAACCAAAAAGAACACACAGATCCCTGGAGAAATGCCCGCCG	305		
Db	572	TTCCACACACAGAGAACCAAAAAGAACACACAGATCCCTGGAGAAATGCCCGCCG	513		

QY	306	CCATCTGGGGCATCGAATGAGACCTCGGCCCTGGCTGGTCCCGCTTGGAGGGAAAGACA	365
Db	512	CCATCTTGGGTCATCGATGATGAGCCTCGGCCCTCTGGCTGGTCCCGCTTGGAGGGAAAGACA	453
QY	366	TTAGAAATGAAATGATGTGTCTCCCTTAAAGGATGGCGAGAAACAGATCCTGTGTGGGA	425
Db	452	TTAGAAATGAAATGATGTGTCTCCCTTAAAGGATGGCGAGAAACAGATCCTGTGTGGGA	393
QY	426	TATTTATTTGAACGGGATTTACAGATTTTGAATTGAAGTGCACAAAGTGAGCATTTACCAATGA	485
Db	392	TATTTATTTGAACGGGATTTACAGATTTTGAATTGAAGTGCACAAAGTGAGCATTTACCAATGA	333
QY	486	GAGGAAACACAGCGAATACTTGATGGCTTCCACAAGACATGCGAACAAACAAATGGAA	545
Db	332	GAGGAAACACAGCGAATACTTGATGGCTTCCACAAGACATGCGAACAAACAAATGGAA	273
QY	546	TACTGTGATGACATGAGGCGAGCCAAAGCTGGGGAGAGATTAACCAAGGGGGCAGAGGCTCAG	605
Db	272	TACTGTGATGACATGAGGCGAGCCAAAGCTGGGGAGAGATTAACCAAGGGGGCAGAGGCTCAG	213
QY	606	GATTCGTGCCCGCTGCTTAAACGTGGCTTCATTAACCAATTCATTTATTTCTTAAC	665
Db	212	GATTCGTGCCCGCTGCTTAAACGTGGCTTCATTAACCAATTCATTTATTTCTTAAC	153
QY	666	CTCAAAACAAAGCTGTGTGTAATATCTGATCTCAAGGTTCTTCTGGGCCCAACATTCCTC	725
Db	152	CTCAAAACAAAGCTGTGTGTAATATCTGATCTCAAGGTTCTTCTGGGCCCAACATTCCTC	93
QY	726	CATATATCCAGCACATCATTTTAAATATTTAGTCCCAATCGATCGTATCTGACGCTTTC	785
Db	92	CATATATCCAGCACATCATTTTAAATATTTAGTCCCAATCTGTACTGTGACCTTTC	33
QY	786	TACACTGATAGATAACATTTACTCATTTTGTTC	817
Db	32	TACACTGATAGATAACATTTACTCATTTTGTTC	1

	RESULT 4				
	AR278570/c				
LOCUS	AR278570	812 bp	DNA	linear	PAT 10-APR-2003
DEFINITION	Sequence 471 from patent US 6512094.				
ACCESSION	AR278570				
VERSION	AR278570.1	GI:29712816			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 812)				
	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,				
	Kalos,M.D., Fanger,G.R., Reltter,M.W., Stolk,J.A., Day,C.H.,				
	Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,				
	Hepner,W.T. and Henderson,R.A.				
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer				
JOURNAL	Patent: US 6512094-A 471 28-JUN-2003;				
FEATURES	Location/Qualifiers				
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	/organism="unknown"				
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Db	652	TACCACTTCGAGGCCACACATCTGCGGAAATGAGAGTAATTAACATCTACTAGAAACAGCA	633
QY	186	GATGACCAATATATCTTAAGTAGGACATGTTTTTGCCATTTCCAGGCCCTTTAAATA	245
Db	632	GATGACCAATATATCTTAAGTAGGACATGTTTTTGCCATTTCCAGGCCCTTTAAATA	573
QY	246	TCCACACACACAGGAGGACAAAGAGACACAGAGATCCCTGGGAGAAATGCCGCCG	305
Db	572	TCCACACACACAGGAGGACAAAGAGACACAGAGATCCCTGGGAGAAATGCCGCCG	513
QY	306	CCATCTTGGGTCATGATGAGCGTCGCCCTGGCCCTGGCCCGCTTGAGAGGAGAGCA	365
Db	512	CCATCTTGGGTCATGATGAGCGTCGCCCTGGCCCTGGCCCGCTTGAGAGGAGAGCA	453
QY	366	TTAGAAAATGAATTTGATGTCCTCTTAAAGATGGGCGAGAAACAGATCCTGTTGGA	425
Db	452	TTAGAAAATGAATTTGATGTCCTCTTAAAGATGGGCGAGAAACAGATCCTGTTGGA	393
QY	426	TATTTATTTGAACGGGATTTACAGATTTGAAATGAAGTCACAAAGTGAGCATTACCAATGA	485
Db	392	TATTTATTTGAACGGGATTTACAGATTTGAAATGAAGTCACAAAGTGAGCATTACCAATGA	333
QY	486	GAGGAAAACAGCGGAAATCTTATGCGCTTCACAAAGCATGCAACAAACAAATGGA	545
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QY	546	TACTTGTGATGACATGAGCGAGCCAGCTGGGGAGAGATATACCAGGGGCGAGAGGTCAG	605
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QY	726	CATATATCCAGGCACACATCTTAAATATTTAGTTCACAGATCTGTACTGACCTTTC	785
Db	92	CATATATCCAGGCACACATCTTAAATATTTAGTTCACAGATCTGTACTGACCTTTC	33
QY	786	TACACTGTAGATAACATTTACTCATTTGTTTC	817
Db	32	TACACTGTAGATAACATTTACTCATTTGTTTC	1
RESULT 5			
AX106207/c			
LOCUS	AX106207	812 bp	DNA
DEFINITION	Sequence 345 from Patent WO0125273.		
ACCESSION	AX106207		
KEYWORDS	AX106207.1	GI:13921896	
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	1 Skelky,Y.A., Xu,J., Cheever,M.A. and Reed,S.G.		
TITLE	Compositions and methods for wt1 specific immunotherapy		
JOURNAL	PATENT: WO 0125273-A 345 12-APR-2001;		
FEATURES			
SOURCE	1..812		
BASE COUNT			
ORIGIN	198 a 189 c 169 g 256 t		

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QY	126 TACCATCTGAGGCCACACATCTGCTGAAATGGAATATTTAACTACTAGAAACAGCA	185		
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QY	366 TTAGAAAATGAAATGATGTGTCCTTAAAGATGGGAGGAAACAGATCCTGTTGGA	425		
Db	452 TTAGAAAATGAAATGATGTGTCCTTAAAGATGGGAGGAAACAGATCCTGTTGGA	393		
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QY	606 GATTCCTGGCCCTGCTGCTTAACGTGCGTTCATTAACCAAAATCATTTATATTTCTTAAC	665		
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Db	152 CTCAAAACAAAGCTGTGTGTAATATCTGATCTCTACGCTTCCTTCTGGGCCCAACATTC	93		
QY	726 CATATATCCACCCACACATCTTTTAAATATTTAATTTCCAGATCTGTACCTTC	785		
Db	92 CATATATCCACCCACACATCTTTTAAATATTTAATTTCCAGATCTGTACCTTC	33		
QY	786 TACACGTGAGAAATTAACATTAATTTTGTTC	817		
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LOCUS	AX106690/c	812 bp	DNA	linear
DEFINITION	Sequence 471 from Patent WO0125272.			
ACCESSION	AX106690			
VERSION	AX106690.1			
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1			

AUTHORS Xu, J., Skelky, Y. A., Reed, S. G. and Cheever, M. A.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0125272-A 471 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 198 a 189 c 169 g 256 t
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Query Match 99.0%; Score 812; DB 6; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCAGCCGAGGAGACAGAGAGA 65
DB 812 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCAGCCGAGGAGACAGAGAGA 753
QY 66 TCTGCATGTGGGAGGAGACCTGATGATACAGAGGAGAGAAATAAGAAAGGCTGCTGACTT 125
DB 752 TCTGCATGTGGGAGGAGACCTGATGATACAGAGGAGAGAAATAAGAAAGGCTGCTGACTT 693
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DB 692 TACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAACATCAGTAAGAACAGCAA 633
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DB 32 TACACTGTAGATAACATTAATCTCATTTTCTC 1

RESULT 7
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LOCUS Sequence 471 from Patent WO0134802.
DEFINITION AX140981
ACCESSION AX140981
VERSION AX140981.1 GI:14281078
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y.,
Reed, S. G., Kalos, M. D., Retter, M. W., Stolk, J. A., Day, C. H.,
Skelky, Y. A. and Wang, A.
Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0134802-A 471 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN
Query Match 99.0%; Score 812; DB 6; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 812 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCAGCCGAGGAGACAGAGAGA 753
QY 66 TCTGCATGTGGGAGGAGACCTGATGATACAGAGGAGAGAAATAAGAAAGGCTGCTGACTT 125
DB 752 TCTGCATGTGGGAGGAGACCTGATGATACAGAGGAGAGAAATAAGAAAGGCTGCTGACTT 693
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QY 246 TCCACACACACAGAGAACCAAAAGAGAGACAGAGATCCCTGGGAGAAATGCCGGCCG 305
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QY 606 GATTGGGCCCTGCTGCCTTAAACGCTGGCTTACATAACCAATCATTTCTATTCTTAAC 665

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Db 92 CATATATCCAGCCACACTCATTTTAAATATTTAGTCCGACATCTGTAAGCTTTC 33
QY 786 TACACTGAGATAAATCACTCAATTTGTTTC 817
Db 32 TACACTGAGATAAATCACTCAATTTGTTTC 1

RESULT 8
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LOCUS Sequence 471 from Patent WO0151633. 812 bp DNA linear PAT 29-AUG-2001
ACCESSION AX200841
VERSION AX200841.1 GI:15390744
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 471 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
SOURCE Location/Qualifiers
1..812
/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 198 a 189 c 169 g 256 t
ORIGIN
Query Match 99.0%; Score 812; DB 6; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 812 CTGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACCAAGAGA 753
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QY 246 TCCACACACAGAGAGACAGAAAAAGAACAGACAGAGATCCCTGGAGAAATGCCGCG 305
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Db 32 TACACTGAGATAAATCACTCAATTTGTTTC 1

RESULT 9
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LOCUS Sequence 471 from Patent WO0173032. 812 bp DNA linear PAT 26-OCT-2001
ACCESSION AX267497
VERSION AX267497.1 GI:16516261
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 471 04-OCT-2001;
CORIXA CORPORATION (US)
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SOURCE Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 32 TACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1
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AR261037/c 2229 bp DNA linear PAT 29-JAN-2003
LOCUS AR261037 Sequence 469 from patent US 6321716.
DEFINITION AR261037
ACCESSION AR261037
VERSION AR261037.1 GI:28071800
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 2229)
AUTHORS Mashiki, Z. and Harada, J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 469 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..2229
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
Query Match 88.3%; Score 724; DB 6; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 277 CAGAGATCCCTGGAGAAATGCGCGCGCCATCTTGGGTCATCGATGAGCTCGCCCTG 336
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QY 337 TGGCGTCCCTGCTGAGGAGAGACATTTGAAATTAATTAATGATGATGATGATGATG 396
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RESULT 11
AR278568/c 2229 bp DNA linear PAT 10-APR-2003
LOCUS AR278568 Sequence 469 from patent US 6512094.
DEFINITION AR278568
ACCESSION AR278568
VERSION AR278568.1 GI:29712814
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 2229)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Ketter, M.W., Stolk, J.A., Day, C.H.,
Vedrick, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A.W.,
Hepler, W.T., and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 469 28-JAN-2003;
FEATURES Location/Qualifiers
source 1..2229
BASE COUNT 654 a 447 c 481 g 647 t

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Db	1776 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTTACATCTGAGGCCACACATCTGCTGAATG 1717			
QY	157 GAGTAATTAATCACTACATAGAAACAGACAGATGACATATATATATAGTAAGTGAATG 216			
Db	1716 GAGTAATTAATCACTACATAGAAACAGACAGATGACATATATATATAGTAAGTGAATG 1657			
QY	217 TTTTGGACATTTTCCAGCCCTTTAAATATCCACACACAGAGAACAAAGAGCA 276			
Db	1656 TTTTGGACATTTTCCAGCCCTTTAAATATCCACACACAGAGAACAAAGAGCA 1597			
QY	277 CAGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTGATGATGAGCCTGCGCCTG 336			
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Db	1056 CAAA 1053			
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DEFINITION	Sequence 343 from Patent WO0125273.			
ACCESSION	AX106205.1			
VERSION	AX106205.1 GI:13921894			
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Skeiky,Y.A.; Xu,J.; Cheever,M.A. and Reed,S.G.			
TITLE	Compositions and methods for wt1 specific immunotherapy			

JOURNAL	Patent: WO 0125273-A 343 12-APR-2001;	FEATURES	CORIXA CORPORATION (US)	Location/Qualifiers	1..2229	source	/organism="Homo sapiens"	/mol_type="genomic DNA"	/db_xref="taxon:9606"
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Db	1176 CTACGGTTCCTTGGGCCCAACATCTCCATATATCCAGCACACATCTTTTAATAT 1117								
QY	757 TAGTCCCAATCTGTACTGTGACCTTTCTACACTGAGAAATACATTACTATTTGTT 816								
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Db	1056 CAAA 1053								
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LOCUS	AX106688								
DEFINITION	Sequence 469 from Patent WO0125272.								
ACCESSION	AX106688								
VERSION	AX106688.1 GI:13922353								

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0125272-A 469 12-APR-2001;
CORLIX CORPORATION (US)
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BASE COUNT 654 a 447 c 481 g 647 t
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1716 GAGATAATTAACATCACTAGTAAGAAAGCAAGATGACAAATTAATGCTTAAGTAGTGCATG 1657
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DB 1656 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACACAGAGGCAAAAGGAAGA 1597
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DB 1056 CAAA 1053
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LOCUS Sequence 469 from Patent W00134802.
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ACCESSION AXI40979
VERSION AXI40979.1 GI:14281076
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skeiky,Y.A. and Wang,A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0134802-A 469 17-MAY-2001;
CORLIX CORPORATION (US)
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source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
Query Match 88.3%; Score 724; DB 6; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGCTTACCATCTGAGCCACACATCTGCTGAATG 156
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QY 157 GAGATAATTAACATCACTAGTAAGAAAGCAAGATGACAAATTAATGCTTAAGTAGTGCATG 216
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DEFINITION AX200839
ACCESSION AX200839
VERSION AX200839.1 GI:15390742
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 469 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..2229
Location/Qualifiers
BASE COUNT 654 a 447 c 481 g 647 t
ORIGIN
Query Match 88.3%; Score 724; DB 6; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATG 156
1776 AGGTGAGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATG 1717
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C	11	812	99.0	812	25	AAV62429	Prostate cancer th
C	12	724	88.3	2229	21	AAV62429	Human immunogenic
C	13	724	88.3	2229	22	AAV62429	Human prostate-cdn
C	14	724	88.3	2229	22	AAV62429	Human prostate-spe
C	15	724	88.3	2229	22	AAV62429	Prostate tumour an
C	16	724	88.3	2229	22	AAV62429	Human P710P invent
C	17	724	88.3	2229	22	AAV62429	Human P710P CDNA s
C	18	724	88.3	2229	24	AAV62429	Prostate cancer th
C	19	724	88.3	2229	25	AAV62429	Human immunogenic
C	20	724	88.3	2426	21	AAV62429	Human prostate-cdn
C	21	724	88.3	2426	22	AAV62429	Human prostate-spe
C	22	724	88.3	2426	22	AAV62429	Human prostate-spe
C	23	724	88.3	2426	22	AAV62429	Human prostate-spe
C	24	724	88.3	2426	22	AAV62429	Human prostate-spe
C	25	724	88.3	2426	22	AAV62429	Human prostate-spe
C	26	724	88.3	2426	24	AAV62429	Human P710P CDNA s
C	27	724	88.3	2426	25	AAV62429	Prostate cancer th
C	28	724	88.3	3112	21	AAV62429	Human immunogenic
C	29	724	88.3	3112	22	AAV62429	Human prostate-cdn
C	30	724	88.3	3112	22	AAV62429	Human prostate-spe
C	31	724	88.3	3112	22	AAV62429	Human prostate-spe
C	32	724	88.3	3112	22	AAV62429	Human prostate-spe
C	33	724	88.3	3112	22	AAV62429	Human prostate-spe
C	34	724	88.3	3112	22	AAV62429	Human prostate-spe
C	35	724	88.3	3112	25	AAV62429	Human P710P CDNA s
C	36	724	88.3	3112	25	AAV62429	Prostate cancer th
C	37	724	88.3	3112	19	AAV62429	Prostate cancer th
C	38	724	88.3	3112	19	AAV62429	Prostate cancer th
C	39	724	88.3	3112	22	AAV62429	Human P710P CDNA s
C	40	724	88.3	3112	22	AAV62429	Human P710P CDNA s
C	41	724	88.3	3112	22	AAV62429	Human P710P CDNA s
C	42	724	88.3	3112	22	AAV62429	Human P710P CDNA s
C	43	724	88.3	3112	22	AAV62429	Human P710P CDNA s
C	44	724	88.3	3112	22	AAV62429	Human P710P CDNA s
C	45	724	88.3	3112	22	AAV62429	Human P710P CDNA s

ALIGNMENTS

RESULT 1	AAV62429	standard; CDNA; 820 BP.
ID	AAV62429	
XX	AAV62429	
AC	AAV62429	
XX	AAV62429	
DT	30-DEC-1998	(first entry)
XX	30-DEC-1998	
DE	Prostate cancer antigen (PCA3) CDNA splice variant 3.	
XX	Prostate cancer antigen (PCA3) CDNA splice variant 3.	
KW	Prostate cancer antigen CDNA splice variant 3; PCA3; prostatic cancer;	
XX	PC; ds.	
OS	Homo sapiens.	
XX	Homo sapiens.	
PN	WO9845420-A1.	
XX	WO9845420-A1.	
PD	15-OCT-1998.	
XX	15-OCT-1998.	
PF	09-APR-1998;	98WO-CA00346.
XX	09-APR-1998;	
PR	10-APR-1997;	97US-0041836.
XX	10-APR-1997;	
PA	(DIAG-) DIAGNOCURE INC.	
XX	(DIAG-) DIAGNOCURE INC.	
PI	Bussemakers M/G;	
XX	Bussemakers M/G;	
DR	WPI; 1998-568347/48.	
XX	WPI; 1998-568347/48.	
PT	New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,	
XX	prevention and treatment of prostatic cancer	

XX Claim 4; Pages 77-78; 11pp; English.
PS
XX The present sequence represents the prostate cancer antigen (PCA3)
CC cDNA splice variant 3 sequence comprising of exons 1, 3, and 4a
CC of the PCA3 gene. The PCA3 cDNA splice variant 3 sequence,
CC isolated from a human primary prostatic tumour tissue cDNA library,
CC was found in approximately 15% of the cDNA clones isolated. The
CC invention claims for PCA3 cDNA variants and the proteins they encode.
CC The invention also claims for antibodies against PCA3 protein. The
CC antibodies are claimed to be useful for detecting PCA3 protein in
CC immunosay tests, for diagnosing, assessing and prognosing of
CC prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed
CC to be useful for treating PC, while determining elevated levels of
CC PCA3 (as RNA or protein) is useful for detecting a predisposition
CC to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
CC allows differentiation between malignant and benign prostatic disease,
CC and the level of PCA3 expression allows correlation with the grade of
CC tumour. PCA3 protein and its fragments are also claimed to be useful
CC in vaccines for preventing PC; in drug screens for identifying
CC specific (ant)agonists (potentially useful therapeutically) and for
CC studying protein-DNA interactions.
CC
XX
SQ Sequence 820 BP; 262 A; 169 C; 191 G; 198 T; 0 other;

Query Match 100.0%; Score 820; DB 19; Length 820;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGATCAGAAAAACAGAGGAGATTTGTGCTGACGCCGAGGAGACCAG 60
DB 1 AGAAGCTGGATCAGAAAAACAGAGGAGATTTGTGCTGACGCCGAGGAGACCAG 60
QY 61 GAAGATCTGATGGTGGGAAGGACCTGATGATACAGAGTGAGAAATAGAAAGCTGCT 120
DB 61 GAAGATCTGATGGTGGGAAGGACCTGATGATACAGAGTGAGAAATAGAAAGCTGCT 120
QY 121 GACTTACCATCTGAGGCCACACATCTGCTGAAAATGAGATTAATTAACATCATAAGAAC 180
DB 121 GACTTACCATCTGAGGCCACACATCTGCTGAAAATGAGATTAATTAACATCATAAGAAC 180
QY 181 AGCAAGATGACAAATATATGTCATAGTAGACATGTTTTGGCATTTCAGCCCTTT 240
DB 181 AGCAAGATGACAAATATATGTCATAGTAGACATGTTTTGGCATTTCAGCCCTTT 240
QY 241 AATATCCACACACACAGAGGACCAAAAGAAAGACAGAGATCCCTGGGAGAAATGCC 300
DB 241 AATATCCACACACACAGAGGACCAAAAGAAAGACAGAGATCCCTGGGAGAAATGCC 300
QY 301 GCGCGCCATCTTGGGTCATGATGAGCGCTGCGCTGTGCTGCTGCCCTTGTGAGGAA 360
DB 301 GCGCGCCATCTTGGGTCATGATGAGCGCTGCGCTGTGCTGCTGCCCTTGTGAGGAA 360
QY 361 GGACATTAGAAATGATGATGTCCTTAAGAGATGGGCGAGGAAACAGATCCCTGT 420
DB 361 GGACATTAGAAATGATGATGTCCTTAAGAGATGGGCGAGGAAACAGATCCCTGT 420
QY 421 GTGGATTTTATTTGAAAGGATTTACAGATTTGAAATGAAGTCAAAAGTGAGCATTAAC 480
DB 421 GTGGATTTTATTTGAAAGGATTTACAGATTTGAAATGAAGTCAAAAGTGAGCATTAAC 480
QY 481 AATGAGAGGAAAAACAGAGGAAATCTGATGGCTTCAAGACATGCAACAAACAAA 540
DB 481 AATGAGAGGAAAAACAGAGGAAATCTGATGGCTTCAAGACATGCAACAAACAAA 540
QY 541 TGAATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 TGAATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 GTGAGATCTGAGCCCTGCTGCTAAACTGCTGCTTAATACCAATCATTTCTATTTTC 660
DB 601 GTGAGATCTGAGCCCTGCTGCTAAACTGCTGCTTAATACCAATCATTTCTATTTTC 660

QY 661 TAACCTTCAAAACAAAGCTGTGTATATCTGATCTACGGTTCCTTGCGGCCAACA 720
DB 661 TAACCTTCAAAACAAAGCTGTGTATATCTGATCTACGGTTCCTTGCGGCCAACA 720
QY 721 TTCTCCATATATCCAGCCACACATCTTTAATATTTAGTTCCAGATCTGTACTGTAC 780
DB 721 TTCTCCATATATCCAGCCACACATCTTTAATATTTAGTTCCAGATCTGTACTGTAC 780
QY 781 CTTTCTACCTGTAGAAATACATTAATCATTTGTTGCAA 820
DB 781 CTTTCTACCTGTAGAAATACATTAATCATTTGTTGCAA 820

RESULT 2

AAD38815
ID AAD38815 standard; cDNA; 876 BP.

AC AAD38815;

DT 23-SEP-2002 (first entry)

DE Human PSNA cDNA, Pro123.

XX Human, prostate specific protein; PSP; prostate specific nucleic acid;

KW vaccine; transgenic; prostate cancer; gene therapy; transgenic animal;

KM PSNA; ss.

OS Homo sapiens.

XX WO200224718-A1.

PD 28-MAR-2002.

PF 19-SEP-2001; 2001WO-US29386.

PR 19-SEP-2000; 2000US-233746P.

XX (DIAD-) DIADEXUS INC.

PA Sun Y, Recipon H, Cafferty R, Ali S;

DR WPI; 2002-471216/50.

XX Novel isolated prostate specific polypeptide useful for identifying,

PT diagnosing, monitoring, staging, imaging, and treating prostate cancer

PT and non-cancerous disease states in prostate

PS Claim 1; Page 179; 210pp; English.

XX The invention relates to prostate specific proteins (PSP) and prostate

CC specific nucleic acids (PSNA). Sequences of the invention are useful

CC for identifying, diagnosing, monitoring, staging, imaging and treating

CC prostate cancer and non-cancerous disease states in prostate. They are

CC also useful for producing engineered prostate tissue for treatment and

CC research. The PSNA sequences are used in gene therapy and for producing

CC transgenic animals and cells. The invention is also used as vaccines.

CC The present sequence is human PSNA cDNA.

XX
SQ Sequence 876 BP; 275 A; 183 C; 207 G; 211 T; 0 other;

Query Match 100.0%; Score 820; DB 24; Length 876;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGCTGGATCAGAAAAACAGAGGAGGAGATTTGTGCTGACGCCGAGGAGACCAG 60
DB 30 AGAAGCTGGATCAGAAAAACAGAGGAGGAGATTTGTGCTGACGCCGAGGAGACCAG 89
QY 61 GAAGATCTGATGGTGGGAAGGACCTGATGATACAGAGTGAGAAATAGAAAGCTGCT 120
DB 90 GAAGATCTGATGGTGGGAAGGACCTGATGATACAGAGTGAGAAATAGAAAGCTGCT 149

QY 121 GACCTTACCATCTGAGCCACACATCTGCTGAATGAGATTAATTAACATCACTAGAAC 180
PI |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 150 GACCTTACCATCTGAGCCACACATCTGCTGAATGAGATTAATTAACATCACTAGAAC 209
QY 181 AGCAAGATGACATATATATGCTTAAGTAGTGACATGTTTTTGGACATTTCCAGCCCTTT 240
PI |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 210 AGCAAGATGACATATATATGCTTAAGTAGTGACATGTTTTTGGACATTTCCAGCCCTTT 269
QY 241 AATATCCACACACAGAGAGACACAAAAGAACACAGAGATCCTGGAGAAATGCC 300
PI |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 270 AATATCCACACACAGAGAGACACAAAAGAACACAGAGATCCTGGAGAAATGCC 329
QY 301 GGGCCGCATCTTGGGTCATGATGAGCCTCGCCCTGGCTGGCTGGCTGGAGGAA 360
DB 330 GGGCCGCATCTTGGGTCATGATGAGCCTCGCCCTGGCTGGCTGGAGGAA 389
QY 361 GGACATTTAGAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 390 GGACATTTAGAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 449
QY 421 GTGATATTTATTTGACGGGATTTACAGATTTGAATGAATGACACAAAGTACATACC 480
DB 450 GTGATATTTATTTGACGGGATTTACAGATTTGAATGAATGACACAAAGTACATACC 509
QY 481 AATGAGAGGAAAAACAGAGAGAGAAATCTTGATGCTTCAAGACATGCAACAAACAAA 540
DB 510 AATGAGAGGAAAAACAGAGAGAGAAATCTTGATGCTTCAAGACATGCAACAAACAAA 569
QY 541 TGGAACTACTGTATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 570 TGGAACTACTGTATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 629
QY 601 GTGAGATTTCTGGCCCTGCTGCTAAAGCTGCTGCTAAAGCTGCTGCTGCTGCTGCT 660
DB 630 GTGAGATTTCTGGCCCTGCTGCTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689
QY 661 TAACCTCAAAACAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 690 TAACCTCAAAACAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 749
QY 721 TTCTCATATATTCACGACCACTCATTTTAAATATTAGTCCAGATCTGATCTGAC 780
DB 750 TTCTCATATATTCACGACCACTCATTTTAAATATTAGTCCAGATCTGATCTGAC 809
QY 781 CTTTACACCTGAGAGATTAACATTAATTAATTAATTAATTAATTAATTAATTAAT 820
DB 810 CTTTACACCTGAGAGATTAACATTAATTAATTAATTAATTAATTAATTAATTAAT 849

RESULT 3
AAV62428
ID AAV62428 standard; cDNA: 1872 BP.
AC AAV62428;
XX
DT 30-DEC-1998 (first entry)
XX
DE Prostate cancer antigen (PCA3) cDNA splice variant 2.
XX
KW Prostate cancer antigen cDNA splice variant 2; PCA3; prostatic cancer;
KM PC; ds.
XX
OS Homo sapiens.
XX
PN WO9845420-A1.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98WO-CA00346.
XX
PR 10-APR-1997; 97US-0041836.
XX
PA (DIAG-) DIAGNOCURE INC.

XX
XX Bussemakers MUG;
PI
PI
DR WPI: 1998-568347/48.
XX
PT New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
PT prevention and treatment of prostatic cancer
XX
PS Claim 4: Pages 76-77; 111pp; English.
XX
XX The present sequence represents the prostate cancer antigen (PCA3)
CC cDNA splice variant 2 sequence comprising of exons 1, 3, 4a and
CC 4b of the PCA3 gene. The PCA3 cDNA splice variant 2 sequence,
CC isolated from a human primary prostatic tumor tissue cDNA library,
CC was found in approximately 65% of the cDNA clones isolated. The
CC invention claims for PCA3 cDNA variants and the proteins they encode.
CC The invention also claims for antibodies against PCA3 protein. The
CC antibodies are claimed to be useful for detecting PCA3 protein in
CC immunosassay tests, for diagnosing, assessing and prognosing of
CC prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed
CC to be useful for treating PC, while determining elevated levels of
CC PCA3 (as RNA or protein) is useful for detecting a predisposition
CC to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
CC allows differentiation between malignant and benign prostatic disease,
CC and the level of PCA3 expression allows correlation with the grade of
CC tumour. PCA3 protein and its fragments are also claimed to be useful
CC in vaccines for preventing PC; in drug screens for identifying
CC specific (ant)agonists (potentially useful therapeutically) and for
CC studying protein-DNA interactions.
XX
SO Sequence 1872 BP; 567 A; 389 C; 369 G; 539 T; 8 other;
Query Match 100.0%; Score 820; DB 19; Length 1872;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAAGCTGGCATCAGAAAAACAGAGGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
DB 1 AGAAGCTGGCATCAGAAAAACAGAGGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 61 GAAGATCTGCATGCTGGAAGGACCTGATGATACAGAGGTGAGAAATGAAGAGCTGCT 120
DB 61 GAAGATCTGCATGCTGGAAGGACCTGATGATACAGAGGTGAGAAATGAAGAGCTGCT 120
QY 121 GACTTTACCATCTGAGGCCACACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 GACTTTACCATCTGAGGCCACACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 AGCAAGATGACATATATATGCTTAAGTAGTGACATGTTTTTGGACATTTCCAGCCCTTT 240
DB 181 AGCAAGATGACATATATATGCTTAAGTAGTGACATGTTTTTGGACATTTCCAGCCCTTT 240
QY 241 AATATCCACACACAGAGAGACACAAAAGAACACAGAGATCCTGGAGAAATGCC 300
DB 241 AATATCCACACACAGAGAGACACAAAAGAACACAGAGATCCTGGAGAAATGCC 300
QY 301 GGGCCGCATCTTGGGTCATGATGAGCCTCGCCCTGGCTGGCTGGCTGGAGGAA 360
DB 301 GGGCCGCATCTTGGGTCATGATGAGCCTCGCCCTGGCTGGCTGGAGGAA 360
QY 361 GGACATTTAGAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 GGACATTTAGAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 GTGATATTTATTTGACGGGATTTACAGATTTGAATGAATGACACAAAGTACATACC 480
DB 421 GTGATATTTATTTGACGGGATTTACAGATTTGAATGAATGACACAAAGTACATACC 480
QY 481 AATGAGAGGAAAAACAGAGAGAGAAATCTTGATGCTTCAAGACATGCAACAAACAAA 540
DB 481 AATGAGAGGAAAAACAGAGAGAGAAATCTTGATGCTTCAAGACATGCAACAAACAAA 540

QY 541 TGAATAGTGTGATGACATGAGGACCAAGCTGGGGAGAGATACACGGGGCAGAG 600
Db 541 TGAATAGTGTGATGACATGAGGACCAAGCTGGGGAGAGATACACGGGGCAGAG 600
QY 601 GTCAGAGATTCGGCCCTGCTCCTAAACTGTCGCTTCAACCAATCATTTATATTC 660
Db 601 GTCAGAGATTCGGCCCTGCTCCTAAACTGTCGCTTCAACCAATCATTTATATTC 660
QY 661 TAACCTTCAAAACAAAGCTGTTGTAATATCTGATCTACGTTCTCTGGGCCAACA 720
Db 661 TAACCTTCAAAACAAAGCTGTTGTAATATCTGATCTACGTTCTCTGGGCCAACA 720
QY 721 TTCCTCAATATTCACGACACATCTATTTTAAATTTAGTCCAGATCTACTGTAC 780
Db 721 TTCCTCAATATTCACGACACATCTATTTTAAATTTAGTCCAGATCTACTGTAC 780
QY 781 CTTCTACACTGTAGAAATTAACATTACTATTTGTTCAA 820
Db 781 CTTCTACACTGTAGAAATTAACATTACTATTTGTTCAA 820

RESULT 4
ID AAA06690/c
AAA06690 standard; cDNA: 812 BP.

XX AAA06690;
XX 13-JUN-2000 (first entry)

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:471.

KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW Immunogenic; cytosolic; vaccine; ss.

OS Homo sapiens.

PN WO200004149-A2.

PD 27-JAN-2000.

PE 14-JUL-1999; 99WO-US15838.

PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.

PA (CORI-) CORIXA CORP.

PI Dillon DC, Harlocker SL, Yung J, Xu J, Mitcham JL;

XX WPL; 2000-171268/15.

PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -

PS Claim 1; Page 262; 263pp; English.

CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AA06200 to AA06202 represent sequences used in the exemplification of

CC the present invention.
XX SQ Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;

Query Match 99.0%; Score 812; DB 21; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGGCATCAGAAAAACAGAGGGGAGATTTGTGTGGCTGCACCCAGGAGACACAGAGA 65
Db 812 CTGGCATCAGAAAAACAGAGGGGAGATTTGTGTGGCTGCACCCAGGAGACACAGAGA 753
QY 66 TCTGCATGTGTGGGAAGACCTGATGATACAGAGGTGAGAAATTAAGAAAGCTGCTG 125
Db 752 TCTGCATGTGTGGGAAGACCTGATGATACAGAGGTGAGAAATTAAGAAAGCTGCTG 693
QY 126 TACATCTGAGGCGCACACATCTGCGTGAATGAGATTAATTAACATCTAACAACAGAA 185
Db 692 TACATCTGAGGCGCACACATCTGCGTGAATGAGATTAATTAACATCTAACAACAGAA 633
QY 186 GATGACATATTAATGCTAAAGTACATGATCTTTTTCACATTTCCAGCCCTTTAATA 245
Db 632 GATGACATATTAATGCTAAAGTACATGATCTTTTTCACATTTCCAGCCCTTTAATA 573
QY 246 TCCACACACACAGAGACACAAAAGAAAGACACAGATCCCTGGAGAAATGCCGGCG 305
Db 572 TCCACACACACAGAGACACAAAAGAAAGACACAGATCCCTGGAGAAATGCCGGCG 513
QY 306 CCATCTGGGTCATGATGATGAGCCCTGCGCTGGCTGCTGCTGCTGGAGGAGAGACA 365
Db 512 CCATCTGGGTCATGATGATGAGCCCTGCGCTGGCTGCTGCTGCTGGAGGAGAGACA 453
QY 366 TTAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 425
Db 452 TTAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 393
QY 426 TATTTATTTGAGCGGATTTACAGATTTGAATGAAGTCACAAAGTACGATTTACAA 485
Db 392 TATTTATTTGAGCGGATTTACAGATTTGAATGAAGTCACAAAGTACGATTTACAA 333
QY 486 GAGGAAACACAGAGAGAAATCTGATGCGCTTCAAGACATGCAACAAACAAATGAA 545
Db 332 GAGGAAACACAGAGAGAAATCTGATGCGCTTCAAGACATGCAACAAACAAATGAA 273
QY 546 TACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 605
Db 272 TACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 213
QY 606 GATTCCTGGCCCTGCTGCTTAACTGTGCTTCAATACCAATCATTTCTATTTCTAAC 665
Db 212 GATTCCTGGCCCTGCTGCTTAACTGTGCTTCAATACCAATCATTTCTATTTCTAAC 153
QY 666 CTCAAAACAAAGCTGTTGTAATATCTGATCTCTAGGCTCTTGGGCCCAACATCTC 725
Db 152 CTCAAAACAAAGCTGTTGTAATATCTGATCTCTAGGCTCTTGGGCCCAACATCTC 93
QY 726 CATATATTCACGACCACTCATTTTAAATTTAGTCCAGATCTGATCTGACCTTTC 785
Db 92 CATATATTCACGACCACTCATTTTAAATTTAGTCCAGATCTGATCTGACCTTTC 33
QY 786 TACACTGTAGATTAACATTTACTCTATTTGTTTC 817
Db 32 TACACTGTAGATTAACATTTACTCTATTTGTTTC 1

RESULT 5
ID AAS63899/c
AAS63899 standard; cDNA: 812 BP.
XX AAS63899;
XX 29-JAN-2002 (first entry)

Db	572	TTCCACACACACAGSAGACCAAAAAGAAACACAGATTCCTTGGAGAAATGCCGGCCG	513
QY	306	CCATCTTGGGTCATCGATGAGCCCTGGCCCTGTGCTGTGCCGCTTGTGAGGGAAGGACA	365
Db	512	CCATCTTGGGTCATCGATGAGCCCTGGCCCTGTGCTGTGCCGCTTGTGAGGGAAGGACA	453
QY	366	TTAGAAATGATTAATGATGTGTTCTTAAAGAGTGGCAGGAAACACATCTGTTGTGA	425
Db	452	TTAGAAATGATTAATGATGTGTTCTTAAAGAGTGGCAGGAAACACATCTGTTGTGA	393
QY	426	TATTTATTTGAACGGGATTACAGATTGAAATGAAATGAAGTACAAAGTGAAGCATTACCATTGA	485
Db	392	TATTTATTTGAACGGGATTACAGATTGAAATGAAATGAAGTACAAAGTGAAGCATTACCATTGA	333
QY	486	GAGGAAAAACAGACGAGAAAAATCTTGATGGCTTCCACAAGACATGCAACAAACAAATGGAA	545
Db	332	GAGGAAAAACAGACGAGAAAAATCTTGATGGCTTCCACAAGACATGCAACAAACAAATGGAA	273
QY	546	TACTGTGATGACATGAGGACGACCAGAGCTGGGGGAGAGTAAACACGGGGCAGAGGGTCAG	605
Db	272	TACTGTGATGACATGAGGACGACCAGAGCTGGGGGAGAGTAAACACGGGGCAGAGGGTCAG	213
QY	606	GATCTGTGGCCCTGGTGCCTAAACGTCGTGGCTCATTAACCAATTCATTTCTTAACC	665
Db	212	GATCTGTGGCCCTGGTGCCTAAACGTCGTGGCTCATTAACCAATTCATTTCTTAACC	153
QY	666	CTCAAAACAAAGCTGTTGTAATATCTGATCTCTACAGGTTCCCTTGGGCCCAACATTCTC	725
Db	152	CTCAAAACAAAGCTGTTGTAATATCTGATCTCTACAGGTTCCCTTGGGCCCAACATTCTC	93
QY	726	CATATATTCACGACACACTCATTTTAAATATTAGTCCACAGATCTGTACGTGACCTTTC	785
Db	92	CATATATTCACGACACACTCATTTTAAATATTAGTCCACAGATCTGTACGTGACCTTTC	33
QY	786	TACACTGTAGATTAACATTTACTCTGTTTCTTC	817
Db	32	TACACTGTAGATTAACATTTACTCTGTTTCTTC	1
RESULT 6			
AAH93806/c			
ID	AAH93806	standard; cDNA: 812 BP.	
XX	AAH93806;		
AC			
XX	04-OCT-2001	(first entry)	
DT			
XX	Human prostate-specific cDNA sequence P710P #4.		
DE			
XX	Human; prostate cancer; prostate-specific; diagnosis; vaccine;		
KW	cytostatic; gene therapy; metastasis; ss.		
KW			
XX	Homo sapiens.		
CS			
XX	MO200151633-A2.		
PN			
XX	19-JUL-2001.		
PD			
XX	16-JAN-2001; 2001WO-US01574.		
PF			
XX	14-JAN-2000; 2000US-0483672.		
PR			
XX	(CORI-) CORIXA CORP.		
PA			
XX	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;		
PL	Kalos MD, Fanger GR, Day CH, Retter MM, Stolk JA, Skelky YAW;		
PI	Wang A, Meagher MJ;		
XX			
DR	WPI: 2001-425873/45.		
XX			
PT	New polynucleotide encoding a prostate-specific protein, for		
PT	diagnosing, monitoring and treating prostate cancer in a patient and		

for use in vaccines -

Claim 1; Page 385; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytosstatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.

Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;

Query Match 99.0%; Score 812; DB 22; Length 812;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 6 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCACCCGAGGAGACCAAGAGA 65
Db 812 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCACCCGAGGAGACCAAGAGA 753
QY 66 TCTGCATGTGGGAGAGACCTGATGATACAGAGGTGAAGAAATGAAGAGCTGCTGACTT 125
Db 752 TCTGCATGTGGGAGAGACCTGATGATACAGAGGTGAAGAAATGAAGAGCTGCTGACTT 693
QY 126 TACCATGTAGGCCACACATCTGCTGAATGAGATATTACATCACTAGAAACAGCA 185
Db 692 TACCATGTAGGCCACACATCTGCTGAATGAGATATTACATCACTAGAAACAGCA 633
QY 186 GATGACATATATATGTCTAAGTAGTGCATGTTTGGACATTTCCAGCCCTTTAATA 245
Db 632 GATGACATATATATGTCTAAGTAGTGCATGTTTGGACATTTCCAGCCCTTTAATA 573
QY 246 TCACACACACAGGAGACCAAAAGAGACAGAGATCCCTGGGAGAAATGCCGCGC 305
Db 572 TCACACACACAGGAGACCAAAAGAGACAGAGATCCCTGGGAGAAATGCCGCGC 513
QY 306 CCATCTTGGGTCATCGATGAGCTCGCCCTGCTGCTGCCCTTGTGAGGAGAGACA 365
Db 512 CCATCTTGGGTCATCGATGAGCTCGCCCTGCTGCTGCCCTTGTGAGGAGAGACA 453
QY 366 TTAGAAATGATGATGTGTCTTCTTAAAGATGGGAGAGAAACAGATCCTGTGGA 425
Db 452 TTAGAAATGATGATGTGTCTTCTTAAAGATGGGAGAGAAACAGATCCTGTGGA 393
QY 426 TATTATTTGAACGGGATTCAGATTTGAATGAAGTCACAAATGAGCATTTACAA 485
Db 392 TATTATTTGAACGGGATTCAGATTTGAATGAAGTCACAAATGAGCATTTACAA 333
QY 486 GAGGAAAAACAGACGAGAAATCTTGATGCGCTTCACAAAGATGCAACAAATGGA 545
Db 332 GAGGAAAAACAGACGAGAAATCTTGATGCGCTTCACAAAGATGCAACAAATGGA 273
QY 546 TACTGTATGATGATGAGGAGCCAAAGCTGGGAGAGATTAACACGGGGGAGAGGTCAG 605
Db 272 TACTGTATGATGATGAGGAGCCAAAGCTGGGAGAGATTAACACGGGGGAGAGGTCAG 213
QY 606 GATTCTGGCCCTGCTGCTAAACTGTGCTCATTAACCAATCTTCAATATTTCTAAC 665
Db 212 GATTCTGGCCCTGCTGCTAAACTGTGCTCATTAACCAATCTTCAATATTTCTAAC 153
QY 666 CTCAAAACAAAGCTGTGTAATATCTGATCTCTAGCGTTCTTGGGCCCAACATCTC 725
Db 152 CTCAAAACAAAGCTGTGTAATATCTGATCTCTAGCGTTCTTGGGCCCAACATCTC 93
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```
QY 726 CATATATCCAGCCACACTCATTTTAAATATTAGTCCAGATCTGACTGTGACCTTTC 785
Db 92 CATATATCCAGCCACACTCATTTTAAATATTAGTCCAGATCTGACTGTGACCTTTC 33
QY 786 TACACTGTAGAAATACATTAATCTACTTGTGTC 817
Db 32 TACACTGTAGAAATACATTAATCTACTTGTGTC 1
```

RESULT 7

AAH85120/C

ID AAH85120 standard; CDNA; 812 BP.

AAH85120;

25-SEP-2001 (first entry)

Human prostate-specific cDNA sequence P710P #4.

Human; prostate cancer; therapy; diagnosis; cat eye syndrome; chromosome 22q11.2; prostate-specific protein; chromosome 1; prostate specific antigen; PSA; ss.

Homo sapiens.

WO200134802-A2.

17-MAY-2001.

09-NOV-2000; 2000WO-US30904.

12-NOV-1999; 99US-0439313.

18-NOV-1999; 99US-0443686.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG; Kairos MD, Retter KM, Stolk JA, Day CH, Skeiky IAW, Wang A;

WPI: 2001-308785/32.

Isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, useful in the diagnosis and therapy of prostate cancer -

Claim 5; Page 284-285; 325pp; English.

The present invention describes an isolated polypeptide (PI) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (NI) encoding (PI). (PI) and (NI) have cytosstatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P774P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. AAH84671 to AAH85143 and AA699000 to AA699077 represent polynucleotide and polypeptide sequences used in the exemplification of the present invention.

Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;

Query Match 99.0%; Score 812; DB 22; Length 812;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 6 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCACCCGAGGAGACCAAGAGA 65
Db 812 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGGCTGCACCCGAGGAGACCAAGAGA 753
QY 66 TCTGCATGTGGGAGAGACCTGATGATACAGAGGTGAAGAAATGAAGAGCTGCTGACTT 125
Db 752 TCTGCATGTGGGAGAGACCTGATGATACAGAGGTGAAGAAATGAAGAGCTGCTGACTT 693
```


QY	126	ACCACCTGAGGCGACACATCGCGGAAATGAGATAATTAACATCCTACTGAAACAGCAA	185
Db	692	THACATCTTAGGCGACACATCTGCTGAAATGAGATAATTAACATCCTACTGAAACACCAA	633
QY	186	GATGACAAATATATGTCCTAAGTAGACATGTTTTGGACATTTCCAGCCCTTTAAATA	245
Db	632	GATGACAAATATATGTCCTAAGTAGACATGTTTTGGACATTTCCAGCCCTTTAAATA	573
QY	246	TCCACACACACAGGAAGCACAAGAGACACAGAGATCCTCGGAGAAATGCCCGCG	305
Db	572	TCCACACACACAGGAAGCACAAGAGACACAGAGATCCTCGGAGAAATGCCCGCG	513
QY	306	CCATCTGGGTCATCGATGAGCCCTGCGCTGCTGCTGCCGCTTGAGAGGAAGACA	365
Db	512	CCATCTGGGTCATCGATGAGCCCTGCGCTGCTGCTGCCGCTTGAGAGGAAGACA	453
QY	366	TTTGAAAAATGAATTGATGTCCTTTCTTAAAGATGGGCGAGAAAACAGTCTCTGTGGGA	425
Db	452	TTTGAAAAATGAATTGATGTCCTTTCTTAAAGATGGGCGAGAAAACAGTCTCTGTGGGA	393
QY	426	TATTTATTTGAACGGGATTACAGATTTGAAATGAAGTCACAAAGTGGAGCATTTACCAATGA	485
Db	392	TATTTATTTGAACGGGATTACAGATTTGAAATGAAGTCACAAAGTGGAGCATTTACCAATGA	333
QY	486	GAGGAAAAACAGACGAGAAAAATCTTGATGCTTCACACAGATGCAACAAACAAAATGGAA	545
Db	332	GAGGAAAAACAGACGAGAAAAATCTTGATGCTTCACAAACATGCAACAAACAAAATGGAA	273
QY	546	TACTGATGATGATGAGGCGACGCAAGCGGGGAGAGATTAACACAGGGGCGAGAGGGTCAG	605
Db	272	TACTGATGATGATGAGGCGACGCAAGCGGGGAGAGATTAACACAGGGGCGAGAGGGTCAG	213
QY	606	GATTCGAGCCCTGCTGCCCTAAACCTGCTGGTTCATTAACCAATTCATTTCAATTTCAAC	665
Db	212	GATTCGAGCCCTGCTGCCCTAAACCTGCTGGTTCATTAACCAATTCATTTCAATTTCAAC	153
QY	666	CTTAAACCAAACTGTTGTATATCTGATCTCTACGGTTCCTTTGGGCCCAACATTTCTC	725
Db	152	CTTAAACCAAACTGTTGTATATCTGATCTCTACGGTTCCTTTGGGCCCAACATTTCTC	93
QY	726	CATATATCCAGCACACCTCATTTTAAATTAATTTAGTCCCAATCTGTACTGTGACCTTTC	785
Db	92	CATATATCCAGCACACCTCATTTTAAATTAATTTAGTCCCAATCTGTACTGTGACCTTTC	33
QY	786	THACCTGTGAATTAACATTACTCATTTTGGTTC	817
Db	32	THACCTGTGAATTAACATTACTCATTTTGGTTC	1

	RESULT 8
XX	AAH02871/c
ID	AAH02871 standard; cDNA; 812 BP.
AC	AAH02871;
XX	
DF	14-JUN-2001 (first entry)
XX	
DE	Prostate tumour antigen cDNA sequence for P710P #4.
XX	
KW	Human; prostate tumour antigen; prostate tumour; diagnosis;
KM	prostate cancer; immunogenic; cytosolic; vaccine; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200125272-A2.
XX	
PD	12-APR-2001.
XX	
PX	04-OCT-2000; 2000WO-US27464.
PF	
XX	
PR	04-OCT-1999; 99US-0157455.
XX	

PA (CORI-) CORIXA CORP.
 XX
 XX
 PI Xu J, Skeiky YAM, Reed SG, Cheever MA;
 XX
 DR WPI; 2001-245062/25.
 XX
 PT Prostate specific protein and its encoding polynucleotide, useful for
 XX the treatment and diagnosis of prostate cancer -
 PS
 XX Claim 4; Page 267; 276pp; English.
 XX
 XX The present invention describes an isolated polypeptide (I) comprising
 CC at least an immunogenic portion of a prostate tumour antigen protein or
 CC its variant. (I) have cytostatic activity and can be used in vaccine
 CC production.. (I)' prostate tumour antigen polynucleotides, an antigen
 CC presenting cell (APC e.g. a dendritic cell) that expresses (I)', and a
 CC pharmaceutical composition containing (I) are useful for inhibiting the
 CC development of cancer in a patient. Antibodies specific for prostate
 CC specific proteins and oligonucleotides that hybridise to a
 CC polynucleotide that encodes a prostate specific protein are useful
 CC for detecting the presence or absence of a cancer or monitoring the
 CC progression the progression of a cancer, especially prostate cancer.
 CC AA002422 to AAH2872; AAB74798 to AAB74821 and AAB74830 are sequences
 CC used in the exemplification of the present invention.
 XX
 XX Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
 XQ

[illegible]

[illegible]

QY	126	TACATCTGAGGCCACACATCTGCTGCTAAATGAGATTAATTAACATCACTAGAAAACAGCA	183
Db	692	TACATCTGAGGCCACACATCTGCTGCTAAATGAGATTAATTAACATCACTAGAAAACAGCA	633
QY	186	GATGACAACTTAATGCTCTAAGTAGTACATGTTTTGGACATTTCCAGCCCTTTAATA	245
Db	632	GATGACAACTTAATGCTCTAAGTAGTACATGTTTTGGACATTTCCAGCCCTTTAATA	573
QY	246	TCACACACACAGSAAAGCAGAAAAGSAGACAGAGATCCTGGAGAAATGCCGGCCG	305
Db	572	TCACACACACAGSAAAGCAGAAAAGSAGACAGAGATCCTGGAGAAATGCCGGCCG	513
QY	306	CCATCTGGGCTCATTCATGATGAGCTCGCCCTGTGCTCGCTGGCTTGGAGGAAGACA	365
Db	512	CCATCTGGGCTCATTCATGATGAGCTCGCCCTGTGCTCGCTTGGAGGAAGACA	453
QY	366	TTAGAAATTAATTTGATGTTGTTCTTAAAGATGGGCGAGAAAACAGATCCTGTTGGA	425
Db	452	TTAGAAATTAATTTGATGTTGTTCTTAAAGATGGGCGAGAAAACAGATCCTGTTGGA	393
QY	426	TATTTATTTGGAACGGGATTACAGATTTGAAATGAAGTCACAAAGTGAGCATTTACAA	485
Db	392	TATTTATTTGGAACGGGATTACAGATTTGAAATGAAGTCACAAAGTGAGCATTTACAA	333
QY	486	GAGGAAAAACGACGAGAAAAATCTTGATGCTTCACAGACATTCGACAAACAAATGGAA	545
Db	332	GAGGAAAAACGACGAGAAAAATCTTGATGCTTCACAGACATTCGACAAACAAATGGAA	273
QY	546	TACTGTGATGATGATGAGGCGACCAAGCTGGGAGAGATTAACCAACGGGCGAGAGGGTCAG	605
Db	272	TACTGTGATGATGATGAGGCGACCAAGCTGGGAGAGATTAACCAACGGGCGAGAGGGTCAG	213
QY	606	GATTCGTGGCCCTGCTGCTAAACCTGTGCTCATTAACCAATCATTTCAATTTCTAAC	665
Db	212	GATTCGTGGCCCTGCTGCTAAACCTGTGCTCATTAACCAATCATTTCAATTTCTAAC	153
QY	666	CTCAAAACAAAGCTGTGTAATATCTGATCTCTAGAGTCTCTCTGGGCCCAACATTTCTC	725
Db	152	CTCAAAACAAAGCTGTGTAATATCTGATCTCTAGAGTCTCTCTGGGCCCAACATTTCTC	93
QY	726	CATATATCCAGCCACACTCATTTTAAATATTAGTCCAGATCTGACTGTGACCTTTC	785
Db	92	CATATATCCAGCCACACTCATTTTAAATATTAGTCCAGATCTGACTGTGACCTTTC	33
QY	786	TACACTGTAGAAATTAACATTAATTTGTTTC	817
Db	32	TACACTGTAGAAATTAACATTAATTTGTTTC	1
RESULT 10			
ABL95270/c			
XX	ABL95270	standard; cDNA; 812 bp.	
XX	ABL95270;		
XX	19-JUL-2002	(first entry)	
XX	Human P710P	cDNA sequence SPO ID NO 471.	
DE	Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;		
KW	gene therapy; gene; ss.		
KW	gene therapy; gene; ss.		
XX	Human sapiens.		
XX	OS		
XX	PN	US2002022248-A1.	
XX	21-FEB-2002.		
XX	12-JAN-2001; 2001US-0759143.		
PR	25-FEB-1997.	97US-080609.	
PR	01-AUG-1997.	97US-0904804.	
PR	09-FEB-1998;	98US-0020956.	

PR 25-FEB-1998; 9805-0030607.
PR 14-JUL-1998; 9805-0115453.
PR 23-SEP-1998; 9805-0159812.
PR 15-JAN-1999; 9905-0232149.
PR 09-APR-1999; 9905-0288946.
PR 13-JUL-1999; 9905-0352616.
PR 12-NOV-1999; 9905-0439313.
PR 18-NOV-1999; 9905-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX

PA (XUJ/) XU J.
PA (DILL/) DILLON D. C.
PA (MITC/) MITCHAM J. L.
PA (HARL/) HARLOCKER S. L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M. D.
PA (FANG/) FANGER G. R.
PA (RETT/) RETTER M. W.
PA (STOL/) STOLK J. A.
PA (DAYC/) DAY C. H.
PA (VEDV/) VEDVICK T. S.
PA (CART/) CARTER D.
PA (LISX/) LI S. X.
PA (MANG/) MANG A.
PA (SKET/) SKETKY Y. A. W.
PA (HEPL/) HEPLER W. T.
PA (HEND/) HENDERSON R. A.
XX

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Sketky YAW, Hepler WT, Henderson RA;
XX

DR WPI, 2002-255649/30.
XX

PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX

PS Claim 1; SEQ ID NO 471; 87pp; English.
XX

CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX

XX Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
SQ

Query Match 99.0%; Score 812; DB 24; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACAGAGA 65
DB 812 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGAGACAGAGA 753
QY 66 TCTGCATGGTGGGAAGACCTGATGATACAGAGTGAGAAATAGAAAAGGCTGACTT 125
DB 752 TCTGCATGGTGGGAAGACCTGATGATACAGAGTGAGAAATAGAAAAGGCTGACTT 693
QY 126 TACCATCTGAGGCCACACATCTGCTGAATGAGATTAATACATCAGTAAAGCA 185
DB 692 TACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAACATCAGTAAAGCA 633

QY 186 GATGACAAATATATGCTATAGTAGACATGTTTTGGACATTTCCAGCCCTTAATA 245
DB 632 GATGACAAATATATGCTATAGTAGACATGTTTTGGACATTTCCAGCCCTTAATA 573
QY 246 TCCACACACACAGGAAGACAAAGAGACACAGATTCCTGGGAAATCCCGCGC 305
DB 572 TCCACACACACAGGAAGACAAAGAGACACAGATTCCTGGGAAATCCCGCGC 513
QY 306 CCATCTGGGTCATGATGATGAGCTGCGCCCTGTCGCTGCGCGCTTGTAGGAAGACA 365
DB 512 CCATCTGGGTCATGATGATGAGCTGCGCCCTGTCGCTGCGCGCTTGTAGGAAGACA 453
QY 366 TTAGAAATGAATGATGATGCTCTTAAAGATGGGACAGAAACAGATCCTGTGTGA 425
DB 452 TTAGAAATGAATGATGATGCTCTTAAAGATGGGACAGAAACAGATCCTGTGTGA 393
QY 426 TATTTATTTTGAACGGGATTAACAGATTTGAATGAAGTCAACAGTACATTACAN 485
DB 392 TATTTATTTTGAACGGGATTAACAGATTTGAATGAAGTCAACAGTACATTACAN 333
QY 486 GAGGAAACACAGACGAAATCTGTATGCTGCCTCACAGACATGCAACAAACAAATGGA 545
DB 332 GAGGAAACACAGACGAAATCTGTATGCTGCCTCACAGACATGCAACAAACAAATGGA 273
QY 546 TACTGTGATGATGATGAGCAGCCCAAGCTGGGAGAGATTAACACAGGAGGCTCAG 605
DB 272 TACTGTGATGATGATGAGCAGCCCAAGCTGGGAGAGATTAACACAGGAGGCTCAG 213
QY 606 GATTCGTGCGCTGCTGCTCTAAACGTGCTCATTAACCAATTCATTATTTCTAAC 665
DB 212 GATTCGTGCGCTGCTGCTCTAAACGTGCTCATTAACCAATTCATTATTTCTAAC 153
QY 666 CTCAAACAAACCTGTGTGAATATCTGATGATCTAGGTCCTTCTGGGCGCAACATTC 725
DB 152 CTCAAACAAACCTGTGTGAATATCTGATGATCTAGGTCCTTCTGGGCGCAACATTC 93
QY 726 CATATATCCAGCCACACTCATTTTAAATTAATTAATTCAGATCTGTACTGTGACTTTC 785
DB 92 CATATATCCAGCCACACTCATTTTAAATTAATTAATTCAGATCTGTACTGTGACTTTC 33
QY 786 TACACTGTGAATTAACATTACTCATTTTGTTC 817
DB 32 TACACTGTGAATTAACATTACTCATTTTGTTC 1
RESULT 11
ACA59707/c
ID ACA59707 standard; cDNA; 812 BP.
AC ACA59707;
XX
AC ACA59707;
XX
DT 10-JUN-2003 (first entry)
XX
DE Prostate cancer therapy associated cDNA #450.
XX
DE Prostate cancer: vaccine; gene therapy; cytostatic; fusion protein;
XX immunogen; cancer; prostate specific antigen; PSA;
XX prostatic acid phosphatase; PAP; prostate specific membrane antigen;
XX PSMa; gene; ss.
OS Homo sapiens.
XX
PN US2002192763-A1.
XX
PD 19-DEC-2002.
XX
XX 29-JUN-2001; 2001US-0895793.
XX
XX 17-APR-2000; 2000US-157455P.
PR 04-OCT-2000; 2000US-0679272.
PR 28-MAR-2001; 2001US-0822827.
XX
XX (XUJ/) XU J.

PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUN/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
 PI Fanger GR, Retter MM, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
 PI McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;
 XX
 DR WPI: 2003-352711/33.
 XX
 PT New fusion protein comprising prostate-specific polypeptides, or its
 PT immunogenic portions, useful for diagnosing, preventing and/or treating
 PT cancer, particularly prostate cancer.
 PS
 PS Example 16; SEQ ID NO 471; 85pp; English.
 XX
 CC The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 35 sequences defined in the USPTO
 CC web site, which is encoded by any of the 4 nucleotide sequences not
 CC defined in the specification. The fusion protein, composition and
 CC methods are useful for diagnosing, preventing and/or treating cancer,
 CC particularly prostate cancer. The proteins are useful as markers to
 CC indicate the presence or absence of cancer. This sequence
 CC represents a prostate cancer therapy associated cDNA.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from the US patent office at
 CC seqdata.uspto.gov/sequence.html?DocID=US20020192763.
 CC
 XX
 SQ Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;
 Query Match 99.0%; Score 812; DB 25; Length 812;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 812: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 572 TCACACACACAGGAGACAAAAAGAACACAGAGATCCCTGGAGAAATGCCCCGCCG 513
 Oy CCATCTGGGTCATCATGATGACCCGCGCCCTGGCTGGCTGCCCTGGTGGAGGAGAC 365
 Db 512 CCATCTGGGTCATCATGATGACCCGCGCCCTGGCTGGCTGCCCTGGTGGAGGAGAC 453
 Oy 366 TTAGAAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
 Db 452 TTAGAAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 393
 Oy 426 TATTTATTTGACGGGATTTACAGATTTGAATGAATGACAAAGTACATTTACCAATGA 485
 Db 392 TATTTATTTGACGGGATTTACAGATTTGAATGAATGACAAAGTACATTTACCAATGA 333
 Oy 486 GAGGAAACAGACAGAGAAATCTGATGGCTTCACAGACATGACAAACAAATGAA 545
 Db 332 GAGGAAACAGACAGAGAAATCTGATGGCTTCACAGACATGACAAACAAATGAA 273
 Oy 546 TACTGTGATGACATGAGGACAGCCAGCTGGGAGAGATTAACACAGGGGAGAGGTCAG 605
 Db 272 TACTGTGATGACATGAGGACAGCCAGCTGGGAGAGATTAACACAGGGGAGAGGTCAG 213
 Oy 606 GATTCGCGCCCTGCTGCTTAACCTGCTGCTTAACCTGCTGCTTAACCTGCTGCTAAC 665
 Db 212 GATTCGCGCCCTGCTGCTTAACCTGCTGCTTAACCTGCTGCTTAACCTGCTGCTAAC 153
 Oy 666 CTCAAAACAAAGCTGTGATATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 725
 Db 152 CTCAAAACAAAGCTGTGATATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 93
 Oy 726 CATATATCCAGCCACACTCATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 785
 Db 92 CATATATCCAGCCACACTCATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 33
 Oy 786 TACACTGTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 817
 Db 32 TACACTGTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1
 RESULT 12
 AAA06688/C
 ID AAA06688 standard; cDNA: 2229 BP.
 XX
 AC AAA06688;
 XX
 DE 13-JUN-2000 (first entry)
 XX
 DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:469.
 XX
 KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
 KW immunogenic; cytostatic; vaccine; ss.
 XX
 OS Homo sapiens.
 PN WO200004149-A2.
 XX
 PD 27-JAN-2000.
 XX
 PF 14-JUL-1999; 99NO-US15838.
 XX
 PR 14-JUL-1998; 98US-0115453.
 PR 14-JUL-1998; 98US-0116134.
 PR 23-SEP-1998; 98US-0159812.
 PR 23-SEP-1998; 98US-0159822.
 PR 15-JAN-1999; 99US-0232149.
 PR 15-JAN-1999; 99US-0232860.
 PR 09-APR-1999; 99US-0288946.
 XX
 PA (CORI-) CORIXA CORP.
 PI
 PI Dillon DC, Harlocker SL, Yudin J, Xu J, Mitcham JL;

DR WPI: 2000-171268/15.
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
XX
PS Claim 1: Page 260-261; 263pp; English.
XX
XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PrP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AY82000 to AY82020 represent sequences used in the exemplification of
CC the present invention.
XX
XX Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;
SQ
Query Match 88.3%; Score 724; DB 21; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGGAATTAAGAAAGGCTGCTGACCTTACCATCTGAGGCCACACATCTGCTGAATG 156
DB 1776 AGGTGGAATTAAGAAAGGCTGCTGACCTTACCATCTGAGGCCACACATCTGCTGAATG 1717
QY 157 GAGATATTAACATCACTGAGAAACAGCAGATGACATATATAGTAAAGTAGTACATG 216
DB 1716 GAGATATTAACATCACTGAGAAACAGCAGATGACATATATAGTAAAGTAGTACATG 1657
QY 217 TTTTTCACATTTCCAGCCCTTTAATATCCACACACAGCAGACACAAAAGAAAGCA 276
DB 1656 TTTTTCACATTTCCAGCCCTTTAATATCCACACACAGCAGACACAAAAGAAAGCA 1597
QY 277 CAGAGATCCCTGGGAGAAATGCCCGCCGACATCTGGTGCATGATGAGCTGCCCTG 336
DB 1596 CAGAGATCCCTGGGAGAAATGCCCGCCGACATCTGGTGCATGATGAGCTGCCCTG 1537
QY 337 TGCTTGTCCTCCGCTTGTGAGGAGAGACATTAGAAATGATGATGTTCTTTAAGG 396
DB 1536 TGCTTGTCCTCCGCTTGTGAGGAGAGACATTAGAAATGATGATGTTCTTTAAGG 1477
QY 397 ATGGCAGAGAAAACAGATCCTGTTGTGATATTTTGAACGGGATTAACAGATTGAAA 456
DB 1476 ATGGCAGAGAAAACAGATCCTGTTGTGATATTTTGAACGGGATTAACAGATTGAAA 1417
QY 457 TGAAGTCACAAAGTGCACATTACCAATGAGAGAAAACAGCAGAAAATCTTGATGCT 516
DB 1416 TGAAGTCACAAAGTGCACATTACCAATGAGAGAAAACAGCAGAAAATCTTGATGCT 1357
QY 517 TCACAAGACATGCAACAAACAAATGAAATGATGATGATGAGGAGCCCAAGTGGG 576
DB 1356 TCACAAGACATGCAACAAACAAATGAAATGATGATGATGAGGAGCCCAAGTGGG 1297
QY 577 GAGGAGATAACCAAGGGGAGAGAGGTGAGGATCTGGCCCTGCTTAAAGTGGCT 636
DB 1296 GAGGAGATAACCAAGGGGAGAGAGGTGAGGATCTGGCCCTGCTTAAAGTGGCT 1237
QY 637 CATACCAAAATCTTTTCATATTTCTAACCTCTCAAAACAAAGCTGTTGTAATATCTGATCT 696
DB 1236 CATACCAAAATCTTTTCATATTTCTAACCTCTCAAAACAAAGCTGTTGTAATATCTGATCT 1177
QY 697 CTACGGTTCCTTGGGCCCAACATCTCATATATTCAGCCACACATCTTTAATAT 756
DB 1176 CTACGGTTCCTTGGGCCCAACATCTCATATATTCAGCCACACATCTTTAATAT 1117
QY 757 TAGTCCAGATCTGACTGTGACCTTCTACACTGATAGAAATTAACATTACTCATTTTGT 816
|||||

DB 1116 TAGTCCAGATCTGACTGTGACCTTTCTACACTGATAGAAATTAACATTACTCATTTTGT 1057
QY 817 CAAA 820
DB 1056 CAAA 1053
RESULT 13
AAS63897/C
ID AAS63897 standard; cDNA; 2229 BP.
XX
XX AAS63897;
AC
XX
XX 29-JAN-2002 (first entry)
DE Human prostate cDNA sequence #431.
XX
XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
XX Homo sapiens.
OS
XX
XX WO200173032-A2.
PN
XX
XX 04-OCT-2001.
PD
XX
XX 27-MAR-2001; 2001MO-US09919.
PF
XX
XX 27-MAR-2000; 2000US-0536857.
PR
XX 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (CORI-) CORIAX CORP.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skelky YAM, Hepler WT, Henderson RA;
XX
XX WPI: 2001-639232/73.
DR
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
PT
XX
PS Claim 1: Page 385; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
XX Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;
SQ
Query Match 88.3%; Score 724; DB 22; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGGAATTAAGAAAGGCTGCTGACCTTACCATCTGAGGCCACACATCTGCTGAATG 156
|||||

Db	1776	AGGTGAGAAATATAGAAAGGCGTGTGACCTTTACATCTGAGGCCACACATCTGCTGAATG	1717
QY	157	GAGATAAATTAACATCTACTAGAAACAGCAGATGACAAATATATAGTCTTAAGTAGACATG	216
Db	1716	GAGATAAATTAACATCTACTAGAAACAGCAGATGACAAATATATAGTCTTAAGTAGACATG	1657
QY	217	TTTTTGCACATTTCCAGGCCCTTTTAAATATCCACACACACAGGAAAGCAACAAAGGAACA	276
Db	1656	TTTTTGCACATTTCCAGGCCCTTTTAAATATCCACACACACAGGAAAGCAACAAAGGAACA	1597
QY	277	CAGAGATCCCTGGGAGAAATGCCGCGCCCATCTTGGGTATGATGAGAGCCTGCGCCTG	336
Db	1596	CAGAGATCCCTGGGAGAAATGCCGCGCCCATCTTGGGTATGATGAGAGCCTGCGCCTG	1537
QY	337	TGCGTGGTCCCGCTTGTGAGGGAAGACATTAAGAAAAATGATGTGTCTTTAAAG	396
Db	1356	TGCGTGGTCCCGCTTGTGAGGGAAGACATTAAGAAAAATGATGTGTCTTTAAAG	1477
QY	397	ATGGGACAGAAACAGATCCTGTTGTGGATATTTATTTGAACGGGATTAACAGATTTGAA	456
Db	1476	ATGGGACAGAAACAGATCCTGTTGTGGATATTTATTTGAACGGGATTAACAGATTTGAA	1417
QY	457	TGAAGTCAACAAAGTAGCATTACCAATGAGAGGAAACAGACGAGAAAAATCTTATGGCT	516
Db	1416	TGAAGTCAACAAAGTAGCATTACCAATGAGAGGAAACAGACGAGAAAAATCTTATGGCT	1357
QY	517	TCACAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACGACCAAGCTGGG	576
Db	1356	TCACAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACGACCAAGCTGGG	1297
QY	577	GAGAGATATACACGCGGGCAGAGGGTCAGATTCCTGCGCTTAAACTGTGCGTT	636
Db	1296	GAGAGATATACACGCGGGCAGAGGGTCAGATTCCTGCGCTTAAACTGTGCGTT	1237
QY	637	CATTAACCAATCATTTTCATTTTCTTAACCCCTCAAAACCAACCTGTGTAATATCTGATCT	696
Db	1236	CATTAACCAATCATTTTCATTTTCTTAACCCCTCAAAACCAACCTGTGTAAATATCTGATCT	1177
QY	697	CTACGGTTCCTTCTGGGCCCAACATTCATCATATATCCAGCACATCATTTTAAATAT	756
Db	1176	CTACGGTTCCTTCTGGGCCCAACATTCATCATATATCCAGCACATCATTTTAAATAT	1117
QY	757	TAGTTCCAGATCTGTACTGTGACCTTCTTCACTGTAGAAATTAACATTTACTTTGT	816
Db	1116	TAGTTCCAGATCTGTACTGTGACCTTCTTCACTGTAGAAATTAACATTTACTTTGT	1057
QY	817	CAAA 820	
Db	1056	CAAA 1053	
RESULT 14			
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ID	AAH93804	standard; cDNA; 2229 BP.	
XX	AAH93804;		
AC			
XX	04-OCT-2001	(first entry)	
DT			
XX			
DE		Human prostate-specific cDNA sequence p710p #2.	
XX			
KW		Human; prostate cancer; prostate-specific; diagnosis; vaccine;	
XX		cytostatic; gene therapy; metastasis; ss.	
OS		Homo sapiens.	
XX			
PN	MO200151633-A2.		
XX			
PD	19-JUL-2001.		
XX			
EF	16-JAN-2001; 2001WO-US01574.		
XX			
PR	14-JAN-2000; 2000US-0483672.		

XX	(CORI-) CORIXA CORP.
PA	
XX	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
PI	Kalos MD, Fanger GR, Day CH, Retter MM, Stolk JB, Skeiky YAM,
PI	Wang A, Meagher MJ;
XX	WPT, 2001-425873/45.
DR	
XX	New polynucleotide encoding a prostate-specific protein, for
PT	diagnosing, monitoring and treating prostate cancer in a patient and
PT	for use in vaccines -
XX	
PS	Claim 1; Page 363-384; 543pp; English.
XX	
CC	The present invention describes polynucleotide sequences (I) which encode
CC	prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC	and can be used in vaccine production and gene therapy. (I), (II),
CC	antibodies to (II), fusion proteins comprising (II), and isolated
CC	T cells prepared using (I) or (II) are used treat cancer in a patient.
CC	(I) and the antibodies are also used in the detection of cancer in a
CC	patient. The cancer that is diagnosed or treated is particularly
CC	prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC	(I) can be used for monitoring the progression of cancer in a patient.
CC	(I) and (II) can also be used to improve diagnostic and therapeutic
CC	methods for prostate cancer. They can indicate the level of metastasis
CC	as well as the prostate volume. AA93357 to AA93944 and AMO1115 to
CC	AAO1318 represent polynucleotide and amino acid sequences used in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;
Query Match	88.3%; Score 724; DB 22; Length 2229;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 724;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	97 AGTGAGAATATAGAAAGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATG 156 DB 1776 AGGTGAGAAATAAAGAAAGCGTCGTGTAATTACCATCTGAGGCCACACATCTGCTGAATG 1717
OY	157 GAGTAAATTTAACATCATTACAGAAAGCAAGACAATGCAATTAATAGTAAAGTAGTGACATG 216
DB	1716 GAGTAAATTTAACATCATTACAGAAAGCAAGACAATGCAATTAATAGTAAAGTAGTGACATG 1657
OY	217 TTTTGGACATTTCCACCCTTTAAATATCCACACACACAGGAACACAAAAAGGAAGCA 276
DB	1656 TTTTGGACATTTCCACCCTTTAAATATCCACACACACAGGAACACAAAAAGGAAGCA 1597
OY	277 CAGAGATTCCTGGGAGAAATGCCGGCGGCATCTTGGGTCATGCATGAGCCTCGCCCTG 336
DB	1596 CAGAGATTCCTGGGAGAAATGCCGGCGGCATCTTGGGTCATGCATGAGCCTCGCCCTG 1537
OY	337 TGCCGTGTCGCCGCTTGGAGGAGGAAGCATTTAAGAAATGAATGTATCTTCCCTTAAAG 396
DB	1536 TGCCGTGTCGCCGCTTGGAGGAGGAAGCATTTAAGAAATGAATGTATCTTCCCTTAAAG 1477
OY	397 ATGGCGAGGAAGACAGATCTCTGTGGATATTTTGAACGGGATTCACAGATTTGAAA 456
DB	1476 ATTGGCGAGGAAGACAGATCTCTGTGGATATTTTGAACGGGATTCACAGATTTGAAA 1417
OY	457 TGAAGTCACAAAGGACATTTACCAATGAGAGGAAACAGAGAGAAATCTTGATGGCT 516
DB	1416 TGAAGTCACAAAGGACATTTACCAATGAGAGGAAACAGAGAGAAATCTTGATGGCT 1357
OY	517 TCACAGAATGCAACAACAAATGGAATACTGTGATGACATGAGGCGACCAAGCTGGG 576
DB	1356 TCACAGAATGCAACAACAAATGGAATACTGTGATGACATGAGGCGACCAAGCTGGG 1297
OY	577 GAGAGATTAACACAGGGGGCAGAGGATCAGGATTCCTGGCCCTGCTCTAACTGTGCGTT 636
DB	1296 GAGAGATTAACACAGGGGGCAGAGGATCAGGATTCCTGGCCCTGCTCTAACTGTGCGTT 1237
OY	637 CATTAACCAATTCATTTCTATTTCTTAACCTCAAACAAAGCGTGTGAATCTGCATCT 666

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DB      1236 CATAACCAATATTTATTTCTTAACCTCAAAACAAAGCTGTGTAATCTGATCT 1177
QY      697 CTACGGTTCCTTCTGGGCCCAACATTCCTCCATATATCCAGCCACACTCTTTTAATAT 756
DB      1176 CTACGGTTCCTTCTGGGCCCAACATTCCTCCATATATCCAGCCACACTCTTTTAATAT 1117
QY      757 TAGTCCCAAGATCTGTACTGTAGCTTCTTACACTGTAGATTAACATTAATCTATTTGTT 816
DB      1116 TAGTCCCAAGATCTGTACTGTAGCTTCTTACACTGTAGATTAACATTAATCTATTTGTT 1057
QY      817 CAAA 820
DB      1056 CAAA 1053

RESULT 15
AAH85118/c
ID      AAH85118 standard; cDNA; 2229 BP.
XX
AC      AAH85118;
XX
DT      25-SEP-2001 (first entry)
XX
DE      Human prostate-specific cDNA sequence P710P #2.
XX
KW      Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KM      chromosome 22q11.2; prostate-specific protein; chromosome 1;
KN      prostate specific antigen; PSA; ss.
XX
OS      Homo sapiens.
XX
PN      MO200134802-A2.
XX
PD      17-MAY-2001.
XX
PF      09-NOV-2000; 2000MO-US30904.
XX
PR      12-NOV-1999; 99US-0439313.
XX
PR      18-NOV-1999; 99US-0443686.
XX
PA      (CORI-) CORIXA CORP.
PI      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI      Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAM, Wang A;
DR      WPI; 2001-308785/32.
XX
PT      Isolated polypeptide comprising at least an immunogenic portion of a
PT      prostate-specific protein, useful in the diagnosis and therapy of
XX      prostate cancer
XX
PS      Claim 5; Page 283-284; 325pp; English.
XX
CC      The present invention describes an isolated polypeptide (P1) comprising
CC      at least an immunogenic portion of a prostate-specific protein, or its
CC      variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC      (N1) have cytostatic activity and can be used in vaccine production.
CC      The polypeptides, nucleic acids and antibodies from the present
CC      invention are useful in the diagnosis and therapy of prostate cancer.
CC      Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC      in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC      region. Prostate specific antigen (PSA) P501S was located on
CC      chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC      polynucleotide and polypeptide sequences used in the exemplification
CC      of the present invention.
XX
SQ      Sequence 2229 BP; 654 A; 447 C; 481 G; 647 T; 0 other;

```

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Query Match      88.3%; Score 724; DB 22; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      97 AGGTGAATAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG 156
DB      1776 AGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG 1717
QY      157 GAGATTAATTAACATCTACTGTAAGAAACAGCAAGATGACATTAATGTCTAAGTGTGACATG 216
DB      1716 GAGATTAATTAACATCTACTGTAAGAAACAGCAAGATGACATTAATGTCTAAGTGTGACATG 1657
QY      217 TTTTTCACATTTTCCGCCCCCTTTAATTAATTCACACACAGCAAGAAACAAAAGGAAGA 276
DB      1656 TTTTTCACATTTTCCGCCCCCTTTAATTAATTCACACACAGCAAGAAACAAAAGGAAGA 1597
QY      277 CAGAGATCCCTGGGAGAAATGCCCCGCCATCTTGGGTCAATGATGAGCCCTCGCCCTG 336
DB      1596 CAGAGATCCCTGGGAGAAATGCCCCGCCATCTTGGGTCAATGATGAGCCCTCGCCCTG 1537
QY      337 TGCTGTGTCCTCCGCTTGTGAGGAGAGACATTAAGAAATGAATTAATGTGTTCTTAAAG 396
DB      1536 TGCTGTGTCCTCCGCTTGTGAGGAGAGACATTAAGAAATGAATTAATGTGTTCTTAAAG 1477
QY      397 ATGGCGAGGAAAAACAGATCTGCTGTGATTTATTTGAAGGGATTAACAGATTGAAA 456
DB      1476 ATGGCGAGGAAAAACAGATCTGCTGTGATTTATTTGAAGGGATTAACAGATTGAAA 1417
QY      457 TGAAGTCACAAAAGTGAGCATTTACCAATGAGAGGAAAAACAGAGAAAAATCTTGATGCT 516
DB      1416 TGAAGTCACAAAAGTGAGCATTTACCAATGAGAGGAAAAACAGAGAAAAATCTTGATGCT 1357
QY      517 TCACAAGACATGCACAAAACAAAATGAATTAATCTGTATGACATGAGGACGCAAGCTGGG 576
DB      1356 TCACAAGACATGCACAAAACAAAATGAATTAATCTGTATGACATGAGGACGCAAGCTGGG 1297
QY      577 GAGGAGATTAACACAGGGGGCAGAGGGTCAGAGATTCGCGCCCTGCTCTAACTGTCGCT 636
DB      1296 GAGGAGATTAACACAGGGGGCAGAGGGTCAGAGATTCGCGCCCTGCTCTAACTGTCGCT 1237
QY      637 CATAACCAATCATTTTCATATTTCTTAACCTCAAAACAAAGCTGTGTAATTAATGATCT 696
DB      1236 CATAACCAATCATTTTCATATTTCTTAACCTCAAAACAAAGCTGTGTAATTAATGATCT 1177
QY      697 CTACGGTTCCTTCTGGGCCCAACATTCCTCCATATATCCAGCCACACTCTTTTAATAT 756
DB      1176 CTACGGTTCCTTCTGGGCCCAACATTCCTCCATATATCCAGCCACACTCTTTTAATAT 1117
QY      757 TAGTCCCAAGATCTGTACTGTAGCTTCTTACACTGTAGATTAACATTAATCTATTTGTT 816
DB      1116 TAGTCCCAAGATCTGTACTGTAGCTTCTTACACTGTAGATTAACATTAATCTATTTGTT 1057
QY      817 CAAA 820
DB      1056 CAAA 1053

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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:40:03 : Search time 47.0629 Seconds

(without alignments)
7690.430 Million cell updates/sec

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Perfect score: 820

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Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	812	99.0	812	4	US-09-439-313-471	Sequence 471, App
C 2	812	99.0	812	4	US-09-352-616A-471	Sequence 471, App
C 3	724	88.3	2229	4	US-09-439-313-469	Sequence 469, App
C 4	724	88.3	2229	4	US-09-352-616A-469	Sequence 469, App
C 5	724	88.3	2426	4	US-09-439-313-470	Sequence 470, App
C 6	724	88.3	2426	4	US-09-352-616A-470	Sequence 470, App
C 7	724	88.3	3112	4	US-09-439-313-468	Sequence 468, App
C 8	724	88.3	3112	4	US-09-352-616A-468	Sequence 468, App
C 9	257	31.3	718	4	US-09-439-313-313	Sequence 313, App
C 10	257	31.3	718	4	US-09-352-616A-313	Sequence 313, App
C 11	257	31.3	718	4	US-09-232-149A-313	Sequence 313, App
C 12	179	21.8	301	4	US-09-439-313-287	Sequence 287, App
C 13	179	21.8	301	4	US-09-352-616A-287	Sequence 287, App
C 14	179	21.8	301	4	US-09-232-149A-287	Sequence 287, App
C 15	2.4	1664976	4	US-08-916-421B-1	Sequence 1, App	
C 16	1.6	161	1	US-08-450-834-3	Sequence 3, App	
C 17	1.6	4527	2	US-08-944-449-8	Sequence 8, App	
C 18	1.6	4527	2	US-09-353-362-8	Sequence 8, App	
C 19	1.6	8930	4	US-09-077-098A-1	Sequence 1, App	
C 20	1.6	17000	4	US-09-679-299A-18	Sequence 18, App	
C 21	1.6	590	4	US-09-364-206-25	Sequence 25, App	
C 22	1.6	831	1	US-08-450-834-5	Sequence 5, App	
C 23	1.6	1017	4	US-09-328-475C-104	Sequence 104, App	
C 24	1.6	2920	3	US-08-976-259-10	Sequence 10, App	
C 25	1.6	3247	3	US-08-718-388-4	Sequence 4, App	
C 26	1.6	3661	3	US-08-718-388-5	Sequence 5, App	
C 27	1.6	3675	3	US-08-793-331-5	Sequence 5, App	

28	17	2.1	5128	4	US-09-364-206-1	Sequence 1, Appl1
29	17	2.1	6792	4	US-09-374-454-20	Sequence 20, Appl1
C 30	17	2.1	7824	3	US-08-718-388-6	Sequence 75, Appl1
C 31	17	2.1	13857	4	US-09-620-312D-75	Sequence 21, Appl1
C 32	17	2.1	15202	3	US-08-922-635-21	Sequence 8, Appl1
C 33	17	2.1	16382	3	US-08-718-388-8	Sequence 2, Appl1
C 34	17	2.1	36519	3	US-08-923-137-2	Sequence 3, Appl1
C 35	17	2.1	46718	4	US-09-816-093-3	Sequence 1, Appl1
C 36	17	2.1	64467	4	US-08-803-671B-3	Sequence 79, Appl1
C 37	17	2.1	164976	4	US-08-916-421B-1	Sequence 45, Appl1
C 38	16	2.0	20	4	US-09-705-299-79	Sequence 2419, Ap
C 39	16	2.0	51	3	US-09-046-247-45	Sequence 27, Appl1
C 40	16	2.0	89	2	US-08-379-482A-3	Sequence 27, Appl1
C 41	16	2.0	219	4	US-09-328-352-2419	Sequence 27, Appl1
C 42	16	2.0	430	1	US-08-466-033-27	Sequence 27, Appl1
C 43	16	2.0	430	1	US-08-444-733-27	Sequence 27, Appl1
C 44	16	2.0	430	2	US-08-464-134-27	Sequence 27, Appl1
C 45	16	2.0	430	2	US-08-461-361-27	Sequence 27, Appl1

ALIGNMENTS

RESULT 1						
US-09-439-313-471/c						
; Sequence 471, Application US/09439313						
; Patent No. 6329505						
; GENERAL INFORMATION:						
; APPLICANT: Xu, Jiangchun						
; APPLICANT: Dillon, David C.						
; APPLICANT: Mitcham, Jennifer L.						
; APPLICANT: Harlocker, Susan Louise						
; APPLICANT: Jiang Yuqun						
; APPLICANT: Reed, Steven G.						
; APPLICANT: Kalos, Michael						
; APPLICANT: Fanger, Gary						
; APPLICANT: Retter, Mark						
; APPLICANT: Solk, John						
; APPLICANT: Day, Craig						
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND						
; FILE REFERENCE: 210121.427C9						
; CURRENT APPLICATION NUMBER: US/09/439, 313						
; CURRENT FILING DATE: 1999-11-12						
; NUMBER OF SEQ ID NOS: 575						
; SOFTWARE: FastSeq for Windows Version 3.0						
; SEQ ID NO 471						
; LENGTH: 812						
; TYPE: DNA						
; ORGANISM: Homo sapiens						
US-09-439-313-471						
Query Match						
Best Local Similarity 99.0%; Score 812; DB 4; Length 812;						
Matches 812; Conservative 100.0%; Pred. No. 0;						
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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DB	812	CTGGCATCATGAAAAACAGAGGGGAGATTTGTGTGCTGCAGCCGAGGAGACAGAA	753			
QY	66	TCTGATGCTGGGAAGACCTGATATACAGAGGAGAAATTAAGAAAGCGCTGACCT	125			
DB	752	TCTGATGCTGGGAAGACCTGATATACAGAGGAGAAATTAAGAAAGCGCTGACCT	693			
QY	126	TACCATCTGAGGCCACACATCTGCTGAATATGAGATTAATTAACATCACTAGAACAGAA	185			
DB	692	TACCATCTGAGGCCACACATCTGCTGAATATGAGATTAATTAACATCACTAGAACAGAA	633			
QY	186	GATGCAATATATATCTCTAAGTAGACATGTTTGGACATTTCCAGCCCTTTAATA	245			
DB	632	GATGCAATATATATCTCTAAGTAGACATGTTTGGACATTTCCAGCCCTTTAATA	573			
QY	246	TCCACACACACAGAAAGCAAAAGAGACAGAGATCCCTGGGAGAAATGCCGGGCG	305			

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|||||
Db 572 TCCACACACAGAGAACACAAAAGAGACAGAGATCCCTGGAGAAAAGCCGGCCG 513
QY 306 CCATCTTGGGTCATCATGAGACCCCGCCCTGTGCTGCTCCGCTTGAGAGAGACA 365
Db 512 CCATCTTGGGTCATCATGAGACCCCGCCCTGTGCTGCTCCGCTTGAGAGAGACA 453
QY 366 TTGAAAATGAATGATGTGTTCTTAAAGAGTGGCAGAAAACAGATCCTGTGTGGA 425
Db 452 TTGAAAATGAATGATGTGTTCTTAAAGAGTGGCAGAAAACAGATCCTGTGTGGA 393
QY 426 TATTATTTGAAGGAGATTACAGATTGAATGAAGTACAAAGTGGAGCATTTACCAATGA 485
Db 392 TATTATTTGAAGGAGATTACAGATTGAATGAAGTACAAAGTGGAGCATTTACCAATGA 333
QY 486 GAGAAAACAGACAGAGAAAATCTTGATGCTTCCAAAGACATGCAACAAACAAATGAA 545
Db 332 GAGAAAACAGACAGAGAAAATCTTGATGCTTCCAAAGACATGCAACAAACAAATGAA 273
QY 546 TACTGTATGATGATGAGGACCCAGAGTGGGAGAGAAATACACCGGGGAGAGGTCAG 605
Db 272 TACTGTATGATGATGAGGACCCAGAGTGGGAGAGAAATACACCGGGGAGAGGTCAG 213
QY 606 GATTCGGCCCTGCTGCTAAACTGTGCTCATACCAATCATTTCTATTTCTAAC 665
Db 212 GATTCGGCCCTGCTGCTAAACTGTGCTCATACCAATCATTTCTATTTCTAAC 153
QY 666 CTCAAAACAAAGCTGTTGTAATATCTGATCTACAGGTTCCCTTGGGCCCAACATTC 725
Db 152 CTCAAAACAAAGCTGTTGTAATATCTGATCTACAGGTTCCCTTGGGCCCAACATTC 93
QY 726 CATATATCCAGCACACTCATTTTATATTTAGTCCAGAGTGTGACGTGACCTTC 785
Db 92 CATATATCCAGCACACTCATTTTATATTTAGTCCAGAGTGTGACGTGACCTTC 33
QY 786 TACACTGTAGATTAACATTAATCTCATTTTGTTC 817
Db 32 TACACTGTAGATTAACATTAATCTCATTTTGTTC 1

RESULT 2
US-09-352-616A-471/C
: Sequence 471, Application US/09352616A
: Patent No. 6395278
: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang, Yugu
: APPLICANT: Xu, Jiangchun
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: FILE REFERENCE: 210121.427C8
: CURRENT APPLICATION NUMBER: US/09/352,616A
: CURRENT FILING DATE: 1999-07-13
: NUMBER OF SEQ ID NOS: 472
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 471
: LENGTH: 812
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-352-616A-471

Query Match 99.0%; Score 812; DB 4; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTGGCATCAAAAAACAGAGGAGATTTGTGTGCTGCAGCCGAGGAGACAGAGAGA 65
Db 812 CTGGCATCAAAAAACAGAGGAGATTTGTGTGCTGCAGCCGAGGAGACAGAGAGA 753
QY 66 TCGCATGTGGGAGGAGCACTGATGATACAGAGGTGAATAAGAAAGCTGTGACTT 125
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Db 752 TCGCATGTGGGAGGAGCACTGATGATACAGAGGTGAGAAATAGAAAGGCTGTGACTT 693
QY 126 TACCATCTGAGGCGCCACATCTGCTGAAATGAGAGATATTAACATCACTAGAAACAGCAA 185
Db 692 TACCATCTGAGGCGCCACATCTGCTGAAATGAGAGATATTAACATCACTAGAAACAGCAA 633
QY 186 GATGACAAATATATGTCTAAGTAGTACATGTTTTTGCACATTTCCAGCCCTTTAAATA 245
Db 632 GATGACAAATATATGTCTAAGTAGTACATGTTTTTGCACATTTCCAGCCCTTTAAATA 573
QY 246 TCCACACACAGAGAACACAAAAGAGACAGAGATCCCTGGAGAAATGGCCGGCCG 305
Db 572 TCCACACACAGAGAACACAAAAGAGACAGAGATCCCTGGAGAAATGGCCGGCCG 513
QY 306 CCATCTTGGGTCATCATGAGACCCCGCCCTGTGCTGCTCCGCTTGAGAGAGACA 365
Db 512 CCATCTTGGGTCATCATGAGACCCCGCCCTGTGCTGCTCCGCTTGAGAGAGACA 453
QY 366 TTGAAAATGAATGATGTGTTCTTAAAGAGTGGCAGAAAACAGATCCTGTGTGGA 425
Db 452 TTGAAAATGAATGATGTGTTCTTAAAGAGTGGCAGAAAACAGATCCTGTGTGGA 393
QY 426 TATTATTTGAAGGAGATTACAGATTGAATGAAGTACAAAGTGGAGCATTTACCAATGA 485
Db 392 TATTATTTGAAGGAGATTACAGATTGAATGAAGTACAAAGTGGAGCATTTACCAATGA 333
QY 486 GAGAAAACAGACAGAGAAAATCTTGATGCTTCCAAAGACATGCAACAAACAAATGAA 545
Db 332 GAGAAAACAGACAGAGAAAATCTTGATGCTTCCAAAGACATGCAACAAACAAATGAA 273
QY 546 TACTGTATGATGATGAGGACCCAGAGTGGGAGAGAAATACACCGGGGAGAGGTCAG 605
Db 272 TACTGTATGATGATGAGGACCCAGAGTGGGAGAGAAATACACCGGGGAGAGGTCAG 213
QY 606 GATTCGGCCCTGCTGCTAAACTGTGCTCATACCAATCATTTCTATTTCTAAC 665
Db 212 GATTCGGCCCTGCTGCTAAACTGTGCTCATACCAATCATTTCTATTTCTAAC 153
QY 666 CTCAAAACAAAGCTGTTGTAATATCTGATCTACAGGTTCCCTTGGGCCCAACATTC 725
Db 152 CTCAAAACAAAGCTGTTGTAATATCTGATCTACAGGTTCCCTTGGGCCCAACATTC 93
QY 726 CATATATCCAGCACACTCATTTTATATTTAGTCCAGAGTGTGACGTGACCTTC 785
Db 92 CATATATCCAGCACACTCATTTTATATTTAGTCCAGAGTGTGACGTGACCTTC 33
QY 786 TACACTGTAGATTAACATTAATCTCATTTTGTTC 817
Db 32 TACACTGTAGATTAACATTAATCTCATTTTGTTC 1

RESULT 3
US-09-439-313-469/C
: Sequence 469, Application US/09439313
: Patent No. 6329505
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang Yugu
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael
: APPLICANT: Fanger, Gary
: APPLICANT: Retler, Mark
: APPLICANT: Solk, John
: APPLICANT: Day, Craig
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: FILE REFERENCE: 210121.427C9
: CURRENT APPLICATION NUMBER: US/09/439,313
: CURRENT FILING DATE: 1999-11-12
: NUMBER OF SEQ ID NOS: 575
```

QY	97	AGGAGAGAAATTAAGAAAGCGTGCATCTTTACATCTGAGGCCACACATCTGCTGAATG	156
Db	1776	AGGTGAGAAATTAAGAAAGCGTGCATCTTTACATCTGAGGCCACACATCTGCTGAATG	1711
QY	157	GAGATTAATTAACATCTACTAGAAACGCAAGATGACAAATATAATGTCTAAGTAGACATG	216
Db	1716	GAGATTAATTAACATCTACTAGAAACGCAAGATGACAAATATAATGTCTAAGTAGACATG	165
QY	217	TTTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGAAAGCACAAAAGAGCA	276
Db	1656	TTTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGAAAGCACAAAAGAGCA	1593
QY	277	CAGAGATCCCTGGGAGAAATGCCGCCGCCCATCTGGGTATCGATGAGCCTCGCCCTG	336
Db	1596	CAGAGATCCCTGGGAGAAATGCCGCCGCCCATCTGGGTATCGATGAGCCTCGCCCTG	1533
QY	337	TGCCTGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATTGATGTCTCTTAAAG	396
Db	1536	TGCCTGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATTGATGTCTCTTAAAG	1477
QY	397	ATGGGCGAGAAACAGATCCTGTGTGTGATATTTATTTGAACGGGATTTACAGATTTGAAA	456
Db	1476	ATGGGCGAGAAACAGATCCTGTGTGTGATATTTATTTGAACGGGATTTACAGATTTGAAA	1411
QY	457	TGAAGTCCAAAGTGAGCATTAACCAATGAGAGGAAACAGACAGAAATCTTGATGGCT	516
Db	1416	TGAAGTCCAAAGTGAGCATTAACCAATGAGAGGAAACAGACAGAAATCTTGATGGCT	1357
QY	517	TCACAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACGCCAAGCTGGG	576
Db	1356	TCACAAGACATGCAACAAACAAATGGAATCTGTGATGACATGAGGACGCCAAGCTGGG	1297
QY	577	GAGAGATTAACACGCGGGCAGAGGGTGCAGAAATCTGGGCCCTGCTCCCAACTGTGCGTT	636
Db	1296	GAGAGATTAACACGCGGGCAGAGGGTGCAGAAATCTGGGCCCTGCTCCCAACTGTGCGTT	1233
QY	637	CATAAACCAATCATATTCATATTTCTAACCCCTCAAAACAAAGCTGTTGAATATCGATCT	696
Db	1236	CATAAACCAATCATATTCATATTTCTAACCCCTCAAAACAAAGCTGTTGAATATCGATCT	1177
QY	697	CTACGGTTCCTTGTGGGCCAACAATCTCCATATATCCAGCCACACTCATTTTATAATTT	756
Db	1176	CTACGGTTCCTTGTGGGCCAACAATCTCCATATATCCAGCCACACTCATTTTATAATTT	1111
QY	757	TAGTTCACAGATCTGTACTGTGACCTTCTACAGCTGTGAATTAACATTAACATCTTCTGTT	816
Db	1116	TAGTTCACAGATCTGTACTGTGACCTTCTACAGCTGTGAATTAACATTAACATCTTCTGTT	1057
QY	817	CAAA 820	
Db	1056	CAAA 1053	

Sequence 470, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 470
LENGTH: 2426
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-470

Query Match 88.3%; Score 724; DB 4; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGGCCACACATCTGCTGAATG 156
DB 1770 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGGCCACACATCTGCTGAATG 1711
QY 157 GAGATAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTTAAGTAGACATG 216
DB 1710 GAGATAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTTAAGTAGACATG 1651
QY 217 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGAAAGCA 276
DB 1650 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGAAAGCA 1591
QY 277 CAGGATCCCTGGGAGAAATGCCCGGCCCATCTTTGGGTCATGATGAGCCCTGCCCTG 336
DB 1590 CAGGATCCCTGGGAGAAATGCCCGGCCCATCTTTGGGTCATGATGAGCCCTGCCCTG 1531
QY 337 TGCCTGGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGATGCTCTTAAGG 396
DB 1530 TGCCTGGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGATGCTCTTAAGG 1471
QY 397 ATGGCAGGAAACAGATCCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAA 456
DB 1470 ATGGCAGGAAACAGATCCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAA 1411
QY 457 TGAAGTACAAAGGACATTTACCATGAGAGGAAACAGACGAAATCTTGATGGCT 516
DB 1410 TGAAGTACAAAGGACATTTACCATGAGAGGAAACAGACGAAATCTTGATGGCT 1351
QY 517 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGGAGGCAAGCTGGG 576
DB 1350 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGGAGGCAAGCTGGG 1291
QY 577 GAGGAGATAACACAGGGGAGAGGCTGAGATTCCTGGCCCTGCTGCTAAACTGTGGCT 636
DB 1290 GAGGAGATAACACAGGGGAGAGGCTGAGATTCCTGGCCCTGCTGCTAAACTGTGGCT 1231
QY 637 CATTAACCAATCATTTATATTTCTAACCTCAAAAGAGCTGTTGATATATCTGATCT 696
DB 1230 CATTAACCAATCATTTATATTTCTAACCTCAAAAGAGCTGTTGATATATCTGATCT 1171
QY 697 CTACGGTCTCTGGGCCCAACATCTCATATATCAGCAACTCATTTTAATAT 756
DB 1171 CTACGGTCTCTGGGCCCAACATCTCATATATCAGCAACTCATTTTAATAT 1111

DB 1170 CTACGGTCTCTGGGCCCAACATCTCATATATCAGCAACTCATTTTAATAT 1111
QY 757 TAGTCCAGATCTGTACTGTGACCTTTTACACTGAGATAACATTAATCAATTTGTT 816
DB 1110 TAGTCCAGATCTGTACTGTGACCTTTTACACTGAGATAACATTAATCAATTTGTT 1051
QY 817 CAAA 820
DB 1050 CAAA 1047

RESULT 6
US-09-352-616A-470/C
Sequence 470, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Devin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 470
LENGTH: 2426
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616A-470

Query Match 88.3%; Score 724; DB 4; Length 2426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGGCCACACATCTGCTGAATG 156
DB 1770 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGGCCACACATCTGCTGAATG 1711
QY 157 GAGATAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTTAAGTAGACATG 216
DB 1710 GAGATAATTAACATCACTAGAAACAGCAAGATGACATATATATGCTTAAGTAGACATG 1651
QY 217 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGAAAGCA 276
DB 1650 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACAGCAAGCAAAAGAAAGCA 1591
QY 277 CAGGATCCCTGGGAGAAATGCCCGGCCCATCTTTGGGTCATGATGAGCCCTGCCCTG 336
DB 1590 CAGGATCCCTGGGAGAAATGCCCGGCCCATCTTTGGGTCATGATGAGCCCTGCCCTG 1531
QY 337 TGCCTGGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGATGCTCTTAAGG 396
DB 1530 TGCCTGGTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGATGCTCTTAAGG 1471
QY 397 ATGGCAGGAAACAGATCCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAA 456
DB 1470 ATGGCAGGAAACAGATCCTGTTGTGATATTTTGAACGGGATTAAGATTTGAAA 1411
QY 457 TGAAGTACAAAGGACATTTACCAATGAGAGGAAACAGACGAAATCTTGATGGCT 516
DB 1410 TGAAGTACAAAGGACATTTACCAATGAGAGGAAACAGACGAAATCTTGATGGCT 1351
QY 517 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGGAGGCAAGCTGGG 576
DB 1350 TCACAGACATGCAACAAACAAATGGAATACGTGTGATGACATGAGGAGGCAAGCTGGG 1291
QY 577 GAGGAGATAACACAGGGGAGAGGCTGAGATTCCTGGCCCTGCTGCTAAACTGTGGCT 636
DB 1290 GAGGAGATAACACAGGGGAGAGGCTGAGATTCCTGGCCCTGCTGCTAAACTGTGGCT 1231

QY 637 CATACCAATCATTTTCTATTTCTAACCCCTCAAAACAAAGCTGTGTATATCTGATCT 696
DB 1230 CATACCAATCATTTTCTATTTCTAACCCCTCAAAACAAAGCTGTGTATATCTGATCT 1171
QY 697 CTACGGTCTCTTGCGCCCAACATCTCATATATCCAGCCACACTCTTTTATATTT 756
DB 1170 CTACGGTCTCTTGCGCCCAACATCTCATATATCCAGCCACACTCTTTTATATTT 1111
QY 757 TAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTAATCTGATTT 816
DB 1110 TAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTAATCTGATTT 1051
QY 817 CAAA 820
DB 1050 CAAA 1047

RESULT 7
US-09-439-313-468
Sequence 468, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Rafter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-468

Query Match 88.3%; Score 724; DB 4; Length 3112;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG 156
DB 1312 AGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG 1371
QY 157 GAGATATTAACATCTAGAAACAGCAAGATGACATTAATAGTCTAGTGCATG 216
DB 1372 GAGATATTAACATCTAGAAACAGCAAGATGACATTAATAGTCTAGTGCATG 1431
QY 217 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGGAAGA 276
DB 1432 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGGAAGA 1491
QY 277 CAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGGGTGATGATGAGCTCGCCCTG 336
DB 1492 CAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGGGTGATGATGAGCTCGCCCTG 1551
QY 337 TGCTGTGCTCCGCTGTGAGGAAGACATTAAGAAATGAATGATGATGATGATGATG 396
DB 1552 TGCTGTGCTCCGCTGTGAGGAAGACATTAAGAAATGAATGATGATGATGATGATG 1611
QY 397 ATGGCAGGAGAAACAGATCTGTGATATTTATTTGACGGATACAGATTTGAAA 456
DB 1111

DB 1612 ATGGCAGGAGAAACAGATCTGTGATATTTATTTGACGGATACAGATTTGAAA 1671
QY 457 TGAAGTCACAAAGTAGCATTTACCAATGAGAGAGAAACAGACAGAGAAATCTTGATGCT 516
DB 1672 TGAAGTCACAAAGTAGCATTTACCAATGAGAGAGAAACAGACAGAGAAATCTTGATGCT 1731
QY 517 TCACAGACATGCAACAAACAAATGGAATACGTGATGATGATGATGATGATGATGATG 576
DB 1732 TCACAGACATGCAACAAACAAATGGAATACGTGATGATGATGATGATGATGATGATG 1791
QY 577 GAGGATATACACAGCGGGGAGAGGGTCAGAGATTTGCGCCCTGCTGCTTAACGTGCTG 636
DB 1792 GAGGATATACACAGCGGGGAGAGGGTCAGAGATTTGCGCCCTGCTGCTTAACGTGCTG 1851
QY 637 CATACCAATCATTTTCTATTTCTAACCCCTCAAAACAAAGCTGTGTATATCTGATCT 696
DB 1852 CATACCAATCATTTTCTATTTCTAACCCCTCAAAACAAAGCTGTGTATATCTGATCT 1911
QY 697 CTACGGTCTCTTGCGCCCAACATCTCATATATCCAGCCACACTCTTTTATATTT 756
DB 1912 CTACGGTCTCTTGCGCCCAACATCTCATATATCCAGCCACACTCTTTTATATTT 1971
QY 757 TAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTAATCTGATTT 816
DB 1972 TAGTCCAGATCTGTACTGTGACCTTTCTACACTGTAGAAATACATTAATCTGATTT 2031
QY 817 CAAA 820
DB 2032 CAAA 2035

RESULT 8
US-09-352-616A-468
Sequence 468, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616A-468

Query Match 88.3%; Score 724; DB 4; Length 3112;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG 156
DB 1312 AGGTGAGAAATAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG 1371
QY 157 GAGATATTAACATCTAGAAACAGCAAGATGACATTAATAGTCTAGTGCATG 216
DB 1372 GAGATATTAACATCTAGAAACAGCAAGATGACATTAATAGTCTAGTGCATG 1431
QY 217 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGGAAGA 276
DB 1432 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGAACACAAAAGGAAGA 1491
QY 277 CAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGGGTGATGATGAGCTCGCCCTG 336
DB 1492 CAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGGGTGATGATGAGCTCGCCCTG 1551

Qy	337	TGCGTGGTCCCGGCTT	TGAGGGAGAGACATTAA	AAATGAATGAGTGTCTTCTTAAGG	396
Db	1552	TGCGTGGTCCCGGCTT	TGAGGGAGAGACATTAA	AAATGAATGAGTGTCTTCTTAAGG	1611
Qy	397	ATGGGCGAGAAAACAGAT	CTCTGTGTGATATTTAT	TGACGGGATTACAGATTGAAA	456
Db	1612	ATGGGCGAGAAAACAGAT	CTCTGTGTGATATTTAT	TGACGGGATTACAGATTGAAA	1671
Qy	457	TGAAGTACAAAGT	GAGCATTTACCAATGAGAG	AAAAACAGACAGAAAAATCTTGATGGCT	516
Db	1672	TGAAGTACAAAGT	GAGCATTTACCAATGAGAG	AAAAACAGACAGAAAAATCTTGATGGCT	1731
Qy	517	TCACAAGACATGCAACAA	AAAAATGGAATACGTATG	ATGATGAGGGCCGACCAACCTGGG	576
Db	1732	TCACAAGACATGCAACAA	AAAAATGGAATACGTATG	ATGATGAGGGCCGACCAACCTGGG	1791
Qy	577	GAGAGATTAACCAAGGGG	CAGAGGATTCAGGATTCGG	CCCTGCTTAACTGTCGCTT	636
Db	1792	GAGAGATTAACCAAGGGG	CAGAGGATTCAGGATTCGG	CCCTGCTTAACTGTCGCTT	1851
Qy	637	CATTAACCAATTCATTTCAT	TTTCTTAACCTCAAAA	CAAAAGCTGTTGTAATCTGATCT	696
Db	1852	CATTAACCAATTCATTTCAT	TTTCTTAACCTCAAAA	CAAAAGCTGTTGTAATCTGATCT	1911
Qy	697	CTACGGTTCCTTGGGGCC	CAACATTCCTCATATATAC	AGCAACCTCATTTTATATNT	756
Db	1912	CTACGGTTCCTTGGGGCC	CAACATTCCTCATATATAC	AGCAACCTCATTTTATATNT	1971
Qy	757	TAGTTCAGATCTGTACTGT	AGCTTTCTACACTGTAGAT	TAACATTAATCTATTTTCTT	816
Db	1972	TAGTTCAGATCTGTACTGT	AGCTTTCTACACTGTAGAT	TAACATTAATCTATTTTCTT	2031
Qy	817	CAAA 820			
Db	2032	CAAA 2035			
RESULT 9					
US-09-439-313-313					
: Sequence 313, Application US/09439313					
: Patent No. 6329505					
: GENERAL INFORMATION:					
: APPLICANT: Xu, Jianshun					
: APPLICANT: Dillon, Davin C.					
: APPLICANT: Mitcham, Jennifer L.					
: APPLICANT: Harlocker, Susan Louise					
: APPLICANT: Jiang, Yuyu					
: APPLICANT: Reed, Steven G.					
: APPLICANT: Kalos, Michael					
: APPLICANT: Fanger, Gary					
: APPLICANT: Retler, Mark					
: APPLICANT: Solk, John					
: APPLICANT: Day, Craig					
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND					
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER					
: FILE REFERENCE: 210121.427C9					
: CURRENT APPLICATION NUMBER: US/09/439,313					
: CURRENT FILING DATE: 1999-11-12					
: NUMBER OF SEQ ID NOS: 575					
: SOFTWARE: FastSeq for Windows Version 3.0					
: SEQ ID NO 313					
: LENGTH: 718					
: TYPE: DNA					
: ORGANISM: Homo sapien					
: FEATURE:					
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: OTHER INFORMATION: n = A,T,C or G					
: US-09-439-313-313					
Query Match					
Best Local Similarity 31.3%; Score 257; DB 4; Length 718;					
: 99.4%; Pred. No. 3,1e-125;					

RESULT 12
US-09-439-313-287/c
Sequence 287, Application US/09439313
Patent No 6329605
GENERAL INFORMATION:
APPLICANT: Xu, Jlangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Hatclough, Susan Louise

	Query Match	Similarity	Score	DB	Length
Best Local	229	99.6%	179	301	
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				Indels	0
				Gaps	0
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Db	301	AGCATTTACCATGAGAGGAAAAACAGACGAGAAATCTTGATGGCTTCCACAGACATGCCA	242		
OY	532	CAAAACAAAATGGAACTACTGTGATGATGACATGAGAGGCCCAAGCTGGGGAGAGAAATCAACCG	591		

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Db      241 CAAACAAAATGAACTGATGATACATGAGCAGCACCAGCTGGGAGAGATTAACACAG 182
Oy      592 GGGCAGAGGCTCAGGATCTGGCCCTGCTGCTAAAGCTGGCTCATTAACCAATCTTT 651
Db      181 GGGCAGAGGCTCAGGATCTGGCCCTGCTGCTAAAGCTGGCTCATTAACCAATCTTT 122
Oy      652 TCATATTTCTAACCTCAAAACAAAGCTGTTGTAATATCTGATCTCTACG 701
Db      121 TCATATTTCTAACCTCAAAACAAAGCTGTTGTAATATCTGATCTCTACG 72

RESULT 14
US-09-232-149A-287/c
; Sequence 287, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427c6
; CURRENT APPLICATION NUMBER: US/09/232.149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 287
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-287

Query Match      21.8%; Score 179; DB 4; Length 301;
Best Local Similarity 99.6%; Pred. No. 2.8e-84;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      472 AGCATTTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCTTCAACAGATGCAA 531
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Oy      532 CAAACAAAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 591
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Oy      592 GGGCAGAGGCTCAGGATCTGGCCCTGCTGCTAAAGCTGCTTCAATTAACCAATCATTT 651
Db      181 GGGCAGAGGCTCAGGATCTGGCCCTGCTGCTAAAGCTGCTTCAATTAACCAATCATTT 122
Oy      652 TCATATTTCTAACCTCAAAACAAAGCTGTTGTAATATCTGATCTCTACG 701
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RESULT 15
US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916.421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
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US-08-916-421B-1

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Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 51.0629 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:44:18 : Search time 190.028 Seconds
(without alignments)
10742.554 Million cell updates/sec

Title: US-09-402-713a-4

Perfect score: 820

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Searched: 1678620 seqs, 1244745471 residues

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Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	820	100.0	876	11 US-09-957-708-3	Sequence 3, Appli
2	812	99.0	812	9 US-09-759-143-471	Sequence 471, App
3	812	99.0	812	9 US-09-780-669-471	Sequence 471, App
4	812	99.0	812	9 US-09-822-827-471	Sequence 471, App
5	812	99.0	812	10 US-09-895-793-471	Sequence 471, App
6	812	99.0	812	10 US-09-895-814-471	Sequence 471, App
7	812	99.0	812	12 US-10-144-678A-471	Sequence 471, App
8	812	99.0	812	13 US-10-012-896-471	Sequence 471, App
9	812	99.0	812	14 US-10-010-940-471	Sequence 471, App
10	724	88.3	2229	9 US-09-759-143-469	Sequence 469, App
11	724	88.3	2229	9 US-09-780-669-469	Sequence 469, App
12	724	88.3	2229	9 US-09-822-827-469	Sequence 469, App
13	724	88.3	2229	10 US-09-895-793-469	Sequence 469, App
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15	724	88.3	2229	12 US-10-144-678A-469	Sequence 469, App
16	724	88.3	2229	13 US-10-012-896-469	Sequence 469, App

C 17	724	88.3	2229	14 US-10-010-940-469	Sequence 469, App
C 18	724	88.3	2426	9 US-09-759-143-470	Sequence 470, App
C 19	724	88.3	2426	9 US-09-780-669-470	Sequence 470, App
C 20	724	88.3	2426	9 US-09-822-827-470	Sequence 470, App
C 21	724	88.3	2426	10 US-09-895-793-470	Sequence 470, App
C 22	724	88.3	2426	10 US-09-895-814-470	Sequence 470, App
C 23	724	88.3	2426	13 US-10-144-678A-470	Sequence 470, App
C 24	724	88.3	2426	13 US-10-012-896-470	Sequence 470, App
C 25	724	88.3	2426	14 US-10-010-940-470	Sequence 470, App
C 26	724	88.3	2426	14 US-10-205-823-448	Sequence 448, App
C 27	724	88.3	3112	9 US-09-759-143-468	Sequence 468, App
C 28	724	88.3	3112	9 US-09-780-669-468	Sequence 468, App
C 29	724	88.3	3112	9 US-09-822-827-468	Sequence 468, App
C 30	724	88.3	3112	10 US-09-895-793-468	Sequence 468, App
C 31	724	88.3	3112	10 US-09-895-814-468	Sequence 468, App
C 32	724	88.3	3112	12 US-10-144-678A-468	Sequence 468, App
C 33	724	88.3	3112	13 US-10-012-896-468	Sequence 468, App
C 34	724	88.3	3112	14 US-10-010-940-468	Sequence 468, App
C 35	723	88.2	3923	9 US-09-759-143-690	Sequence 690, App
C 36	723	88.2	3923	9 US-09-780-669-690	Sequence 690, App
C 37	723	88.2	3923	9 US-09-822-827-690	Sequence 690, App
C 38	723	88.2	3923	10 US-09-895-793-690	Sequence 690, App
C 39	723	88.2	3923	10 US-09-895-814-690	Sequence 690, App
C 40	723	88.2	3923	12 US-10-144-678A-690	Sequence 690, App
C 41	723	88.2	3923	13 US-10-012-896-690	Sequence 690, App
C 42	723	88.2	3923	14 US-10-205-823-316	Sequence 316, App
C 43	473	57.7	597	12 US-10-195-730-46	Sequence 46, Appl
C 44	467	57.0	1102	14 US-10-198-846-11000	Sequence 11000, A
C 45	287	35.0	4097	12 US-09-814-353-20144	Sequence 20144, A

ALIGNMENTS

RESULT 1					
US-09-957-708-3					
: Sequence 3, Application US/09957708					
: Publication No. US20030031678A1					
GENERAL INFORMATION:					
: APPLICANT: Sun, Yongming					
: APPLICANT: Recipon, Hervé					
: APPLICANT: Cafferey, Robert					
: APPLICANT: Ali, Shujath					
: TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific					
: TITLE OF INVENTION: Genes					
: FILE REFERENCE: DEX-0239					
: CURRENT APPLICATION NUMBER: US/09/957,708					
: PRIOR FILING DATE: 2001-09-19					
: PRIOR APPLICATION NUMBER: 60/233,746					
: PRIOR FILING DATE: 2000-09-19					
: NUMBER OF SEQ ID NOS: 40					
: SOFTWARE: Patentin Ver. 2.1					
: SEQ ID NO 3					
: LENGTH: 876					
: TYPE: DNA					
: ORGANISM: Homo sapiens					
US-09-957-708-3					
Query Match					
Best Local Similarity 100.0%; Score 820; DB 11; Length 876;					
Matches 820; Conservative 0; Mismatch 0; Indels 0; Gaps 0;					
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QY	121	GACTTACCATCTGAGGCCACACATCTGCTGAATGAGATTAATTAACATCACTAGAAAC	180		
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QY 481 AATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
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QY 541 TGGAAATCTGTGATGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
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RESULT 2
: Sequence 471, Application us/09759143
: Patent No. US20020022248A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jlangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jlang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hegler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C23
: CURRENT APPLICATION NUMBER: US/09/759,143
: CURRENT FILING DATE: 2001-01-12

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: NUMBER OF SEQ ID NOS: 934
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 471
: LENGTH: 812
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-759-143-471

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Query Match 99.0%; Score 812; DB 9; Length 812;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 752 TCTGCATGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 693
QY 126 TACCATCTGAGGCGCACATCTGCTGAAATGAGATTAATTAACATCACTAGAAACAGCAA 185
Db 692 TACCATCTGAGGCGCACATCTGCTGAAATGAGATTAATTAACATCACTAGAAACAGCAA 633
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Db 632 GATGACAAATATATGTCTAAGTAGTACATGTTTTTGCACATTTCCAGCCCTTTAAATA 573
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Db 452 TTGAGAAATGAATGATGTGTTCTTAAAGATGGGAGGAGGAGGAGGAGGAGGAGGAGG 393
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Db 272 TACTGTATGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 213
QY 606 GATCTGCGCCCTGCTGCTAAAGCTGCTGCTCAATTAACCAATCATTTTCAATTTCTAAC 665
Db 212 GATCTGCGCCCTGCTGCTAAAGCTGCTGCTCAATTAACCAATCATTTTCAATTTCTAAC 153
QY 666 CTCAAAAACAAGCTGTTGTAATATCTGATCTGATGCTGCTGCTGCTGCTGCTGCTGCT 725
Db 152 CTCAAAAACAAGCTGTTGTAATATCTGATCTGATGCTGCTGCTGCTGCTGCTGCTGCT 93
QY 726 CATATATCCAGCCACACATCTTTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 785
Db 92 CATATATCCAGCCACACATCTTTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 33
QY 786 TACACTGTAGATTAACATTTACTATTTTGTTC 817
Db 32 TACACTGTAGATTAACATTTACTATTTTGTTC 1

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RESULT 3
: Sequence 471, Application us/09780669
: Patent No. US20020051977A1

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/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Ketter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darriick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skelky, Yasir A.W.
/ APPLICANT: Hepler, William
/ APPLICANT: Hural, John
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Houghton, Raymond L.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C24
/ CURRENT APPLICATION NUMBER: US/09/780,669
/ CURRENT FILING DATE: 2001-02-09
/ NUMBER OF SEQ ID NOS: 943
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 471
/ LENGTH: 812
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-780-669-471
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Query Match          99.0%; Score 812; DB 9; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGGAGACCAGAGAA 65
DB      812 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGGAGACCAGAGAA 753
QY      66 TCTGCATGTTGGGAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 125
DB      752 TCTGCATGTTGGGAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 693
QY      126 TACCATCTGAGGCCACACATCTGCTGAATGAGATATTTAACTACTAGAAACAGCAA 185
DB      692 TACCATCTGAGGCCACACATCTGCTGAATGAGATATTTAACTACTAGAAACAGCAA 633
QY      186 GATGCAATATATATGCTAAGTAGACATGTTTTGCACTTCCAGCCCTTTAAATA 245
DB      632 GATGCAATATATATGCTAAGTAGACATGTTTTGCACTTCCAGCCCTTTAAATA 573
QY      246 TCCACACACACAGAAAGCAAAAGAGACACAGAGATCCCTGGGAGAAATGCCGCGCG 305
DB      572 TCCACACACACAGAAAGCAAAAGAGACACAGAGATCCCTGGGAGAAATGCCGCGCG 513
QY      306 CCATCTTGGGTCATGATGAGCTCGCCCTGTGCTGCTGCCGCTTGTGAGGGAAGGACA 365
DB      512 CCATCTTGGGTCATGATGAGCTCGCCCTGTGCTGCTGCCGCTTGTGAGGGAAGGACA 453
QY      366 TTAGAAATATGATATGATGCTTCTTAAAGATGGGCAAGAAACAGATCTGTTGTGA 425
DB      452 TTAGAAATATGATATGATGCTTCTTAAAGATGGGCAAGAAACAGATCTGTTGTGA 393
QY      426 TATTTTATGAAGGGATTAAGATTTGAATGAAGTCAAAAGTGAAGATTACCAATGA 485
DB      392 TATTTTATGAAGGGATTAAGATTTGAATGAAGTCAAAAGTGAAGATTACCAATGA 333
QY      486 GAGGAAACAGACGAGAAATCTGTATGCTTCACAAAGACATGCAACAAACAAATATGAA 545
DB      332 GAGGAAACAGACGAGAAATCTGTATGCTTCACAAAGACATGCAACAAACAAATATGAA 273
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QY      546 TACTGTGATGATGAGGACGCAAGCTGGGAGAGGATTAACAGGGGACAGGCTCAG 605
DB      272 TACTGTGATGATGAGGACGCAAGCTGGGAGAGGATTAACAGGGGACAGGCTCAG 213
QY      606 GATTCGGCCCTGCTGCTTAACCTGATGCTTATATAACCAATCATTTCTATTTCTAAC 665
DB      212 GATTCGGCCCTGCTGCTTAACCTGATGCTTATATAACCAATCATTTCTATTTCTAAC 153
QY      666 CTCAAAACAAAGCTGTTGAATATGATCTCTAGCGTTCCTTGGGCCCAACATCTTC 725
DB      152 CTCAAAACAAAGCTGTTGAATATGATCTCTAGCGTTCCTTGGGCCCAACATCTTC 93
QY      726 CATATATCCAGCACACATCTATTTATATTTAGTTCCTCCAGATTCCTACTGACCTTTC 785
DB      92 CATATATCCAGCACACATCTATTTATATTTAGTTCCTCCAGATTCCTACTGACCTTTC 33
QY      786 TACACTGTAGAAATTAACATTAATCTCATTTTGTTC 817
DB      32 TACACTGTAGAAATTAACATTAATCTCATTTTGTTC 1
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RESULT 4
US-09-822-827-471/c
/ Sequence 471, Application US/09822827
/ Patent No. US20020081680A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.534C1
/ CURRENT APPLICATION NUMBER: US/09/822,827
/ CURRENT FILING DATE: 2001-03-28
/ NUMBER OF SEQ ID NOS: 982
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 471
/ LENGTH: 812
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-822-827-471
```

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Query Match          99.0%; Score 812; DB 9; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGGAGACCAGAGAA 65
DB      812 CTGGCATCAGAAAAACAGAGGGAGATTGTGTGCTGCAGCCGAGGGAGACCAGAGAA 753
QY      66 TCTGCATGTTGGGAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 125
DB      752 TCTGCATGTTGGGAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 693
QY      126 TACCATCTGAGGCCACACATCTGCTGAATGAGATATTTAACTACTAGAAACAGCAA 185
DB      692 TACCATCTGAGGCCACACATCTGCTGAATGAGATATTTAACTACTAGAAACAGCAA 633
QY      186 GATGCAATATATATGCTAAGTAGACATGTTTTGCACTTCCAGCCCTTTAAATA 245
DB      632 GATGCAATATATATGCTAAGTAGACATGTTTTGCACTTCCAGCCCTTTAAATA 573
QY      246 TCCACACACACAGAAAGCAAAAGAGACACAGAGATCCCTGGGAGAAATGCCGCGCG 305
DB      572 TCCACACACACAGAAAGCAAAAGAGAGACACAGAGATCCCTGGGAGAAATGCCGCGCG 513
QY      306 CCATCTTGGGTCATGATGAGCTCGCCCTGTGCTGCTGCCGCTTGTGAGGGAAGGACA 365
DB      512 CCATCTTGGGTCATGATGAGCTCGCCCTGTGCTGCTGCCGCTTGTGAGGGAAGGACA 453
QY      366 TTAGAAATATGATATGATGCTTCTTAAAGATGGGCAAGAAACAGATCTGTTGTGA 425
DB      452 TTAGAAATATGATATGATGCTTCTTAAAGATGGGCAAGAAACAGATCTGTTGTGA 393
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OY	446	TATTTATTTGAACGGGATTTACAGATTTTGAATGAAGTCAACAAAGTGAAGATTTCCAAATGA	485
Db	392	TATTTATTTGAACGGGATTTACAGATTTTGAATGAAGTCAACAAAGTGAAGATTTCCAAATGA	333
OY	486	GAGGAAAACAGACGAGAAAATCTTGATGGCTTCACAAAGCATGTCAACAAACAAATGGAA	545
Db	332	GAGGAAAACAGACGAGAAAATCTTGATGGCTTCACAAAGCATGTCAACAAACAAATGGAA	273
OY	546	TACTGTGATGACATAGACGACCCAAAGCTGGGAGAGATTAACACGGGCGAGAGGTCAG	605
Db	272	TACTGTGATGACATAGAGCGACCAAGCTGGGAGAGAGATTAACACAGGGGCGAGGTCAG	213
OY	606	GATTTGGCCCGTCGCTAAACCTGGGCTCATATAACCAATCATTTCAATTTCTTAACC	665
Db	212	GATTTGGCCCGTCGCTAAACCTGGGCTCATATAACCAATCATTTCAATTTCTTAACC	153
OY	666	CTCAAAACAAAGCTTTGTAAATATGTGATCTCTACGGTCTCTCTGGGCCCAACATTCTC	725
Db	152	CTCAAAACAAAGCTTTGTAAATATGTGATCTCTACGGTCTCTCTGGGCCCAACATTCTC	93
OY	726	CATATATCCAGCCACACTCATTTTAAATATTAATTAAGTCCAGATCTGTACTGTGACCTTTC	785
Db	92	CATATATCCAGCCACACTCATTTTAAATATTAATTAAGTCCAGATCTGTACTGTGACCTTTC	33
OY	786	TACACTGTAGATAATACATTACTCATTTTGTTC	817
Db	32	TACACTGTAGATAATACATTACTCATTTTGTTC	1

RESULT 5

US-09-895-793-471/c
; Sequence 471, Application US/09895793

Publication NO. US20020192763A1
; GENERAL INFORMATION:

```

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Ajun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 471
LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
S-09-895-793-471

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Query Match	99.0%	Score 812:	DB 10:	Length 812:
Best Local Similarity	100.0%	Pred. NO. 0:		
Matches 812: Conservative	0:	Mismatches	0:	Gaps 0:

QY	6	CTGGCATCAGAAAAACAGAGGGAGATTGTGTGGCGCCAGCCGAGGAGACAGGAA	65
Db	812	CTGGATCAGAAAAACAGAGGGAGATTGTGTGGCGCCAGCCGAGGAGACAGGAA	75
QY	66	TCTGCATGTGTGGAGGACCTGATGATACAGAGGTGGAAATTAAGAAAGGCTGTGACTT	12
QY	126	TACCATCTGAGGCCACACACATCTGCTGAATGAGATATTAACATCCTAGAAACAGCA	18
Db	692	TACCATCTGAGGCCACACATCTGCTGAATGAGATATTAACATCCTAGAAACAGCA	63
QY	186	GATCACAATATAATGTCTAAGTAGTGTGATGTTTGGACATTTCCAGCCCTTTAAATA	24
Db	632	GATCACAATATAATGTCTAAGTAGTGTGATGTTTGGACATTTCCAGCCCTTTAAATA	57
QY	246	TCCACACACACAGAGAACACAAAAAGAGCAGAGATCCCTGGAGAAATCCCGCGC	30
Db	572	TCCACACACACAGAGAACACAAAAAGAGCAGAGATCCCTGGAGAAATCCCGCGC	51
QY	306	CCATCTTGGGTCATCGATGAGCCTCGCCCTGTGCTGGTCCGCTTGTGAGGAAAGACA	36
Db	512	CCATCTTGGGTCATCGATGAGCCTCGCCCTGTGCTGGTCCGCTTGTGAGGAAAGACA	45
QY	366	TTAAGAAATGAATGTATGTCTTCCTTAAAGATGGGACGAAAAACAGATCTGTTGTGA	42
Db	452	TTAAGAAATGAATGTATGTCTTCCTTAAAGATGGGACGAAAAACAGATCTGTTGTGA	39
QY	426	TATTTATTTGACGGGATTACAGATTTGAAATGAAGTCACAAAAGTAGCATTTACCAATGA	48
Db	392	TATTTATTTGACGGGATTACAGATTTGAAATGAAGTCACAAAAGTAGCATTTACCAATGA	33
QY	486	GAGAAAAACAGAGAGAAAAATCTTGATGGCTTACAAAGCATGTGCAACAAACAAATGGA	54
Db	332	GAGAAAAACAGAGAGAAAAATCTTGATGGCTTACAAAGCATGTGCAACAAACAAATGGA	27
QY	546	TACGTGATGATGAGGACAGCCAGCTGGGGAGAGATTAACCCAGGGCCAAAGGTCAG	60
Db	272	TACGTGATGATGAGGACAGCCAGCTGGGGAGAGATTAACCCAGGGCCAAAGGTCAG	21
QY	606	GATTCGTGGCCCTGCTGACTTAACGTGTGCTTCAATTAACCAATCTTCAATTTCAAC	66
Db	212	GATTCGTGGCCCTGCTGACTTAACGTGTGCTTCAATTAACCAATCTTCAATTTCAAC	15
QY	666	CTCAAAACAAGCGTGTATATATCGATCTCAGAGTTCCTTGGGCCCAACATTCG	72
Db	152	CTCAAAACAAGCGTGTGTATATCTGATCTCAGAGTTCCTTGGGCCCAACATTCG	93
QY	726	CATATATCCAGCCACACTATTTTATAATTTAGTCCAGATCTGTACTGTGACCTTTC	78
Db	92	CATATATCCAGCCACACTATTTTATAATTTAGTCCAGATCTGTACTGTGACCTTTC	33
QY	786	TACACTGTAGATTAACATTTACTATTTTGTTC	817
Db	32	TACACTGTAGATTAACATTTACTATTTTGTTC	1

RESULT 6

US-09-895-814-471/c
; Sequence 471, Application US/09895814

Publication No. US20020193296A1
; GENERAL INFORMATION:

1. APPLICANT: Xu, Jiangchun
2. APPLICANT: Dillon, Davin C.
3. APPLICANT: Hitchcock, Jennifer L.
4. APPLICANT: Harlock, Susan L.
5. APPLICANT: Jiang, Yugu
6. APPLICANT: Kalos, Michael D.
7. APPLICANT: Retter, Marc W.
8. APPLICANT: Stolk, John A.
9. APPLICANT: Day, Craig H.
10. APPLICANT: Vedvyck, Thomas S.
11. APPLICANT: Carter, Darriek

```

; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepier, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-471

Query Match          99.0%; Score 812; DB 10; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGCTGCAGCCGAGGAGACAGAGAA 65
DB 812 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGCTGCAGCCGAGGAGACAGAGAA 753
OY 66 TCTGCATGTGGGAAAGACCTGATATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 125
DB 752 TCTGCATGTGGGAAAGACCTGATATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 693
OY 126 TACCATCTGAGGCCACACATCTGCTGAATGGAGATTAATTAACATCAGTAAAGCA 185
DB 692 TACCATCTGAGGCCACACATCTGCTGAATGGAGATTAATTAACATCAGTAAAGCA 633
OY 186 GATGACAATATATATGTCTAAGTAGTACATGTTTGGCATTTCAGCCCTTTAAATA 245
DB 632 GATGACAATATATATGTCTAAGTAGTACATGTTTGGCATTTCAGCCCTTTAAATA 573
OY 246 TCCACACACACAGAGAACCAAAAGAGACACAGAGATCCCTGGGAAATGCCGCGC 305
DB 572 TCCACACACACAGAGAACCAAAAGAGACACAGAGATCCCTGGGAAATGCCGCGC 513
OY 306 CCATCTGGGTCATGATGATGAGCTGCGCCCTGTGCTGCTGCCGCTTGTGAGGGAAGACA 365
DB 512 CCATCTGGGTCATGATGATGAGCTGCGCCCTGTGCTGCTGCCGCTTGTGAGGGAAGACA 453
OY 366 TTAGAANAATGAATGTATGTCTCTTAAAGATGGGCAAGAAACAGATCCTGTTGTGA 425
DB 452 TTAGAANAATGAATGTATGTCTCTTAAAGATGGGCAAGAAACAGATCCTGTTGTGA 393
OY 426 TATTTATTTTGAACGGGATTAACAGATTGAATGAAGTCAAAAGTAGAGCATTAACCAATGA 485
DB 392 TATTTATTTTGAACGGGATTAACAGATTGAATGAAGTCAAAAGTAGAGCATTAACCAATGA 333
OY 486 GAGGAAAACAGACGAGAAAATCTTGATGGCTTCAAGACATGCAAAACAAATGGA 545
DB 332 GAGGAAAACAGACGAGAAAATCTTGATGGCTTCAAGACATGCAAAACAAATGGA 273
OY 546 TACTGTGATGATGATGAGGAGCCAGCTGGGAGAGATTAACAGGAGGAGAGGAGTCA 605
DB 272 TACTGTGATGATGATGAGGAGCCAGCTGGGAGAGATTAACAGGAGGAGAGGAGTCA 213
OY 606 GATTTCGGCCCTGCTGCTTAACTGTGCTTATTAACCAATATTTTCAATTTCAACC 665
DB 212 GATTTCGGCCCTGCTGCTTAACTGTGCTTATTAACCAATATTTTCAATTTCAACC 153
OY 666 CTCAAAACAAAGCTGTGTATATATCTGATCTCTAGGGTCTCTTGGGGCCCAACATCTGC 725
```

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DB 152 CTCAAAACAAAGCTGTGTATATCTGATCTCTAGGTTCTTGGGGCCCAACATCTGC 93
OY 726 CATATATCCAGCCACACATCTTTTAATATTTAGTTCACAGATCTGTACTGTGACCTTC 785
DB 92 CATATATCCAGCCACACATCTTTTAATATTTAGTTCACAGATCTGTACTGTGACCTTC 33
OY 786 TACACTGTGATTAACATTAATCTTTTCTTC 817
DB 32 TACACTGTGATTAACATTAATCTTTTCTTC 1

RESULT 7
US-10-144-678A-471/C
; Sequence 471, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepier, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-471

Query Match          99.0%; Score 812; DB 12; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGCTGCAGCCGAGGAGACAGAGAA 65
DB 812 CTGGCATCAGAAAAACAGAGGGGAGATTGTGTGCTGCAGCCGAGGAGACAGAGAA 753
OY 66 TCTGCATGTGGGAAAGACCTGATATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 125
DB 752 TCTGCATGTGGGAAAGACCTGATATACAGAGGTGAGAAATTAAGAAAGCTGCTGACTT 693
OY 126 TACCATCTGAGGCCACACATCTGCTGAATGGAGATTAATTAACATCAGTAAAGCA 185
DB 692 TACCATCTGAGGCCACACATCTGCTGAATGGAGATTAATTAACATCAGTAAAGCA 633
OY 186 GATGACAATATATATGTCTAAGTAGTACATGTTTGGCATTTCAGCCCTTTAAATA 245
DB 632 GATGACAATATATATGTCTAAGTAGTACATGTTTGGCATTTCAGCCCTTTAAATA 573
```


US-10-010-940-471/c
; Sequence 471, Application US/10010940
; Publication No. US2003008062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Marc
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-940-471

Query Match 99.0%; Score 812; DB 14; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CTGGCATCGAAGAAACAGAGGAGATTTGTGTGCTGCGACCCGAGGGAGACAGAGA 65
DB 812 CTGGCATCGAAGAAACAGAGGAGATTTGTGTGCTGCGACCCGAGGGAGACAGAGA 753
QY 66 TCTGCATGTGGGAAGGACCTGATGATACAGAGGTGAGAAATTAAGAAAGGCTGCTACTT 125
DB 752 TCTGCATGTGGGAAGGACCTGATGATGATGAGAGGTGAGAAATTAAGAAAGGCTGCTACTT 693
QY 126 TACCATCTGAGGCGACACATCTGCTGAAATGAGATTAATTAACATCTAGAAACAGCAA 185
DB 692 TACCATCTGAGGCGACACATCTGCTGAAATGAGATTAATTAACATCTAGAAACAGCAA 633
QY 186 GATGACATATATATGCTCTAAGTAGACATGTTTTGACATTTCCAGCCCTTTAAATA 245
DB 632 GATGACATATATATGCTCTAAGTAGACATGTTTTGACATTTCCAGCCCTTTAAATA 573
QY 246 TCCACACACAGGAAGCAAAAGGAGACACAGAGATCCCTGGGGAATGCCGGCG 305
DB 572 TCCACACACAGGAAGCAAAAGGAGACACAGAGATCCCTGGGGAATGCCGGCG 513
QY 306 CCATCTGGGTCATGATGAGGCTGCCCTGTGCTGCTGCCGCTTGTAGGGAAGGACA 365
DB 512 CCATCTGGGTCATGATGAGGCTGCCCTGTGCTGCTGCCGCTTGTAGGGAAGGACA 453
QY 366 TTAGAAATGAATGATGCTGCTTCTTAAGATGGGACAGAAACAGATCCTGTTGCA 425
DB 452 TTAGAAATGAATGATGCTGCTTCTTAAGATGGGACAGAAACAGATCCTGTTGCA 393
QY 426 TTTTATTTGAAGGGATTAAGATTTGAATGAATTCACAAAGTAGATTAACCAATGA 485
DB 392 TTTTATTTGAAGGGATTAAGATTTGAATGAATTCACAAAGTAGATTAACCAATGA 333
QY 486 GAGGAAACAGAGGAAATCTTGATGCTTACAAAGACATGCAACAAACAAATGAA 545
DB 332 GAGGAAACAGAGGAAATCTTGATGCTTACAAAGACATGCAACAAACAAATGAA 273
QY 546 TACTGTGATGATGAGGACAGCCAGCTGGGAGAGATTAACACGGGAGAGGCTGAG 605
DB 272 TACTGTGATGATGAGGACAGCCAGCTGGGAGAGATTAACACGGGAGAGGCTGAG 213
QY 606 GATTCGGCCCTGCTCCTAAACTGTGCTTATTAACCAATCATTTCTTAAC 665

|||||
DB 212 GATTCGGCCCTGCTCCTAAACTGTGCTTATTAACCAATCATTTCTTAAC 153
QY 666 CTCGAAACAAAGCTGTTGTAATATCTGATCTAGCGTTCCTTGGGCCCAACATTC 725
DB 152 CTCGAAACAAAGCTGTTGTAATATCTGATCTAGCGTTCCTTGGGCCCAACATTC 93
QY 726 CATATATCCAGCCACACTATTTTAATATTTAGTCCAGATCTGACTGACCTTC 785
DB 92 CATATATCCAGCCACACTATTTTAATATTTAGTCCAGATCTGACTGACCTTC 33
QY 786 TACACTGTAGAAATTAACATTAATTTGTTTC 817
DB 32 TACACTGTAGAAATTAACATTAATTTGTTTC 1

RESULT 10

US-09-759-143-469/c
; Sequence 469, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Solk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-469

Query Match 88.3%; Score 724; DB 9; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTGGAATTAAGAAAGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 156
DB 1776 AGGTGGAATTAAGAAAGCTGCTGACTTTACATCTGAGGCCACACATCTGCTGAATG 1717
QY 157 GAGATTAATTAACCTACTGAAACAGCAAGATGACAAATTAATGCTTAAGTAGTGCATG 216
DB 1716 GAGATTAATTAACCTACTGAAACAGCAAGATGACAAATTAATGCTTAAGTAGTGCATG 1657
QY 217 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAAACACAAAAAGGAAGA 276
DB 1656 TTTTTCACATTTCCAGCCCTTTAAATATCCACACACAGGAAACACAAAAAGGAAGA 1597
QY 277 CAGAGATCCCTGGGAAATATGCCGGCCGCACTTGGGTGATCCATGAGCCTCGCCCTG 336
DB 1596 CAGAGATCCCTGGGAAATATGCCGGCCGCACTTGGGTGATCCATGAGCCTCGCCCTG 1537
QY 337 TGCCTGTCGCCCTTGTGAGGAGACATTAAGAAATGAATGATGCTTCTTAAAG 396
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	Query Match	Similarity	88.3%; Score 724;	DB 9;	Length 2229;
	Batches	Local Similarity	100.0%; Pred. No. 0;	Mismatches 0; Indels 0; Gaps 0;	
QY	. 97	AGGTGACAAATAAACAAGGGCTGCTGACTTTTACATTCGTGAGGCCACACATCTGCTGAATG	156		
Db	1776	AGGTGACAAATAAACAAGGGCTGCTGACTTTTACATTCGTGAGGCCACACATCTGCTGAATG	1717		
QY	157	GAGATTAATTACATCTAGTACAAACAGAACAATGCAATATATATGTCTTAGTAGTGACATG	216		
Db	1716	GAGATTAATTACATCTAGTACAAACAGAACAATGCAATATATATGTCTTAGTAGTGACATG	1657		
QY	217	TTTTTGACATTTCCAGCCCTTTAAATATCCACACACAGGAAGAACAAAAGSAGCA	276		
Db	1556	TTTTTGACATTTCCAGCCCTTTAAATATCCACACACAGGAAGAACAAAAGSAGCA	1597		
QY	277	CAGAGATCCCTGGGAGAAATGCCCCCGCCCATCTTGGTGCATGATGAGCCTCGCCCTG	336		
Db	1596	CAGAGATCCCTGGGAGAAATGCCCCCGCCCATCTTGGTGCATGATGAGCCTCGCCCTG	1537		
QY	337	TGCTGTGTCCTGCTTTGAGGGAAGACATTTAGAAAAATGAATTGATGTCTTTAAAG	396		
Db	1536	TGCTGTGTCCTGCTTTGAGGGAAGACATTTAGAAAAATGAATTGATGTCTTTAAAG	1477		
QY	397	ATGGGCGAGAAACAGATCCCTGTGTGATTTATTTGAACGGGATTTACAGATTTGAA	456		
Db	1476	ATGGGCGAGAAACAGATCCCTGTGTGATTTATTTGAACGGGATTTACAGATTTGAA	1417		
QY	457	TGAAGTACAAAGGTGACATTTACCATGAGAGGAAAAACAGACGAGAAATCTTGATGGCT	516		
Db	1416	TGAAGTACAAAGGTGACATTTACCATGAGAGGAAAAACAGACGAGAAATCTTGATGGCT	1357		
QY	517	TCACACACATGCAACAACAAATGGAATTCGTGATGACATGAGCGACCAAGCTGGG	576		
Db	1356	TCACACACATGCAACAACAAATGGAATTCGTGATGACATGAGCGACCAAGCTGGG	1297		
QY	577	GAGAGATTAACCAAGGGGGAGAGGGTGAAGATTTGGCCCGCTTAAACGTGGGCT	636		
Db	1296	GAGAGATTAACCAAGGGGGAGAGGGTGAAGATTTGGCCCGCTTAAACGTGGGCT	1237		
QY	637	CATTAACCAAATCATTTTATATTTTAAACCCCAAAACAAAGCTTTGTAATATCTGATCT	696		
Db	1236	CATTAACCAAATCATTTTATATTTTAAACCCCAAAACAAAGCTTTGTAATATCTGATCT	1177		
QY	697	CTACGGTTCCCTGTGGGCCCAACATTCATATATCCAGCCACATCTATTTTAATATT	756		
Db	1176	CTACGGTTCCCTGTGGGCCCAACATTCATATATCCAGCCACATCTATTTTAATATT	1117		
QY	757	TAGTCCCAGATCTGTACTGTGACCTTTCTACACTGTAGAATAATTAATTAATCTTTGTT	816		
Db	1116	TAGTCCCAGATCTGTACTGTGACCTTTCTACACTGTAGAATAATTAATTAATCTTTGTT	1057		
QY	817	CAAA 820			
Db	1056	CAAA 1053			
RESULT 12					
US-09-822-827-469/c					
Sequence 469, Application US/09822827					
Patent No. US20020081680A1					
GENERAL INFORMATION:					
APPLICANT: Xu, Jiangchun					
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND					
FILE REFERENCE: 210121.534C1					
CURRENT APPLICATION NUMBER: US/09/822,827					
NUMBER OF SEQ ID NOS: 982					
SOFTWARE: FastSeq for Windows Version 3.0					
SEQ ID NO 469					
LENGTH: 2229					
TYPE: DNA					

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; ORGANISM: Homo sapiens
US-09-822-827-469

Query Match      88.3%; Score 724; DB 9; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  97 AGGTAGAAATTAAGAAAGGCTGTGACTTACCATCTGTAGGCGCACATCTGCTGAAG 156
    |||||||
DB  1776 AGGTAGAAATTAAGAAAGGCTGTGACTTACCATCTGTAGGCGCACATCTGCTGAAG 1717
QY  157 GAGATTAATTAATCACTAGTAAGAACAGCAAGATGACATTAATTAATGCTAGTGCATG 216
    |||||||
DB  1716 GAGATTAATTAATCACTAGTAAGAACAGCAAGATGACATTAATTAATGCTAGTGCATG 1657
QY  217 TTTTTCGACATTTCCAGCCCTTTAAATATCCACACACACAGAGAAACACAAAGAAAGA 276
    |||||||
DB  1656 TTTTTCGACATTTCCAGCCCTTTAAATATCCACACACACAGAGAAACACAAAGAAAGA 1597
QY  277 CAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGGTCAATCCATGAGCCTCGCCCTG 336
    |||||||
DB  1596 CAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGGTCAATCCATGAGCCTCGCCCTG 1537
QY  337 TCCCTGATCCCTGTGAGGAGAGACATTAAGAAATGATGATGCTTCTCTTAAAG 396
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DB  1536 TCCCTGATCCCTGTGAGGAGAGACATTAAGAAATGATGATGCTTCTCTTAAAG 1477
QY  397 ATGGCAGGAAACAGATCTGTGTGATATTTATTTGACGGGATTAACAGATTTGAAA 456
    |||||||
DB  1476 ATGGCAGGAAACAGATCTGTGTGATATTTATTTGACGGGATTAACAGATTTGAAA 1417
QY  457 TGAAGTCACAAAGTAGAGCTTACCAATGAGAGAAACAGAGAAATCTTGATGGCT 516
    |||||||
DB  1416 TGAAGTCACAAAGTAGAGCTTACCAATGAGAGAAACAGAGAAATCTTGATGGCT 1357
QY  517 TCACAAGACATGCAACAACAAATGATGATGATGATGATGATGATGATGATGATGATG 576
    |||||||
DB  1356 TCACAAGACATGCAACAACAAATGATGATGATGATGATGATGATGATGATGATG 1297
QY  577 GAGGAGATTAACCAAGGGGAGAGAGGTCAGGATTTGGCCCTGCTTAACTGTGCGTT 636
    |||||||
DB  1296 GAGGAGATTAACCAAGGGGAGAGAGGTCAGGATTTGGCCCTGCTTAACTGTGCGTT 1237
QY  637 CATTAACCAATTAATTTCAATTTCAACCTCAAAACAAAGCTGTGTAATTCGATCT 696
    |||||||
DB  1236 CATTAACCAATTAATTTCAATTTCAACCTCAAAACAAAGCTGTGTAATTCGATCT 1177
QY  697 CTACGGTTCCTCTGGGCCCAACATTTCCATATATCCAGCCACACTATTTTAAATTT 756
    |||||||
DB  1176 CTACGGTTCCTCTGGGCCCAACATTTCCATATATCCAGCCACACTATTTTAAATTT 1117
QY  757 TAGTTCACAGATCTGTACTGTGACCTTTTACACGTGTAGATTAACATTAATTTGTT 816
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DB  1116 TAGTTCACAGATCTGTACTGTGACCTTTTACACGTGTAGATTAACATTAATTTGTT 1057
QY  817 CAAA 820
    |||||
DB  1056 CAAA 1053

RESULT 13
US-09-895-793-469/c
; Sequence 469, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
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; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Ajun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-469

Query Match      88.3%; Score 724; DB 10; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  97 AGGTAGAAATTAAGAAAGGCTGTGACTTACCATCTGTAGGCGCACATCTGCTGAAG 156
    |||||||
DB  1776 AGGTAGAAATTAAGAAAGGCTGTGACTTACCATCTGTAGGCGCACATCTGCTGAAG 1717
QY  157 GAGATTAATTAATCACTAGTAAGAACAGCAAGATGACATTAATTAATGCTAGTGCATG 216
    |||||||
DB  1716 GAGATTAATTAATCACTAGTAAGAACAGCAAGATGACATTAATTAATGCTAGTGCATG 1657
QY  217 TTTTTCGACATTTCCAGCCCTTTAAATATCCACACACACAGAGAAACACAAAGAAAGA 276
    |||||||
DB  1656 TTTTTCGACATTTCCAGCCCTTTAAATATCCACACACACAGAGAAACACAAAGAAAGA 1597
QY  277 CAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGGTCAATCCATGAGCCTCGCCCTG 336
    |||||||
DB  1596 CAGAGATCCCTGGGAGAAATGCCCGCCCATCTTGGGTCAATCCATGAGCCTCGCCCTG 1537
QY  337 TCCCTGATCCCTGTGAGGAGAGACATTAAGAAATGATGATGATGATGATGATGATGATG 396
    |||||||
DB  1536 TCCCTGATCCCTGTGAGGAGAGACATTAAGAAATGATGATGATGATGATGATGATGATG 1477
QY  397 ATGGCAGGAAACAGATCTGTGTGATATTTATTTGACGGGATTAACAGATTTGAAA 456
    |||||||
DB  1476 ATGGCAGGAAACAGATCTGTGTGATATTTATTTGACGGGATTAACAGATTTGAAA 1417
QY  457 TGAAGTCACAAAGTAGAGCTTACCAATGAGAGAAACAGAGAAATCTTGATGGCT 516
    |||||||
DB  1416 TGAAGTCACAAAGTAGAGCTTACCAATGAGAGAAACAGAGAAATCTTGATGGCT 1357
QY  517 TCACAAGACATGCAACAACAAATGATGATGATGATGATGATGATGATGATGATGATG 576
    |||||||
DB  1356 TCACAAGACATGCAACAACAAATGATGATGATGATGATGATGATGATGATGATG 1297
QY  577 GAGGAGATTAACCAAGGGGAGAGAGGTCAGGATTTGGCCCTGCTTAACTGTGCGTT 636
    |||||||
DB  1296 GAGGAGATTAACCAAGGGGAGAGAGGTCAGGATTTGGCCCTGCTTAACTGTGCGTT 1237
QY  637 CATTAACCAATTAATTTCAATTTCAACCTCAAAACAAAGCTGTGTAATTCGATCT 696
    |||||||
DB  1236 CATTAACCAATTAATTTCAATTTCAACCTCAAAACAAAGCTGTGTAATTCGATCT 1177
QY  697 CTACGGTTCCTCTGGGCCCAACATTTCCATATATCCAGCCACACTATTTTAAATTT 756
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Db 1176 CTAGGTTCTTGGGCCCAACATCTCCATATATCCAGCCACACTATTTTAAATTT 1117
Qy 757 TAGTCCCGAGATCTGTACTGTGACCTTTCTACACTGTAGAATAACATTACTCATTTTGT 816
Db 1116 TAGTCCCGAGATCTGTACTGTGACCTTTCTACACTGTAGAATAACATTACTCATTTTGT 1057
Qy 817 CAAA 820
Db 1056 CAAA 1053

RESULT 14
US-09-895-814-469/C
; Sequence 469, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895, 814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-469

Query Match 88.3%; Score 724; DB 10; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 AGGTGAATAATTAAGAAAGCGTCGCTGACTTACCATCTGAGGCCACACATCTGCTGAATG 156
Db 1776 AGGTGAATAATTAAGAAAGCGTCGCTGACTTACCATCTGAGGCCACACATCTGCTGAATG 1717
Qy 157 GAGATAATTAACATCACTAGAACAGACAGATGACATATATATCTTAAGTAGATG 216
Db 1716 GAGATAATTAACATCACTAGAACAGACAGATGACATATATATCTTAAGTAGATG 1657
Qy 217 TTTTTCGACATTTTCAGCCCTTTAAATATCCACACACAGAAAGCAAAAGAGCA 276
Db 1656 TTTTTCGACATTTTCAGCCCTTTAAATATCCACACACAGAAAGCAAAAGAGCA 1597
Qy 277 CAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCTGCCCTG 336
Db 1596 CAGAGATCCCTGGAGAAATGCCCGGCCCATCTTGGGTCATGATGAGCCTGCCCTG 1537
Qy 337 TGCGTGGTCCCGCTTGAGAGGAAGACATTAGAAATGATGATGTTCTCTTAAGG 396
Db 1116 TGCGTGGTCCCGCTTGAGAGGAAGACATTAGAAATGATGATGTTCTCTTAAGG 396
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Db 1536 TGCGTGGTCCCGCTTGAGAGGAAGACATTAGAAATGATGATGTTCTCTTAAGG 1477
Qy 397 ATGGCAGAGAAACAGATCTGTGTGTGATATTTATTTGAACGGGATTAACAGATTGAAA 456
Db 1476 ATGGCAGAGAAACAGATCTGTGTGTGATATTTATTTGAACGGGATTAACAGATTGAAA 1417
Qy 457 TGAGTCAAAATGAGCATTAACATGAGAGAAACAGACAGAAATCTTGATGCT 516
Db 1416 TGAGTCAAAATGAGCATTAACATGAGAGAAACAGACAGAAATCTTGATGCT 1357
Qy 517 TCACAGACATGCAACAAACAAATGAAATCTGTGATGATGAGGAGGCAAGCTGGG 576
Db 1356 TCACAGACATGCAACAAACAAATGAAATCTGTGATGATGAGGAGGCAAGCTGGG 1297
Qy 577 GAGGATTAACACAGGGGACAGAGGTCAGATTTCTGGCCCTGCTTAACTGTGCTT 636
Db 1296 GAGGATTAACACAGGGGACAGAGGTCAGATTTCTGGCCCTGCTTAACTGTGCTT 1237
Qy 637 CATACCAATATTTCTATTTCTTAACCTCAAAACAAAGCTGTTGTAATCTGATCT 696
Db 1236 CATACCAATATTTCTATTTCTTAACCTCAAAACAAAGCTGTTGTAATCTGATCT 1177
Qy 697 CTAGGTTCTTCTGGGCCCAACATTTCTCATATATCCAGCCACACTATTTTAAATTT 756
Db 1176 CTAGGTTCTTCTGGGCCCAACATTTCTCATATATCCAGCCACACTATTTTAAATTT 1117
Qy 757 TAGTCCCGAGATCTGTACTGTGACCTTTCTACACTGTAGAATAACATTACTCATTTTGT 816
Db 1116 TAGTCCCGAGATCTGTACTGTGACCTTTCTACACTGTAGAATAACATTACTCATTTTGT 1057
Qy 817 CAAA 820
Db 1056 CAAA 1053

RESULT 15
US-10-144-678A-469/C
; Sequence 469, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Gary R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 2229
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TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-469

Query Match 88.3%; Score 724; DB 12; Length 2229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 97 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG 156
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Db 1776 AGGTGAGAAATTAAGAAAGGCTGCTGACTTTACCATCTGAGGCCACACATCTGCTGAATG 1717
QY 157 GAGATATTAACATACATCTGAAGAACGACATGACATATTAATGCTAAGTAGTGACATG 216
    |||||||
Db 1716 GAGATATTAACATACATCTGAAGAACGACATGACATATTAATGCTAAGTAGTGACATG 1657
QY 217 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACACAGAGACACAAAAGAGCA 276
    |||||||
Db 1656 TTTTGGACATTTCCAGCCCTTTAAATATCCACACACACAGAGACACAAAAGAGCA 1597
QY 277 CAGAGATCCCTGGAGAAATGCCCGGCCCACTTTGGGTCAATGATGAGCCTCGCCCTG 336
    |||||||
Db 1596 CAGAGATCCCTGGAGAAATGCCCGGCCCACTTTGGGTCAATGATGAGCCTCGCCCTG 1537
QY 337 TGCCTGTGCTCCGCTGTGAGGAGGACATTAAGAAATGAATTAATGATGTGCTTAAAG 396
    |||||||
Db 1536 TGCCTGTGCTCCGCTGTGAGGAGGACATTAAGAAATGAATTAATGATGTGCTTAAAG 1477
QY 397 ATGGCGAGGAAACAGATCCTGTGTGATATTTATTTGACGGATTAACAGATTTGAAA 456
    |||||||
Db 1476 ATGGCGAGGAAACAGATCCTGTGTGATATTTATTTGACGGATTAACAGATTTGAAA 1417
QY 457 TGAAGTCACAAAGTGAGCATTTACCAATGAGAGAAACAGACAGAAAACTTTGATGCT 516
    |||||||
Db 1416 TGAAGTCACAAAGTGAGCATTTACCAATGAGAGAAACAGACAGAAAACTTTGATGCT 1357
QY 517 TCACAAGACATGCAACAAACAAATGAGATACGTGATGACATGAGGCCAAGCTGGG 576
    |||||||
Db 1356 TCACAAGACATGCAACAAACAAATGAGATACGTGATGACATGAGGCCAAGCTGGG 1297
QY 577 GAGGAGATTAACGAGGGGAGAGGGTCAGGATTTGCCCCCTGCTGAACGTGCGTT 636
    |||||||
Db 1296 GAGGAGATTAACGAGGGGAGAGGGTCAGGATTTGCCCCCTGCTGAACGTGCGTT 1237
QY 637 CATTAACCAATCATTTCAATTTCTAACCTCAAAAAGCTGTTGTAATCTGATCT 696
    |||||||
Db 1236 CATTAACCAATCATTTCAATTTCTAACCTCAAAAAGCTGTTGTAATCTGATCT 1177
QY 697 CTACGGTTCCTTCTGGGGCCCAACATCTCCATATATTCAGCCACACTCAATTTTAATTT 756
    |||||||
Db 1176 CTACGGTTCCTTCTGGGGCCCAACATCTCCATATATTCAGCCACACTCAATTTTAATTT 1117
QY 757 TAGTTCACAGATCTGACTGTGACCTTTCTACACTGTAGAAATACATTAATCTGTTTGT 816
    |||||||
Db 1116 TAGTTCACAGATCTGACTGTGACCTTTCTACACTGTAGAAATACATTAATCTGTTTGT 1057
QY 817 CAAA 820
    ||||
Db 1056 CAAA 1053
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Job time : 192.028 secs

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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:39:38 ; Search time 1720.81 Seconds
(without alignments)
11581.589 Million cell updates/sec

Title: US-09-402-713a-4

Perfect score: 820
Sequence: 1 agaagctgcatcagaagaa.....cattactcatttgcacaa 820

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlinu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
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14: gb_est5:*
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17: em_gss_hum:*
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19: em_gss_pln:*
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21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
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25: em_gss_rpd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	44.8	402	9	AA578773
2	238	29.0	290	9	AA578773
3	213	26.0	332	10	BF373619
4	199	24.3	226	10	BF858286

Result No.	Score	Query Match	Length	DB ID	Description
5	198	24.1	282	10	BF373581
6	167	20.4	167	10	BF373406
7	103	12.6	394	28	AQ206972
8	100	12.2	572	13	BQ292550
9	86	10.5	657	10	AI557495
10	22	2.7	349	10	BE904264
11	22	2.7	569	13	BQ836203
12	22	2.7	804	10	BG119805
13	21	2.6	334	28	A2418181
14	21	2.6	416	28	AQ712816
15	21	2.6	416	29	B2292184
16	21	2.6	484	28	BH072026
17	21	2.6	666	28	BZ007435
18	20	2.4	54	28	A2306177
19	20	2.4	336	9	AV552477
20	20	2.4	480	14	T43985
21	20	2.4	539	9	AV553868
22	20	2.4	547	28	A2812467
23	20	2.4	565	9	AV881136
24	20	2.4	571	29	B2630161
25	20	2.4	575	13	BM185716
26	20	2.4	575	29	B2630159
27	20	2.4	577	29	B2630476
28	20	2.4	597	29	B2630479
29	20	2.4	601	13	BM143969
30	20	2.4	603	29	CNS02108
31	20	2.4	605	13	BM110589
32	20	2.4	617	14	CB003211
33	20	2.4	626	13	BM253300
34	20	2.4	632	13	BM093085
35	20	2.4	632	14	CB004149
36	20	2.4	643	13	BM094987
37	20	2.4	645	13	BM135051
38	20	2.4	645	13	BM165500
39	20	2.4	647	13	BM143965
40	20	2.4	652	9	AV871969
41	20	2.4	656	13	BM119156
42	20	2.4	658	13	BU742900
43	20	2.4	659	14	CA345815
44	20	2.4	661	9	AV983992
45	20	2.4	669	9	AV850520

ALIGNMENTS

RESULT 1
AA578773
LOCUS
DEFINITION
AA578773
ACCESION
AA578773
VERSION
AA578773.1
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

402 bp mRNA linear EST 12-SEP-1997
nh24a04.s1 NCI-CGAP_Prl Homo sapiens CDNA clone IMAGE:953262, mRNA
sequence.
GI:2356957
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/cigap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.
, Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html

Insert Length: 565 Std Error: 0.00
 Seq primer: -40m13 fwd. EP from Amersham
 High quality sequence stop: 373.
 Location/Qualifiers

FEATURES

SOURCE

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1..402
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    /db_xref="taxon:9606"
    /clone="IMAGE:953262"
    /sex="Male"
    /dev_stage="45 years old"
    /lab_host="DH10B"
    /clone_lib="NCL-CGAP_Pri1"
    /note="Vector: PAMP10; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected, histologically normal prostate
epithelial cells. Double-stranded cDNA was ligated to
EcoRI adaptors, 5 cycles of PCR applied to the cDNA with
an adaptor-specific primer, and the resulting PCR product
subcloned into PAMP10 by the UDG-cloning method (Life
Technologies). Average insert size is 600 bp. NOTE: Not
directionally cloned. This library was constructed by
David Krizman."

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BASE COUNT 128 a 86 c 84 g 104 t
 ORIGIN

Query Match 44.8%; Score 367; DB 9; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4e-180;
 Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 430 TATTTGAACGGGATTACAGATTGTAATGAAGTCACAAAGTGAGCATTACCAATGAGAGG 489
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Db 36 TATTTGAACGGGATTACAGATTGTAATGAAGTCACAAAGTGAGCATTACCAATGAGAGG 95
OY 490 AAAACAGACGAGAAATCTGATGCTCACAAGACATGCAAAACAAATGGAAATCT 549
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Db 96 AAAACAGACGAGAAATCTGATGCTCACAAGACATGCAAAACAAATGGAAATCT 155
OY 550 GTGATGACATGAGCGACGCAAGCTGGGGAGAGATTAACACGCGGCGAGAGGTCAGAGATT 609
    |||||||
Db 156 GTGATGACATGAGCGACGCAAGCTGGGGAGAGATTAACACGCGGCGAGAGGTCAGAGATT 215
OY 610 CTGGCCCTGCTGCTTAAACTGTGGTCTATTAACCAATCATTTTCTTAACCTCA 669
    |||||||
Db 216 CTGGCCCTGCTGCTTAAACTGTGGTCTATTAACCAATCATTTTCTTAACCTCA 275
OY 670 AAAAAGAGCTGTGTAATATCTGANTCTAGCTTCCCTTGGGGCCCAACATTCCTCA 729
    |||||||
Db 276 AAAAAGAGCTGTGTAATATCTGANTCTAGCTTCCCTTGGGGCCCAACATTCCTCA 335
OY 730 TATCCAGCCACATCATTTTAAATATTTAGTCCAGATCTGTAAGCTGACCTTCTACA 789
    |||||||
Db 336 TATCCAGCCACATCATTTTAAATATTTAGTCCAGATCTGTAAGCTGACCTTCTACA 395
OY 790 CTGTAGA 796
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Db 396 CTGTAGA 402

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RESULT 2

BF373619

LOCUS BF373619 290 bp mRNA linear EST 24-NOV-2000
 DEFINITION MR0-FT0175-310800-106-n09 FT0175 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF373619
 VERSION BF373619.1 GI:11335644
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 290)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

TITLE Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.G.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

PUBMED

10737800

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?rl=MR06t2-MR0-FT0175-310800-106-h09&rt=2000-08-31&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 290.
 Location/Qualifiers

FEATURES

SOURCE

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    /db_xref="taxon:9606"
    /dev_stage="Adult"
    /clone_lib="FT0175"
    /note="Organ: prostate,tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

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BASE COUNT 78 a 73 c 53 g 86 t
 ORIGIN

Query Match 29.0%; Score 238; DB 10; Length 290;
 Best Local Similarity 100.0%; Pred. No. 8.5e-113;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 575 GGGAGGAGATTAACACGCGGCGAGAGGTCAGAGATTGCGCTGCTCTAACTGTGCG 634
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Db 21 GGGAGGAGATTAACACGCGGCGAGAGGTCAGAGATTGCGCTGCTCTAACTGTGCG 80
OY 635 TTCAATACCAATCATTTTCAATATTTCTAACCTCAAAACAAAGCTGTTGTAATCTGAT 694
    |||||||
Db 81 TTCAATACCAATCATTTTCAATATTTCTAACCTCAAAACAAAGCTGTTGTAATCTGAT 140
OY 695 CTCAGGCTTCCTTGGGGCCCAACATTCCTCATATATCCAGCCACACTCATTTTATA 754
    |||||||
Db 141 CTCAGGCTTCCTTGGGGCCCAACATTCCTCATATATCCAGCCACACTCATTTTATA 200
OY 755 TTTAGTCCAGATCTGACTGTGACCTTTCTACAGCTGTAAGTAATTAATCAATTT 812
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Db 201 TTTAGTCCAGATCTGACTGTGACCTTTCTACAGCTGTAAGTAATTAATCAATTT 258

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RESULT 3

BF858286

LOCUS BF858286 332 bp mRNA linear EST 16-JAN-2001
 DEFINITION RC5-FT0193-201100-012-D06 FT0193 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF858286
 VERSION BF858286.1 GI:12246030
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 332)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL
MEDLINE
20202663
PUBMED
10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-FT0193-201100-012-D06&t3=2000-11-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 332.

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0193"
/note="Organ: prostate-tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
90 a 84 c 64 g 94 t

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 1e-99; Length 332;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 GGAGGAGATTAACACGCGGCGAGAGGTCAGATTCTGGCCCTGCTCAAACTGTGCGT 635
|||||
DB 61 GGAGGAGATTAACACGCGGCGAGAGGTCAGATTCTGGCCCTGCTCAAACTGTGCGT 120
QY 636 TCATTAACCAATCATTTTCATATTTTCAACCCCTCAAAACAAGCTGTTGAATATCTGATC 695
|||||
DB 121 TCATTAACCAATCATTTTCATATTTTCAACCCCTCAAAACAAGCTGTTGAATATCTGATC 180
QY 636 TCTAGGTTCTCTTGGGCGCAACATTCATATATCCAGCCACACATCTTTTAATAT 755
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DB 181 TCTAGGTTCTCTTGGGCGCAACATTCATATATCCAGCCACACATCTTTTAATAT 240
QY 756 TTAGTTCCAGATCTGTACTGTGACCTTTCTAC 788
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DB 241 TTAGTTCCAGATCTGTACTGTGACCTTTCTAC 273

RESULT 4
BF858371/c 226 bp mRNA linear EST 16-JAN-2001
LOCUS
DEFINITION
RC5-FT0193-211100-012-E11 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF858371 GI:12246115
VERSION
BF858371.1
KEYWORDS
EST.
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 226)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL
MEDLINE
20202663
PUBMED
10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-FT0193-211100-012-E11&t3=2000-11-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 226.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0193"
/note="Organ: prostate-tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
79 a 29 c 59 g 59 t

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-92; Length 226;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 622 CCTAAACGTGGGTCATTAACCAATCATTTGATATTTCTAACCCCTCAAAACAAGCTGT 681
|||||
DB 226 CCTAAACGTGGGTCATTAACCAATCATTTGATATTTCTAACCCCTCAAAACAAGCTGT 167
QY 682 TGTAAATATGATCTCTAGGTTCTCTTGGGCGCAACATTCATATATCCAGCCACA 741
|||||
DB 166 TGTAAATATGATCTCTAGGTTCTCTTGGGCGCAACATTCATATATCCAGCCACA 107
QY 742 CTCATTTTAAATTTAGTCCAGATCTGTAAGCTGTGACCTTTCTACACTGTAGATAAC 801
|||||
DB 106 CTCATTTTAAATTTAGTCCAGATCTGTAAGCTGTGACCTTTCTACACTGTAGATAAC 47
QY 802 ATTACGATTTTGTCAAA 820
|||||
DB 46 ATTACGATTTTGTCAAA 28

RESULT 5
BF373581/c 282 bp mRNA linear EST 24-NOV-2000
LOCUS
DEFINITION
MR0-FT0175-210800-101-d05 FT0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF373581
VERSION
BF373581.1
KEYWORDS
EST.

SOURCE	ORGANISM	Human sapiens (human)
REFERENCE	AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 282)
JOURNAL	MEDLINE	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M. R., Nagai, M. A., Carvalho, A. F., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bata, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J., and Simpson, A. J.
COMMENT	TEXT	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
COMMENT	TEXT	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT	TEXT	20202663
COMMENT	TEXT	10737800
COMMENT	TEXT	Contact: Simpson A.J.G.
COMMENT	TEXT	Laboratory of Cancer Genetics
COMMENT	TEXT	Ludwig Institute for Cancer Research
COMMENT	TEXT	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
COMMENT	TEXT	Tel: +55-11-2704922
COMMENT	TEXT	Fax: +55-11-2707001
COMMENT	TEXT	Email: asimpson@ludwig.org.br
COMMENT	TEXT	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
COMMENT	TEXT	(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR0&t2=MR0-FT0175-210800-101-d05&t3=2000-08-21&t4=1)
COMMENT	TEXT	Seq primer: puc 18 forward
COMMENT	TEXT	High quality sequence start: 35
COMMENT	TEXT	High quality sequence stop: 282.
FEATURES	SOURCE	Location/Qualifiers
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FEATURES	SOURCE	/organism="Homo sapiens"
FEATURES	SOURCE	/mol_type="mRNA"
FEATURES	SOURCE	/db_xref="taxon:9606"
FEATURES	SOURCE	/dev_stage="Adult"
FEATURES	SOURCE	/clone_lib="FT0175"
FEATURES	SOURCE	/note="Organ: prostate,tumor; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
FEATURES	SOURCE	low stringency conditions."
FEATURES	SOURCE	BASE COUNT 85 a 51 c 70 g 76 t
FEATURES	SOURCE	ORIGIN
FEATURES	SOURCE	Query Match 24.1%; Score 198; DB 10; Length 282;
FEATURES	SOURCE	Best Local Similarity 100.0%; Prid. No. 6; Gaps 0;
FEATURES	SOURCE	Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FEATURES	SOURCE	588 CACGGGCGAGGGGTACGAGATTCTGGCCCTCTGCTTAACCTGCGCTTACCAAAAT 647
FEATURES	SOURCE	
FEATURES	SOURCE	262 CACGGGCGAGGGGTACGAGATTCTGGCCCTCTGCTTAACCTGCGCTTACCAAAAT 203
FEATURES	SOURCE	648 CATTTCATATTCTTACCCCTCAAAACAAAGCTGTTGAATATCTGATCTCTACGGTTCTT 707
FEATURES	SOURCE	
FEATURES	SOURCE	202 CATTTCATATTCTTACCCCTCAAAACAAAGCTGTTGAATATCTGATCTCTACGGTTCTT 143
FEATURES	SOURCE	708 TCTGGGCGCAACATCTTCCATATATCCAGCCACACCTCATTTTAAATATTTAGTCCAGA 767
FEATURES	SOURCE	
FEATURES	SOURCE	142 TCTGGGCGCAACATCTTCCATATATCCAGCCACACCTCATTTTAAATATTTAGTCCAGA 83
FEATURES	SOURCE	768 TCTGTACGTGACCTTTC 785
FEATURES	SOURCE	
FEATURES	SOURCE	82 TCTGTACGTGACCTTTC 65
RESULT 6	LOCUS	BF373406 167 bp mRNA linear EST 24-NOV-2000
DEFINITION	LOCUS	112-FT0159-070800-120-H01 FT0159 Homo sapiens CDNA, mRNA sequence.

ACCESSION	BR373406
VERSION	BR373406.1
KEYWORDS	GI:11335431
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eumalacostraca; Amniota; Mammalia: Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 167) Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Brites, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
PUBMED	10737800
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=1l2&t2=1l2-FT0159-070800-120-H01&t3=2000-08-07&t4=1) Seq primer: puc 18 forward High quality sequence stop: 167. Location/Qualifiers 1..167 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="FT0159" /note="Organ: prostate tumor; Vector: puc18; Site: 1: Smal; Site: 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT	47 a 38 c 49 g 33 t
ORIGIN	
Query Match	20.4%; Score 167; DB 10; Length 167;
Best Local Similarity	100.0%; Pred. No. 8.3e-76;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	254 CACAGGAAGCACAAGAGAGACAGAGATCCCTGGGAGAAATGCCGGCCGCAATCTTG 313 1 CACAGGAAGCACAAGAGAGACAGAGATCCCTGGGAGAAATGCCGGCCGCAATCTTG 60
OY	314 GGTATGATGATAGAGCTCGCCCTGGGCGCTGGCGCTTGATAGGAAGAGATAGAAA 373 Db 61 GGTATGATGATAGAGCTCGCCCTGGGCGCTGGCGCTTGATAGGAAGAGATAGAAA 120
OY	374 TGAATTGATGTGTTCTTAAAGATGGGACAGAAACAGATCTGTT 420 Db 121 TGAATTGATGTGTTCTTAAAGATGGGACAGAAACAGATCTGTT 167
RESULT 7	
LOCUS	AO206972/c 394 bp DNA linear GSS 17-SEP-1998
DEFINITION	H5.3238_B1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=21 Row=N; genomic survey sequence.

ACCESSION AQ206972
VERSION AQ206972.1 GI:3617542
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 394)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3238 row: N column: 21
Class: BAC ends
High quality sequence stop: 394.
FEATURES
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/sex="male"
/clone_lib="CIR Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"
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Best Local Similarity 100.0%; Pred. No. 3.2e-42;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 718 ACATTCGCATATACCCACACACTCATTTTAAATTAATTAATCCAGATCTGACTGT 777
DB 381 ACATTCGCATATATCCACACACTCATTTTAAATTAATTAATTAATCCAGATCTGACTGT 322
QY 778 GACCTTTCACACTGTAGATATACATTAATCTCATTTTGTTCAA 820
DB 321 GACCTTTCACACTGTAGATATACATTAATCTCATTTTGTTCAA 279
RESULT 8
LOCUS BQ292550 572 bp mRNA linear EST 15-MAY-2002
DEFINITION PMO-AN0087-240501-019-a06 AN0087 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ292550
VERSION BQ292550.1 GI:20801500
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 572)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brlones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM06t2-PM0-AN0087-240501-019-a06t3-2001-05-24t4-1)
Seq primer: puc 18 forward
High quality sequence stop: 572.
FEATURES
source
1..572
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="AN0087"
/note="Organ: amnion,normal; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 150 a 90 c 169 g 163 t
ORIGIN
Query Match 12.2%; Score 100; DB 13; Length 572;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGACGTGGCATCAGAAACAGAGGGAGATTGTGTCGTCACGCCAGAGACCG 60
DB 116 AGACGTGGCATCAGAAACAGAGGGAGATTGTGTCGTCACGCCAGAGACCG 175
QY 61 GAAGATCTGCATGTGGGAGGAGCCGTGATGATACAGAGGT 100
DB 176 GAAGATCTGCATGTGGGAGGAGCCGTGATGATACAGAGGT 215
RESULT 9
LOCUS A1557495 657 bp mRNA linear EST 09-AUG-1999
DEFINITION PT2.1.7_H12.r tumor2 Homo sapiens cDNA 3', mRNA sequence.
ACCESSION A1557495
VERSION A1557495.1 GI:4489858
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 657)
AUTHORS Huang,G.M., Ng,W.L., Farkas,J., He,L., Liang,H.A., Gordon,D., Yu,J. and Hood,L.
TITLE Prostate cancer expression profiling by cDNA sequencing analysis
JOURNAL Genomics 59 (2), 178-186 (1999)
MEDLINE 99359982
PUBMED 10409429
COMMENT Contact: Guyang Mathew Huang
Leroy Hood
University of Washington
Department of Molecular Biotechnology, Box 357730, University of Washington, Seattle, WA 98195
Tel: 5106280100
Fax: 5106280108
Email: huanggm@yahoo.com.

FEATURES
source
Location/Qualifiers
1. .657
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="tumor2"
/note="Organ: Prostate; Vector: pBluescript; Directional cDNA library was constructed using Lambda ZP II Kit (Stratagene). mRNA was extracted from a frozen prostate tumor tissue (Mayo Clinics)." 47 others

BASE COUNT
179 a 112 c 153 g 166 t

ORIGIN

Query Match
Best Local Similarity 10.5%; Score 86; DB 9; Length 657;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CAGAAAAACAGAGGAGATTGTGTGCTCCAGCCGAGGAGACGAGAGATCTGCAT 72
|||||
DB 14 CAGAAAAACAGAGGAGATTGTGTGCTCCAGCCGAGGAGACGAGAGATCTGCAT 73
|||||
QY 73 GGTGGAAGGACCTGATGATACAGAG 98
|||||
DB 74 GGTGGAAGGACCTGATGATACAGAG 99
|||||

RESULT 10
BE904264 349 bp mRNA linear EST 20-OCT-2000
LOCUS 601494521F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896548 5',
DEFINITION mRNA sequence.
ACCESSION BE904264
VERSION BE904264.1 GI:10396339
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 349)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@email.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM9689 row: j column: 05
High quality sequence start: 3
High quality sequence stop: 10.
Location/Qualifiers
1. .349
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3896548"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

BASE COUNT
114 a 61 c 93 g 81 t

ORIGIN

Query Match
Best Local Similarity 2.7%; Score 22; DB 10; Length 349;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 757 TAGTCCAGATCTGACTGTG 778
|||||
DB 64 TAGTCCAGATCTGACTGTG 43
|||||

RESULT 11
BO836203 569 bp mRNA linear EST 09-JAN-2003
LOCUS r143b09.y1 Meloidogyne hapla J2 PAMP1 v1 Meloidogyne hapla cDNA 5',
DEFINITION r143b09.y1 Meloidogyne hapla J2 PAMP1 v1 Meloidogyne hapla cDNA 5',
mRNA sequence.
ACCESSION BO836203
VERSION BO836203.1 GI:22140517
KEYWORDS EST.
SOURCE Meloidogyne hapla
ORGANISM Meloidogyne hapla
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
REFERENCE 1 (bases 1 to 569)
AUTHORS McCarter,J., Clifton,S., Chapell,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Thelning,B., Bowers,Y.,
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisbill,R.,
Ronko,I., Kennedy,S., McGuire,L., Beck,C., Underwood,K., Steptoe
,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone will not be made available due to an unidentified
microbial contamination of the source material.
Seq primer: -40RP from Gibco
High quality sequence stop: 423.
Location/Qualifiers
1. .569
/organism="Meloidogyne hapla"
/mol_type="mRNA"
/db_xref="taxon:6305"
/dev_stage="J2"
/lab_host="DH10B"
/clone_lib="Meloidogyne hapla J2 PAMP1 v1"
/note="Vector: pAMP1 (Gibco); Site:1: NotI; Site:2: SalI;
The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The cDNA was
made by using Dynabead oligo-dt priming (Dynal). PCR based
library using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of PAMP1. J2 were provided by Dr. Valerie
Williamson of the University of California at Davis
(vwilliams@ucdavis.edu)."

BASE COUNT
248 a 86 c 56 g 179 t

ORIGIN

Query Match
Best Local Similarity 2.7%; Score 22; DB 13; Length 569;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAGAAATCTGATGCTTCAC 520
|||||
DB 336 GAGAAATCTGATGCTTCAC 357
|||||

RESULT 12
BG119805 804 bp mRNA linear EST 30-JAN-2001
LOCUS 602352140F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4450424 5',
DEFINITION mRNA sequence.

ACCESSION BG119805
 VERSION BG119805.1 GI:12613311
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 804)
 NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bts-riemail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLM10235 row: p column: 09
 High quality sequence stop: 310.
 Location/Qualifiers
 1..804
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4450424"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH-MGC.90"
 /note="Organ: liver; Vector: pCMV-SPORT6; Site:1; NotI; Site:2; SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."
 BASE COUNT 283 a 200 c 202 g 119 t
 ORIGIN
 Query Match 2.7%; Score 22; DB 10; Length 804;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 483 TGAGAGGAAACAGACGAGAA 504
 DB 734 TGAGAGGAAACAGACGAGAA 755
 RESULT 13
 AZ418181/c 334 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M019409F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M019409 F, genomic survey sequence.
 ACCESSION AZ418181
 VERSION AZ418181.1 GI:10542194
 KEYWORDS GSS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 334)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0194 row: j column: 09
 Seq primer: CGTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 334.
 Location/Qualifiers
 1..334
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 /mol_type="genomic DNA"
 /strain="C57BL/6j"
 /db_xref="taxon:10090"
 /clone="UUGC1M019409"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42uv; Purified genomic DNA from M. musculus C57BL/6j (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (q147321419b1AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 59 a 53 c 99 g 123 t
 ORIGIN
 Query Match 2.6%; Score 21; DB 28; Length 334;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 248 CACACACACGAGACGACAAA 268
 DB 147 CACACACACGAGACGACAAA 127
 RESULT 14
 A0712816 416 bp DNA linear GSS 13-JUL-1999
 LOCUS HS_5387_A2_E08-SP6E RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate=963 Col=16 Row=I, genomic survey sequence.
 ACCESSION A0712816
 VERSION A0712816.1 GI:5462132
 KEYWORDS GSS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 416)
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 963 row: I column: 16
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 416.
Location/Qualifiers
1. .416
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=963 COL=16 Row=I"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC library"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
BASE COUNT 122 a 101 c 75 g 118 t
ORIGIN
Query Match 2.6%; Score 21; DB 28; Length 416;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 660 CTACCTCAACAAACAACTG 680
|||||
Db 186 CTACCTCAACAAACAACTG 206
RESULT 15 416 bp DNA linear GSS 24-OCT-2002
B2292184/c SALK_123591.42.40.x Arabidopsis thaliana TDNA insertion lines
LOCUS Arabidopsis thaliana genomic clone SALK_123591.42.40.x, genomic
DEFINITION Survey sequence.
ACCESSION B2292184
VERSION B2292184.1 GI:24338800
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 416)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g01770.
Class: TDNA tagged.
Location/Qualifiers
1. .416
/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_123591.42.40.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"
BASE COUNT 115 a 77 c 81 g 141 t
ORIGIN
Query Match 2.6%; Score 21; DB 29; Length 416;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 518 CACAAGACATGCACAAACAA 538
|||||
Db 216 CACAAGACATGCACAAACAA 196
Search completed: September 27, 2003, 11:35:46
Job time : 1722.81 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 20:07:52 : Search time 938.707 Seconds
(without alignments)
10300.748 Million cell updates/sec

Title: US-09-402-713a-6

Perfect score: 3582

Sequence: 1 acagaagaataagcaagtcgc.....tgatctcttgttacaacttt 3582

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N.Geneseq_19Jun03:*

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23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3531	98.6	3582	19	AAV62430
2	3036	84.8	3923	22	AAH64026
3	3036	84.8	3923	22	AAH93861
4	3036	84.8	3923	24	ABR92196
5	3036	84.8	3923	24	ABU95397
6	3036	84.8	3923	25	ACA59834
7	1629	45.5	2037	19	AAV62427
8	1367	38.2	1872	19	AAV62428

9	1364	38.1	3112	21	AAH06687	Human immunogenic
10	1364	38.1	3112	22	AAH63896	Human prostate CDN
11	1364	38.1	3112	22	AAH93803	Human prostate-spe
12	1364	38.1	3112	22	AAH85117	Human prostate-spe
13	1364	38.1	3112	22	AAH02868	Prostate tumour an
14	1364	38.1	3112	22	AAH69646	Human P710P Invent
15	1364	38.1	3112	24	ABU95267	Human P710P CDNA s
16	1364	38.1	3112	25	ACA59704	Prostate cancer th
17	1357	37.9	2426	21	AAH06689	Human immunogenic
18	1357	37.9	2426	22	AAH63898	Human prostate CDN
19	1357	37.9	2426	22	AAH93805	Human prostate-spe
20	1357	37.9	2426	22	AAH85119	Human prostate-spe
21	1357	37.9	2426	22	AAH02870	Prostate tumour an
22	1357	37.9	2426	22	AAH69648	Human P710P Invent
23	1357	37.9	2426	24	ABU95269	Human P710P CDNA s
24	1357	37.9	2426	25	ACA59706	Prostate cancer th
25	1123	31.4	2229	21	AAH06688	Human immunogenic
26	1123	31.4	2229	22	AAH63897	Human prostate CDN
27	1123	31.4	2229	22	AAH93804	Human prostate-spe
28	1123	31.4	2229	22	AAH85118	Human prostate-spe
29	1123	31.4	2229	22	AAH02869	Prostate tumour an
30	1123	31.4	2229	22	AAH69647	Human P710P Invent
31	1123	31.4	2229	24	ABU95268	Human P710P CDNA s
32	1123	31.4	2229	25	ACA59705	Prostate cancer th
33	738	20.6	876	24	AAH38815	Human PSNA CDNA, P
34	723	20.2	820	19	AAV62429	Prostate cancer an
35	720	20.1	812	21	AAH06690	Human immunogenic
36	720	20.1	812	22	AAH63899	Human prostate CDN
37	720	20.1	812	22	AAH93806	Human prostate-spe
38	720	20.1	812	22	AAH85120	Human prostate-spe
39	720	20.1	812	22	AAH02871	Prostate tumour an
40	720	20.1	812	22	AAH69649	Human P710P Invent
41	720	20.1	812	24	ABU95270	Human P710P CDNA s
42	720	20.1	812	25	ACA59707	Prostate cancer th
43	538	15.0	1001	23	ABV21323	Human prostate exp
44	538	15.0	1001	23	ABV21496	Human prostate exp
45	538	15.0	1001	23	ABV21705	Human prostate exp

ALIGNMENTS

RESULT 1	
ID	AAV62430
ID	AAV62430 standard; CDNA: 3582 BP.
AC	AAV62430;
XX	
AC	30-DEC-1998 (first entry)
XX	
DE	Prostate cancer antigen (PCA3) wild-type CDNA.
XX	
KW	Prostate cancer antigen CDNA; PCA3; prostatic cancer;
KW	PC; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	401..556
FT	/*tag= a
FT	/*product= "PCA3 protein"
FT	983..987
FT	/*tag= b
FT	2041..2046
FT	polyA_signal
FT	/*tag= c
FT	2597..2602
FT	/*tag= d
FT	3494..3496
FT	/*tag= e
XX	
XX	W09845420-AL.
XX	
PD	15-OCT-1998.

XX 09-APR-1998; 98WO-CA00346.
PF Best Local Similarity 100.0%; Score 3531; DB 19; Length 3582;
XX 10-APR-1997; 97US-0041836.
PR Matches 3581; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX (DIAG-) DIAGNOCURE INC.
PI Bussemakers MUG;
XX WPI: 1998-568347/48.
DR P-PSDB: AAM79738.
XX

PT New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
PT prevention and treatment of prostatic cancer
XX
PS Claim 3; Fig 5B-5F; 11pp; English.

CC The present sequence represents the prostate cancer antigen (PCA3)
CC wild-type cDNA sequence comprising of exons 1, 2, 3, 4a-4d of the
CC PCA3 gene. The invention claims for PCA3 cDNA variants and the
CC proteins they encode. The invention also claims for antibodies
CC against PCA3 protein. The antibodies are claimed to be useful for
CC detecting PCA3 protein in immunoassay tests, for diagnosing, assessing
CC and prognosis of prostatic cancer (PC). Antibodies, optionally
CC coupled to a cytotoxin or radioisotope, and nucleic acids antisense
CC to PCA3 cDNA are claimed to be useful for treating PC, while determining
CC elevated levels of PCA3 (as RNA or protein) is useful for detecting a
CC predisposition to development of PC, e.g. in prenatal tests. Detecting
CC PCA3 protein allows differentiation between malignant and benign
CC prostatic disease, and the level of PCA3 expression allows correlation
CC with the grade of tumour. PCA3 protein and its fragments are also
CC claimed to be useful in vaccines for preventing PC; in drug screens
CC for identifying specific (ant)agonists (potentially useful
CC therapeutically) and for studying protein-DNA interactions.

XX Sequence 3582 BP; 1052 A; 788 C; 679 G; 1063 T; 0 other;

Query Match 98.6%; Score 3531; DB 19; Length 3582;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3581; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAGAGAAATAGCAAGTGGCGAGAGCTGCATCAGAAAAACAGAGGGAGATTGTGT 60
DB 1 ACAGAGAAATAGCAAGTGGCGAGAGCTGCATCAGAAAAACAGAGGGAGATTGTGT 60
QY 61 GCGTCAGCCGAGGAGACACAGAAATCTGATGTTGGAGAGACCTGATGATACAGAG 120
DB 61 GCGTCAGCCGAGGAGACACAGAAATCTGATGTTGGAGAGACCTGATGATACAGAG 120
QY 121 GAATTACACACATATCTAGTGTTCATGAAACACCAATATATAGTGAAGAGCTA 180
DB 121 GAATTACACACATATCTAGTGTTCATGAAACACCAATATATAGTGAAGAGCTA 180
QY 181 GTCCGTGTGAGTCTCCATGACACAGAGGCTGATCACCATGAGCGCATTTCTGAG 240
DB 181 GTCCGTGTGAGTCTCCATGACACAGAGGCTGATCACCATGAGCGCATTTCTGAG 240
QY 241 TACTCAGTCAGCAAGAAAGAGCTACACATCTCAATGSCAGGGGTGAGAAATAGAAA 300
DB 241 TACTCAGTCAGCAAGAAAGAGCTACACATCTCAATGSCAGGGGTGAGAAATAGAAA 300
QY 301 GCGTCGACTTTCACATCTGAGCGCACATCTGCTGCAATGAGAGATTAATACATCAC 360
DB 301 GCGTCGACTTTCACATCTGAGCGCACATCTGCTGCAATGAGAGATTAATACATCAC 360
QY 361 TAGAAGACAGCAAGATGACATATATAGTCTAAGTAGTGTGTTTGCACATTTCCAG 420
DB 361 TAGAAGACAGCAAGATGACATATATAGTCTAAGTAGTGTGTTTGCACATTTCCAG 420
QY 421 CCCCTTTAATATTCACACACACAGAGAACCAAAAGAGACACAGAGATCCCTGGGAGA 480
DB 421 CCCCTTTAATATTCACACACACAGAGAACCAAAAGAGACACAGAGATCCCTGGGAGA 480

QY 481 AATGCCGCGCCGACCTCTGGGTCATGATAGACCTCGCCCTGTGCTGCCGCTTGT 540
DB 481 AATGCCGCGCCGACCTCTGGGTCATGATAGACCTCGCCCTGTGCTGCCGCTTGT 540
QY 541 GAGGGAAGACATTGAAATGAATGATGTGTTCTTAAGAGATGGGACAGAAACAGA 600
DB 541 GAGGGAAGACATTGAAATGAATGATGTGTTCTTAAGAGATGGGACAGAAACAGA 600
QY 601 TCTGTGTTGATATTTTGAACGGGATTCACAGATTTGAAATGAAGTCAACAAAGTAG 660
DB 601 TCTGTGTTGATATTTTGAACGGGATTCACAGATTTGAAATGAAGTCAACAAAGTAG 660
QY 661 CATTAACATAGAGAGAAACACAGACAGAGAAATCTTGATGCTTCACAGATGACACA 720
DB 661 CATTAACATAGAGAGAAACACAGACAGAGAAATCTTGATGCTTCACAGATGACACA 720
QY 721 AACAAAATGSAATCTGATGACATGAGGACCAACCTGGGAGAGATTAACACAGGG 780
DB 721 AACAAAATGSAATCTGATGACATGAGGACCAACCTGGGAGAGATTAACACAGGG 780
QY 781 GCAGAGGGTCAGGATTCGGCCCTGCTCTTAACCTGCTGATACCAATCATTTTC 840
DB 781 GCAGAGGGTCAGGATTCGGCCCTGCTCTTAACCTGCTGATACCAATCATTTTC 840
QY 841 ATATTTCTAACCTCAAAACAAAGCTGTTGTAATATCTGATCTAGGGTCTTCTGAG 900
DB 841 ATATTTCTAACCTCAAAACAAAGCTGTTGTAATATCTGATCTAGGGTCTTCTGAG 900
QY 901 CCCAATCTTCACATATTCACAGACACACATTTTAATTTAGTCCCAAGATCTGTA 960
DB 901 CCCAATCTTCACATATTCACAGACACACATTTTAATTTAGTCCCAAGATCTGTA 960
QY 961 CTGTGACCTTCTACACTGTAGATTAACATTAACATTTTGTCAAAAGACCTTCGTGT 1020
DB 961 CTGTGACCTTCTACACTGTAGATTAACATTAACATTTTGTCAAAAGACCTTCGTGT 1020
QY 1021 GCTGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GCTGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 AACAGGCTGGGAGACATCTCAAGATCTTCCAGAGGTTATATCTAGACACAGCATGA 1140
DB 1081 AACAGGCTGGGAGACATCTCAAGATCTTCCAGAGGTTATATCTAGACACAGCATGA 1140
QY 1141 TCATTAGGAGTGAATATCTAATCAACATCATCTCAGTCTTCCCATTAATATACA 1200
DB 1141 TCATTAGGAGTGAATATCTAATCAACATCATCTCAGTCTTCCCATTAATATACA 1200
QY 1201 TCATTGCCCACCTTTTGGCCCATTTCTCAAGACCTCAAAATGTCATTTCAATTAATACA 1260
DB 1201 TCATTGCCCACCTTTTGGCCCATTTCTCAAGACCTCAAAATGTCATTTCAATTAATACA 1260
QY 1261 GGATTAACCTTTTAACTGGAAGATTCATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 GGATTAACCTTTTAACTGGAAGATTCATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 ATTAATATATTTGTTTCCAGTCAAGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 ATTAATATATTTGTTTCCAGTCAAGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 GATTTTTCCTCAATATTAAGTAAATGCTTACCTGATGATGATGATGATGATGATGATGAT 1440
DB 1381 GATTTTTCCTCAATATTAAGTAAATGCTTACCTGATGATGATGATGATGATGATGATGAT 1440
QY 1441 AGCCTTCCTCCATCCCTCCAGCCTTATCTGATGATGATGATGATGATGATGATGATGAT 1500
DB 1441 AGCCTTCCTCCATCCCTCCAGCCTTATCTGATGATGATGATGATGATGATGATGATGAT 1500
QY 1501 AAACAAATCTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1501 AAACAAATCTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1561 GAGAGAGCTTTCCTGCTCTTAATCTAGATGATGATGATGATGATGATGATGATGATGAT 1620

Dp	1561	GAGAGCTCTTCTTGTCTCTTAAATCTAGATATGTGAAAGTTTGAATTAAGTCACTA	1620
Qy	1561	TCTTACTCTTCATGCAAAAGAGGACACATATAGATTCATCATGACATGACACACAATA	1680
Dp	1521	TCTTACTTCATGCAAAAGAGGACACATATAGATTCATCATGACATGACACACAATA	1680
Qy	1681	CTAAAGGTATTAATTTGATTTATAGAGTTTATGATTAATATATGAATGCAAGAGCCACAGA	1740
Dp	1681	CTAAAGGTATTAATTTGATTTATAGAGTTTATGATTAATATATGAATGCAAGAGCCACAGA	1740
Qy	1741	GGGAAATGTTTAAAGGGGACGTTTAAAGCCGCGGATGTGAAGCAAAAGGACAGGAACCTCA	1800
Dp	1741	GGGAAATGTTTAAAGGGGACGTTTAAAGCCGCGGATGTGAAGCAAAAGGACAGGAACCTCA	1800
Qy	1801	TAGTATCTTAAATATATATCTTCACTTTCTCATCTCATGCAATATCCAAAGAGCTTTT	1860
Dp	1801	TAGTATCTTAAATATATATCTTCACTTTCTCATCTCATGCAATATCCAAAGAGCTTTT	1860
Qy	1861	CACAGAAATTCAGCAGTGCACAAATCCCAAGAGTAACCTTATCCATTTTCATGTGATGC	1920
Dp	1861	CACAGAAATTCAGCAGTGCACAAATCCCAAGAGTAACCTTATCCATTTTCATGTGATGC	1920
Qy	1921	GCTTAAAGTTTGGGCAAAATCATCTGTCTCATCTATCTCAACTTTCAGAAATGTTTGTCC	1980
Dp	1921	GCTTAAAGTTTGGGCAAAATCATCTGTCTCATCTATCTCAACTTTCAGAAATGTTTGTCC	1980
Qy	1981	TTTGATGTTAAATGGAAGAAATAGGGCACCTGTTGAGAGCACCTTAAAGGTTTACACCTGAC	2040
Dp	1981	TTTGATGTTAAATGGAAGAAATAGGGCACCTGTTGAGAGCACCTTAAAGGTTTACACTGTGAC	2040
Qy	2041	AATAAGAAATTTACAAAGAGCTACTCAGAGCAGTTGTTAAGAGCTCTGTGTGTGTGT	2100
Dp	2041	AATAAGAAATTTACAAAGAGCTACTCAGAGCAGTTGTTAAGAGCTCTGTGTGTGTGT	2100
Qy	2101	GTTGTGTGTAGTGTACATGCCAAAGTGTGCTCTCTCTTGAACCATTAATTTGACAG	2160
Dp	2101	GTTGTGTGTAGTGTACATGCCAAAGTGTGCTCTCTCTTGAACCATTAATTTGACAG	2160
Qy	2161	TTTAAACAGAGCATTTTTCAAATGGACATAGAGCTGGCAATGATGTTATCCACACCATAT	2220
Dp	2161	TTTAAACAGAGCATTTTTCAAATGGACATAGAGCTGGCAATGATGTTATCCACACCATAT	2220
Qy	2221	CTCATTTATCTCCAGTAATGTGATTAATATGTATCTGTTAACATATAAAAAAGTTTGAC	2280
Dp	2221	CTCATTTATCTCCAGTAATGTGATTAATATGTATCTGTTAACATATAAAAAAGTTTGAC	2280
Qy	2281	TTTCAAAAAGAGAGCTGGGAAATGGACACACAAATATGATTAATCTAACTCTTCACTATCA	2340
Dp	2281	TTTCAAAAAGAGAGCTGGGAAATGGACACACAAATATGATTAATCTAACTCTTCACTATCA	2340
Qy	2341	GCTCACACAGCTTGCACATATATTTGTTAAGAGCAACCTGCAATTTGGGGTTCCTGTAAAG	2400
Dp	2341	GCTCACACAGCTTGCACATATATTTGTTAAGAGCAACCTGCAATTTGGGGTTCCTGTAAAG	2400
Qy	2401	AAATTAATCTGATTAAGGTCTCAGCTGGGGCTGTGCATCAGAGCGGTTTGAGAAATATTCAA	2460
Dp	2401	AAATTAATCTGATTAAGGTCTCAGCTGGGGCTGTGCATCAGAGCGGTTTGAGAAATATTCAA	2460
Qy	2461	TTTCTCAGCAGAGCCAGAAATTTGAATTCCTCATCTTTTAAAGAAATCATTTTACAGGTTTG	2520
Dp	2461	TTTCTCAGCAGAGCCAGAAATTTGAATTCCTCATCTTTTAAAGAAATCATTTTACAGGTTTG	2520
Qy	2521	GAGAGAAATTCAGAGAGCTCAGAGCTGTTTCAATATATATGTTGAAATCTTGTGCTCTTGG	2580
Dp	2521	GAGAGAAATTCAGAGAGCTCAGAGCTGTTTCAATATATATGTTGAAATCTTGTGCTCTTGG	2580
Qy	2581	TGTTTCATGAGATGCAATAAATATGTTTATCTTTGAACTATAGCTCATAGAGAGATA	2640
Dp	2581	TGTTTCATGAGATGCAATAAATATGTTTATCTTTGAACTATAGCTCATAGAGAGATA	2640
Qy	2641	TAAAGACTCTGAGTGAATATCAACTTAAAGATTTCAAGAAATATTTAGATTTAAGCTCACA	2700
Dp	2641	TAAAGACTCTGAGTGAATATCAACTTAAAGATTTCAAGAAATATTTAGATTTAAGCTCACA	2700

Db	2661	TAAGACCTCTGATGATATTCACAACTTAGGGATTCAAGAATATTAGATTTAAGCTACA	2700
QY	2701	CTGGTCAAAAGAACCAAGATACAAAGAACTGTAGCTGTCACTGCCCTCTCTGTGA	2760
Db	2701	CTGGTCAAAAGAACCAAGATACAAAGAACTGTAGCTGTCACTGCCCTCTCTGTGA	2760
QY	2761	GCACACCAACACAGCAGAGCCCAACGCATGTCTGAGATCCTTAATCAAGAAACAGTG	2820
Db	2761	GCACACCAACACAGAGAGCCCAACGCATGTCTGAGATCCTTAATCAAGAAACAGTG	2820
QY	2821	TCATGAGTTGAATTCCTATTATGAGATGAGTCGTGGGCACTCTGGCTCTCTCTT	2880
Db	2821	TCATGAGTTGAATTCCTATTATGAGATGAGTCGTGGGCACTCTGGCTCTCTCTT	2880
QY	2881	GACACATATTAAGCTTCTAGCCCTTGTGCTCCACGACTTTATCTTTTCTCAACACATCGC	2940
Db	2881	GACACATATTAAGCTTCTAGCCCTTGTGCTCCACGACTTTATCTTTTCTCAACACATCGC	2940
QY	2941	TTACCAATTCCTCTCTCTCTCTGTGTGCTTTGAGACTTCCCAAGAATTTAACGACTCT	3000
Db	2941	TTACCAATTCCTCTCTCTCTCTGTGTGCTTTGAGACTTCCCAAGAATTTAACGACTCT	3000
QY	3001	CAAGCTTTTCTTCCATCCGACACACTTAACGTAATGCGTAGACCCCTATTATTTATTA	3060
Db	3001	CAAGCTTTTCTTCCATCCGACACACTTAACGTAATGCGTAGACCCCTATTATTTATTA	3060
QY	3061	TTTCCAAATAGATGCTGCTATGAGGCTTAATTGGCTTATGATGAACATTAGATATTTAAG	3120
Db	3061	TTTCCAAATAGATGCTGCTATGAGGCTTAATTGGCTTATGATGAACATTAGATATTTAAG	3120
QY	3121	TCATAAGGTTCAAAATCCAACTCATTAATCTCTCTCTCTTCACTCCCTGCTCTCT	3180
Db	3121	TCATAAGGTTCAAAATCCAACTCATTAATCTCTCTCTCTTCACTCCCTGCTCTCTCT	3180
QY	3181	CCCTATATTAAGTGAATGACGAAGAAGATGGTCCCAAGATGCCAGTCAATGGAAGAAC	3240
Db	3181	CCCTATATTAAGTGAATGACGAAGAAGATGGTCCCAAGATGCCAGTCAATGGAAGAAC	3240
QY	3241	CAGTGGCTCCTGTTGGATCATGATGCAAGACTGCTGAAGCCAGAAGATGACTGATTACG	3300
Db	3241	CAGTGGCTCCTGTTGGATCATGATGCAAGACTGCTGAAGCCAGAAGATGACTGATTACG	3300
QY	3301	CCTCATGGGTGAGAGGAGACCACTCCTGGGCTTGTGATGTGCAGAGAACAGACTGAGA	3360
Db	3301	CCTCATGGGTGAGAGGAGACCACTCCTGGGCTTGTGATGTGCAGAGAACAGACTGAGA	3360
QY	3361	TGCTCCCTGCTCTAGTGTCTCTGTCATCTCCCTTCTATGAAGATCCATATAATTGG	3420
Db	3361	TGCTCCCTGCTCTAGTGTCTCTGTCATCTCCCTTCTATGAAGATCCATATAATTGG	3420
QY	3421	CTACATTTGAGAAATTCCAATTAGGAACACATGTTATATCGGCGTATCAATTTTTTAA	3480
Db	3421	CTACATTTGAGAAATTCCAATTAGGAACACATGTTATATCGGCGTATCAATTTTTTAA	3480
QY	3481	ACTTGCTGAAATTAAGTTTTTTCAAAATCTGCTCTGTAAATTAATCTTTTCTTACAGTG	3540
Db	3481	ACTTGCTGAAATTAAGTTTTTTCAAAATCTGCTCTGTAAATTAATCTTTTCTTACAGTG	3540
QY	3541	TCTTGCGACTACTATATCAACTTTGATCTTGTGTACAACTTTT 3582	
Db	3541	TCTTGCGACTACTATATCAACTTTGATCTTGTGTACAACTTTT 3582	
RESULT 2			
AAS64026			
ID	AAS64026	standard; cDNA; 3923 BP.	
XX	AAS64026;		
XX	29-JAN:2002	(first entry)	
XX	Human	CDNA encoding DD3.	
XX			

Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
Homo sapiens.
W0200173032-AZ.
04-OCT-2001.
27-MAR-2001; 2001WO-US09919.
27-MAR-2000; 2000US-0536857.
09-MAY-2000; 2000US-0568100.
12-MAY-2000; 2000US-0570737.
13-JUN-2000; 2000US-0593793.
27-JUN-2000; 2000US-0605783.
10-AUG-2000; 2000US-0636215.
29-AUG-2000; 2000US-0651236.
06-SEP-2000; 2000US-0657279.
02-OCT-2000; 2000US-0679426.
10-OCT-2000; 2000US-0685166.
(CORI-) CORIXA CORP.
Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD, Panger GR, Retter MW, Stoik JA, Day CH, Vedvick TS, Carter D; LI SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA; WPI; 2001-639232/73.
New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
Claim 1; Page 473-474; 579pp; English.
The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumor protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;
Query Match 84.8%; Score 3036; DB 22; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGAGAATAGAGAGCGGAGAGCTGGCATCAGAAAAACAGAGGGAGATTGCT 60
DB 1 ACAGAGAATAGAGAGCGGAGAGCTGGCATCAGAAAAACAGAGGGAGATTGCT 60
QY 61 GGTGACGCGGAGGAGACAGAAATCTGATGTTGGAGGACCTGATGATACAGAG 120
DB 61 GGTGACGCGGAGGAGACAGAAATCTGATGTTGGAGGACCTGATGATACAGAG 120
QY 121 GAATTACACACATATCTAGTGTTCATGAACACACAGATAAATAGTGAAGCTA 180
DB 121 GAATTACACACATATCTAGTGTTCATGAACACACAGATAAATAGTGAAGCTA 180
QY 181 GTCCGCTGTAGTCTCTCACTGACACAGAGGCTGGATCACCATGAGGCACTTTCAG 240
DB 181 GTCCGCTGTAGTCTCTCACTGACACAGAGGCTGGATCACCATGAGGCACTTTCAG 240
QY 241 TACTCAGTGCAGCAAGAAAGACTACAGACATCTCATGAGGAGGAGCAAAATAGAAA 300
DB 241 TACTCAGTGCAGCAAGAAAGACTACAGACATCTCATGAGGAGGAGCAAAATAGAAA 300

QY 301 GGTCTGACTTTTACATCTGAGCCACACATCTGTAATGAGATATTAACATCAC 360
DB 301 GGTCTGACTTTTACATCTGAGCCACACATCTGTAATGAGATATTAACATCAC 360
QY 361 TAGAAGACAGCAGATGACATATATATGCTTAAGTAGACATGTTTTGACATTTCCAG 420
DB 361 TAGAAGACAGCAGATGACATATATATGCTTAAGTAGACATGTTTTGACATTTCCAG 420
QY 421 CCCCTTAATATCCACACACAGGAGGACCAAGGACACAGATCCCGGGAGA 480
DB 421 CCCCTTAATATCCACACACAGGAGGACCAAGGACACAGATCCCGGGAGA 480
QY 481 AATGCCCGCCCATCTTTGGGTATCGATGAGCCCTGCTGCTGCTCCGCTTGT 540
DB 481 AATGCCCGCCCATCTTTGGGTATCGATGAGCCCTGCTGCTGCTCCGCTTGT 540
QY 541 GAGGAGAGACATTAAGAAATGATGATGTTCTTAAGATGGCAGGAAACAGA 600
DB 541 GAGGAGAGACATTAAGAAATGATGATGTTCTTAAGATGGCAGGAAACAGA 600
QY 601 TCTGTGTGATATTTATTTGAACGGGATTAAGATTTGAATGAAGTCAAAAGTAG 660
DB 601 TCTGTGTGATATTTATTTGAACGGGATTAAGATTTGAATGAAGTCAAAAGTAG 660
QY 661 CATTACCAATGAGAGGAAACAGACAGAAAAATCTTGTGCTTACAAAGCATGCAACA 720
DB 661 CATTACCAATGAGAGGAAACAGACAGAAAAATCTTGTGCTTACAAAGCATGCAACA 720
QY 721 AACCAATGGAATCTGATGATGATGAGGACGCAAGCTGGGAGGAGATTAACACGGG 780
DB 721 AACCAATGGAATCTGATGATGATGAGGACGCAAGCTGGGAGGAGATTAACACGGG 780
QY 781 GCAGAGGTCAGGATTCGGCCCTGCTGCCCTAAATGCTGCTTATTAACCAATCATTTT 840
DB 781 GCAGAGGTCAGGATTCGGCCCTGCTGCCCTAAATGCTGCTTATTAACCAATCATTTT 840
QY 841 ATATTTCTAACCCCTCAAAACAAAGCTGTTGTAATATGATCTGACGGTCTCTTGGC 900
DB 841 ATATTTCTAACCCCTCAAAACAAAGCTGTTGTAATATGATCTGACGGTCTCTTGGC 900
QY 901 CCCCAACNTCTCCATATATCCAGCCACACATTTTAAATTTAGTTCCAGATCTGTA 960
DB 901 CCCCAACNTCTCCATATATCCAGCCACACATTTTAAATTTAGTTCCAGATCTGTA 960
QY 961 CTGTGACCTTCTACCTGTGATGATTAACATTAATCTTTGTTCAAGACCTTCGTG 1020
DB 961 CTGTGACCTTCTACCTGTGATGATTAACATTAATCTTTGTTCAAGACCTTCGTG 1020
QY 1021 GCTGCTTAATATGAGTGAAGCTGTTTCTTAAGAGAGTGTCTGCCCCAGGGATCTGTG 1080
DB 1021 GCTGCTTAATATGAGTGAAGCTGTTTCTTAAGAGAGTGTCTGCCCCAGGGATCTGTG 1080
QY 1081 AACAGGCTGGGAACATCTCAAGATCTTCCAGGGTTATCTTACCTAGCACACAGCATGA 1140
DB 1081 AACAGGCTGGGAACATCTCAAGATCTTCCAGGGTTATCTTACCTAGCACACAGCATGA 1140
QY 1141 TCATTAGGAGTGAATATCATCAACATCATCTCAGTGTCTTTGCCATCTGAAT 1200
DB 1141 TCATTAGGAGTGAATATCATCAACATCATCTCAGTGTCTTTGCCATCTGAAT 1200
QY 1201 TCATTTCCACTTTTGTGCCATCTCAAGACCTCAAAATGTCAATTCATTAATATGACA 1260
DB 1201 TCATTTCCACTTTTGTGCCATCTCAAGACCTCAAAATGTCAATTCATTAATATGACA 1260
QY 1261 GGATTAACCTTTTTTTTAACTGGAAGATTCATATGATCATGACCTATGGAAATTTA 1320
DB 1261 GGATTAACCTTTTTTTTAACTGGAAGATTCATATGATCATGACCTATGGAAATTTA 1320
QY 1321 ATTACATATTTTGTTCGAGTGAAGATGACATACTCTTAATCCCTCCCTTGTGTT 1380
DB 1321 ATTACATATTTTGTTCGAGTGAAGATGACATACTCTTAATCCCTCCCTTGTGTT 1380

QY 1381 GATTTTTTCCAGTATATAAGTTAAATGCTTAGCCTTGCTAGAGGCTGTATACAGCAC 1440
|||||
Db 1381 GATTTTTTCCAGTATATAAGTTAAATGCTTAGCCTTGCTAGAGGCTGTATACAGCAC 1440
QY 1441 ACCCTTCGCCATCCCTCCAGGCTTATCTGTATACCAATCAACCCCTCCCATACAGCT 1500
|||||
Db 1441 ACCCTTCGCCATCCCTCCAGGCTTATCTGTATACCAATCAACCCCTCCCATACAGCT 1500
QY 1501 AAACAAAATCTAAGTTGTAATTCCTTGAACATGTGAGACATACATATATCCCTGCGCT 1560
|||||
Db 1501 AAACAAAATCTAAGTTGTAATTCCTTGAACATGTGAGACATACATATATATCCCTGCGCT 1560
QY 1561 GAGAGGCTCTCTGCTCTTAAATCTAGAAATGATGTAAGTTTGAATTAAGTTGACTA 1620
|||||
Db 1561 GAGAGGCTCTCTGCTCTTAAATCTAGAAATGATGTAAGTTTGAATTAAGTTGACTA 1620
QY 1621 TCTTACTTCATGCAAGAAGGAGACATATGAGATTCAATCAGACAGCAAAATA 1680
|||||
Db 1621 TCTTACTTCATGCAAGAAGGAGACATATGAGATTCAATCAGACAGCAAAATA 1680
QY 1681 CTAAGAAGTATTTGATTTAAGATTTAGATTAATATATGAAATGCAAGGCCACAGA 1740
|||||
Db 1681 CTAAGAAGTATTTGATTTAAGATTTAGATTTAATATATGAAATGCAAGGCCACAGA 1740
QY 1741 GGGAAATGTTATGGGGCAGCTTTGTAAGCCTGGAGTGAAGCAAAAGCAGGAACTCA 1800
|||||
Db 1741 GGGAAATGTTATGGGGCAGCTTTGTAAGCCTGGAGTGAAGCAAAAGCAGGAACTCA 1800
QY 1801 TAGTATCTTAT 1860
|||||
Db 1801 TAGTATCTTAT 1860
QY 1861 CACAGAAATCATAGCAGTGAAGTCCCAAGGTAACCTTATCCATTTATATATATATAT 1920
|||||
Db 1861 CACAGAAATCATAGCAGTGAAGTCCCAAGGTAACCTTATCCATTTATATATATATAT 1920
QY 1921 GCTTTAGAAATTTGGCAATCATATGCTGCTACTTATCTCAACTTGGAGTGTGTGTC 1980
|||||
Db 1921 GCTTTAGAAATTTGGCAATCATATGCTGCTACTTATCTCAACTTGGAGTGTGTGTC 1980
QY 1981 TTGTAGTTATTTGGAAGAAATAGGGCAGCTTGTGAGCCACTTTAGGGTTCACTCTG 2040
|||||
Db 1981 TTGTAGTTATTTGGAAGAAATAGGGCAGCTTGTGAGCCACTTTAGGGTTCACTCTG 2040
QY 2041 AATTAAGAAATTTACAAGAGCTACAGAGCAGTGTGTAAGAGCTGTGTGTGTGTGT 2100
|||||
Db 2041 AATTAAGAAATTTACAAGAGCTACAGAGCAGTGTGTAAGAGCTGTGTGTGTGTGT 2100
QY 2101 GT 2160
|||||
Db 2101 GT 2160
QY 2161 TTTAAACAAGCATGTTTTCAATGCGACTATGAGCTGCCAATGATGTATCACACCATAT 2220
|||||
Db 2161 TTTAAACAAGCATGTTTTCAATGCGACTATGAGCTGCCAATGATGTATCACACCATAT 2220
QY 2221 CTCATTTATTCGCCAGTAAATGTGATTAATGTCATCTGTAAACATAAAAAAGTTTGAC 2280
|||||
Db 2221 CTCATTTATTCGCCAGTAAATGTGATTAATGTCATCTGTGTAAACATAAAAAAGTTTGAC 2280
QY 2281 TTTCAAAAAAGCAGCTGAAATGAGACAACCAATATGCAATTAATCACTCTACATCA 2340
|||||
Db 2281 TTTCAAAAAAGCAGCTGAAATGAGACAACCAATATGCAATTAATCACTCTACATCA 2340
QY 2341 GCTACACACTGCTTGACATATTTGTGTAGACACACTGCAATTTGGGTTCTCTTAAGC 2400
|||||
Db 2341 GCTACACACTGCTTGACATATTTGTGTAGACACACTGCAATTTGGGTTCTCTTAAGC 2400
QY 2401 AAAAATCTTGATTTAGGCTCAGCTGGGGCTGTGCAATCGGGGTTTGAAGAAATTTCA 2460
|||||
Db 2401 AAAAATCTTGATTTAGGCTCAGCTGGGGCTGTGCAATCGGGGTTTGAAGAAATTTCA 2460
QY 2461 TTCTGAGCAGAAAGCAGAAATTTGAATTCCTCATCTTTTGAATCATTTTACAGGTTTG 2520

Db 2461 TTCTGAGCAGAAAGCCAGAAATTTGAATTCCTCATCTTTAGAAATCATTTACAGGTTTG 2520
|||||
QY 2521 GAGAGATTCACAGACACTCAGAGTCTTTGACATTAATCTCTGTAACCTTCTGCTCTTG 2580
|||||
Db 2521 GAGAGATTCACAGACACTCAGAGTCTTTGACATTAATCTCTGTAACCTTCTGCTCTTG 2580
QY 2581 TGTTCATGATAGTCCCAATTAATTAATGTTATCTTTGAAGTATGCTATAGAGAAATA 2640
|||||
Db 2581 TGTTCATGATAGTCCCAATTAATTAATGTTATCTTTGAAGTATGCTATAGAGAAATA 2640
QY 2641 TAAGAACTGTGATGATATCAACATTAGGATTCAGAAAGAAATTAAGATTAACTCACA 2700
|||||
Db 2641 TAAGAACTGTGATGATATCAACATTAGGATTCAGAAAGAAATTAAGATTAACTCACA 2700
QY 2701 CTGTCTAAAGAACCAACATATCAAAAGAACTGTGAGCTCTCATCGTCCCATCTGTGA 2760
|||||
Db 2701 CTGTCTAAAGAACCAACATATCAAAAGAACTGTGAGCTCTCATCGTCCCATCTGTGA 2760
QY 2761 GGCACAAACACAGCAGAGCCAGCAGCATGTGAGATGCTTAAATCAAGAAACAGTG 2820
|||||
Db 2761 GGCACAAACACAGCAGAGCCAGCAGCATGTGAGATGCTTAAATCAAGAAACAGTG 2820
QY 2821 TCATGAGTTGAATTCCTATTAATGATGCTAGCTTCTGAGCTCTGCTCTCTCTT 2880
|||||
Db 2821 TCATGAGTTGAATTCCTATTAATGATGCTAGCTTCTGAGCTCTGCTCTCTCTCTT 2880
QY 2881 GACACATATTAAGTTTACCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 2940
|||||
Db 2881 GACACATATTAAGTTTACCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 2940
QY 2941 TTACCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
|||||
Db 2941 TTACCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
QY 3001 CAAGCTTTTCTTCATCCCAACCACTAAGCTGAAT 3036
|||||
Db 3001 CAAGCTTTTCTTCATCCCAACCACTAAGCTGAAT 3036

RESULT 3
AAH93861
ID AAH93861 standard; cDNA; 3923 BP.
XX
AC AAH93861;
DT 04-OCT-2001 (first entry)
DE XX
XX Gene D03 cDNA sequence.
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosolic; gene therapy; metastasis; ss.
OS Homo sapiens.
PN MO200151633-A2.
PD 19-JUL-2001.
PD 16-JAN-2001; 2001MO-US01574.
PR 14-JAN-2000; 2000US-0483672.
PA (CORI-) CORIXA CORP.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YW;
PI Wang A, Meagher MJ;
DR WPI; 2001-425873/45.
XX
XX
XX
PT New polynucleotide encoding a prostate-specific protein, for
diagnosing, monitoring and treating prostate cancer in a patient and

for use in vaccines -
Claim 1: Page 452-453; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AA01115 to AA01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.

Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;

Query Match 84.8%; Score 3036; DB 22; Length 3923;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ACAAGAGAAATAGCAAGTGCAGAGAGCTGCATCAGAAAAACAGAGGGGAGATTGTGT 60
Db 1 ACAAGAGAAATAGCAAGTGCAGAGAGCTGCATCAGAAAAACAGAGGGGAGATTGTGT 60
QY 61 GCGCGAGCGGAGGAGAGCCAGGAAGTCTGATGTTGGGAAGACCTGATGATACAG 120
Db 61 GCGCGAGCGGAGGAGAGCCAGGAAGTCTGATGTTGGGAAGACCTGATGATACAG 120
QY 121 GAATTACACACATATATCTAGTGTTCATGAACACCAAGATAAATAGTGAAGAGTA 180
Db 121 GAATTACACACATATATCTAGTGTTCATGAACACCAAGATAAATAGTGAAGAGTA 180
QY 181 GTCCGCTGTGATCTCTCACTGACACACAGGGCTGTGATCCATCGAGCGCACTTCTGAG 240
Db 181 GTCCGCTGTGATCTCTCACTGACACACAGGGCTGTGATCCATCGAGCGCACTTCTGAG 240
QY 241 TACTCAGTGCAGAAAGAAAGACATACAGACATCTCAATGAGAGGGGTGAGAAATAGAAA 300
Db 241 TACTCAGTGCAGAAAGAAAGACATACAGACATCTCAATGAGAGGGGTGAGAAATAGAAA 300
QY 301 GCGTCTGACTTTCATCTGAGGCCACACATCTGCTGAATGAGATATTAACATCAC 360
Db 301 GCGTCTGACTTTCATCTGAGGCCACACATCTGCTGAATGAGATATTAACATCAC 360
QY 361 TAGAAACAGACAGATGACATATATATGTCTAAGTAGTGACATGTTTTCACATTTCCAG 420
Db 361 TAGAAACAGACAGATGACATATATATGTCTAAGTAGTGACATGTTTTCACATTTCCAG 420
QY 421 CCCCTTTAAATATCCACACACAGAAAGCAAAAGAAAGAACACAGAGATCCCTGGGAGA 480
Db 421 CCCCTTTAAATATCCACACACAGAAAGCAAAAGAAAGAACACAGAGATCCCTGGGAGA 480
QY 481 AATGCCGGCGCCATCTTGCGTATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 AATGCCGGCGCCATCTTGCGTATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 GAGGGAAGGACATTAGAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 GAGGGAAGGACATTAGAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 TCCCTGTGTGATATTTATTTGAACGGGATACAGATTTGAATGAAGTCCAAAGTACAG 660
Db 601 TCCCTGTGTGATATTTATTTGAACGGGATACAGATTTGAATGAAGTCCAAAGTACAG 660
QY 661 CATTAACAATGAGAGAAACAGACAGAGAAATCTTGTGCTTCACAAAGCATGCAACA 720
Db 661 CATTAACAATGAGAGAAACAGACAGAGAAATCTTGTGCTTCACAAAGCATGCAACA 720
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QY 721 AACAAATGATACTGTGATGACATGAGGAGCCAGACCTGGGAGGAGATACCCAGCG 780
Db 721 AACAAATGATACTGTGATGACATGAGGAGCCAGACCTGGGAGGAGATACCCAGCG 780
QY 781 GCAGAGGTCAGAGATTTCTGGCCCTGCTCCCTAACTGTGCTTCAATACCAATCATTTG 840
Db 781 GCAGAGGTCAGAGATTTCTGGCCCTGCTCCCTAACTGTGCTTCAATACCAATCATTTG 840
QY 841 AATATTTCAACCCCAAAACAAAGCTGTTGTAATATGATCTAGAGGTCCTTTGGG 900
Db 841 AATATTTCAACCCCAAAACAAAGCTGTTGTAATATGATCTAGAGGTCCTTTGGG 900
QY 901 CCACAACATCTTCATATATCCAGCCACATCTATTTTAATATTAATAGTCCAGATCTGTA 960
Db 901 CCACAACATCTTCATATATCCAGCCACATCTATTTTAATATTAATAGTCCAGATCTGTA 960
QY 961 CTGAGACCTTCTACAGTGTGAATATACATATATATATATATATATATATATATATAT 1020
Db 961 CTGAGACCTTCTACAGTGTGAATATACATATATATATATATATATATATATATATAT 1020
QY 1021 GCTGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 GCTGCTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 AACAGGCTGGAGAGCATCTCAAGATCTTCCAGGGTATATCTACTAGCACAGCATGA 1140
Db 1081 AACAGGCTGGAGAGCATCTCAAGATCTTCCAGGGTATATCTACTAGCACAGCATGA 1140
QY 1141 TCATTACGAGTGAATATATATATATATATATATATATATATATATATATATATATAT 1200
Db 1141 TCATTACGAGTGAATATATATATATATATATATATATATATATATATATATATATAT 1200
QY 1201 TCATTCCCACTTTTGTGCCATCTCAAGACCTCAAAATGTCAATCCATTAATATACCA 1260
Db 1201 TCATTCCCACTTTTGTGCCATCTCAAGACCTCAAAATGTCAATCCATTAATATACCA 1260
QY 1261 GGATTAACCTTTTAAAACTTAACTGGAAGATTTACATGATGATGATGATGATGATGATG 1320
Db 1261 GGATTAACCTTTTAAAACTTAACTGGAAGATTTACATGATGATGATGATGATGATGATG 1320
QY 1321 ATTACATATTTTGTGTTTCCAGTGAAGATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 ATTACATATTTTGTGTTTCCAGTGAAGATGATGATGATGATGATGATGATGATGATG 1380
QY 1381 GATTTTTCCTCAGTATTAAGTTTAAATGCTTTACCTGTACTAGAGCTGTATACAGAC 1440
Db 1381 GATTTTTCCTCAGTATTAAGTTTAAATGCTTTACCTGTACTAGAGCTGTATACAGAC 1440
QY 1441 AGCCTCTCCCATCCCTCCAGACCTTATCTGATCACCATCAACCCCTCCCATACCACT 1500
Db 1441 AGCCTCTCCCATCCCTCCAGACCTTATCTGATCACCATCAACCCCTCCCATACCACT 1500
QY 1501 AAACAAATCTAACCTGTGAATTTCTGAAACATGTCAGGACATTAATTTCTCTGCT 1560
Db 1501 AAACAAATCTAACCTGTGAATTTCTGAAACATGTCAGGACATTAATTTCTCTGCT 1560
QY 1561 GAGAAGCTCTCTCTGCTCTTAATCTAGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1561 GAGAAGCTCTCTCTGCTCTTAATCTAGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 TCTTACTTCATGCAAGAAGGACACATATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 TCTTACTTCATGCAAGAAGGACACATATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 CTAAAGTGTATATTTGATATTAAGATTTAGATTAATATATATATATATATATATATAT 1740
Db 1681 CTAAAGTGTATATTTGATATTAAGATTTAGATTAATATATATATATATATATATATAT 1740
QY 1741 GGAATGTTTATGAGGACGCTTTGTAAGCCGAGATGGAAGCAAGGACAGGAACTGCA 1800
Db 1741 GGAATGTTTATGAGGACGCTTTGTAAGCCGAGATGGAAGCAAGGACAGGAACTGCA 1800
QY 1801 TAGTATCTTATATATATATATATATATATATATATATATATATATATATATATATAT 1860
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Db      1801 TAGTATCTATATATATATCTTCTATCTCTATACACATATCCACAGCTTTT 1860
QY      1861 CACAGATTCATGACAGTGCATAATCCCAAGGTAACTTTATTCATTCATGCTGAGTGC 1920
Db      1861 CACAGATTCATGACAGTGCATAATCCCAAGGTAACTTTATTCATTCATGCTGAGTGC 1920
QY      1921 GCTTATGATTTTGGCAATCATGCTGCTATTCATTCACCTTGGATGATGTTGTGC 1980
Db      1921 GCTTATGATTTTGGCAATCATGCTGCTATTCATTCACCTTGGATGATGTTGTGC 1980
QY      1981 TTGTAGTTAATTAAGAAATAGGCACTCTGTGAGCCACTTTAGGGTTCACTCCCTGCG 2040
Db      1981 TTGTAGTTAATTAAGAAATAGGCACTCTGTGAGCCACTTTAGGGTTCACTCCCTGCG 2040
QY      2041 AATAAAGATTTTACAAAGAGTACTAGACCAAGTTTAAAGCTCTGTGTGTGTGT 2100
Db      2041 AATAAAGATTTTACAAAGAGTACTAGACCAAGTTTAAAGCTCTGTGTGTGTGT 2100
QY      2101 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
Db      2101 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
QY      2161 TTTAAACAAGCATGTTTTCAAATGACATGAGCTGCCAATGATGATCACCACCATAT 2220
Db      2161 TTTAAACAAGCATGTTTTCAAATGACATGAGCTGCCAATGATGATCACCACCATAT 2220
QY      2221 CTCATTTATTTCCAGTAAATGATATATATGATCTGTGTAAATATTTTGTGAC 2280
Db      2221 CTCATTTATTTCCAGTAAATGATATATGATCTGTGTAAATATTTTGTGAC 2280
QY      2281 TTCACAAAAGCAGTGGAAATGACACCAATATGCAATATGCAATCTCCACCATCA 2340
Db      2281 TTCACAAAAGCAGTGGAAATGACACCAATATGCAATATGCAATCTCCACCATCA 2340
QY      2341 GCTACACACTGCTTGACATATATGTTTAAAGACACCTGCCATTTGGGTTCTCTTAAC 2400
Db      2341 GCTACACACTGCTTGACATATATGTTTAAAGACACCTGCCATTTGGGTTCTCTTAAC 2400
QY      2401 AAAAATCTTGCAATTTAGGCTCTCAGCTGGGCTGTGCATCAGCGGTTTGAAGAATATCAA 2460
Db      2401 AAAAATCTTGCAATTTAGGCTCTCAGCTGGGCTGTGCATCAGCGGTTTGAAGAATATCAA 2460
QY      2461 TTCTCAGCAGAGCCAGATTTGAATTCCTCATCTTTTAAAGAAATCATTTACAGGTTTG 2520
Db      2461 TTCTCAGCAGAGCCAGATTTGAATTCCTCATCTTTTAAAGAAATCATTTACAGGTTTG 2520
QY      2521 GAGAGGATTTACAGACAGCTCAGCTGCTTTCATATGCTCTGAACCTTGTCCCTCTTTG 2580
Db      2521 GAGAGGATTTACAGACAGCTCAGCTGCTTTCATATGCTCTGAACCTTGTCCCTCTTTG 2580
QY      2581 TGTTCATGATATGCTCAATTAATTAATGTTATCTTGAACCTGATGCTCATAGAGAGATA 2640
Db      2581 TGTTCATGATATGCTCAATTAATTAATGTTATCTTGAACCTGATGCTCATAGAGAGATA 2640
QY      2641 TTAGAATCTGTAGTATATCAATTTAGGATTTCAAGAAATTAAGATTTAAGTCACATA 2700
Db      2641 TTAGAATCTGTAGTATATCAATTTAGGATTTCAAGAAATTAAGATTTAAGTCACATA 2700
QY      2701 CTGGTCAAAAGGAAACCAAGATACAAAGAACTCTGAGCTGTCACTGCCCATCTCTGTGA 2760
Db      2701 CTGGTCAAAAGGAAACCAAGATACAAAGAACTCTGAGCTGTCACTGCCCATCTCTGTGA 2760
QY      2761 GCCAACAACCAAGAGAGACCCCAAGCATGTCTGAGATCTTAAATCAAGAGAAACGAGTG 2820
Db      2761 GCCAACAACCAAGAGAGACCCCAAGCATGTCTGAGATCTTAAATCAAGAGAAACGAGTG 2820
QY      2821 TCATGAGTTGAATTTCTCTATATGATGCTAGTCTTGGGCAATCTGCTCTCTCTT 2880
Db      2821 TCATGAGTTGAATTTCTCTATATGATGCTAGTCTTGGGCAATCTGCTCTCTCTT 2880
QY      2881 GACACATATTTAGCTTTAGCCCTTTCACAGCACTTTTATCTTTTCCCAACATCGC 2940
Db      2881 GACACATATTTAGCTTTAGCCCTTTCACAGCACTTTTATCTTTTCCCAACATCGC 2940

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Db      2881 GACACATATTTAGCTTTAGCCCTTTCACAGCACTTTTATCTTTTCCCAACATCGC 2940
QY      2941 TTACCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3000
Db      2941 TTACCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3000
QY      3001 CAAGCTTTTCTTCCATCCCACTAATCTGAAT 3036
Db      3001 CAAGCTTTTCTTCCATCCCACTAATCTGAAT 3036

RESULT 4
ID      ABK92196 standard; DNA; 3923 BP.
AC      ABK92196;
XX      15-AUG-2002 (first entry)
XX      15-AUG-2002 (first entry)
DE      Prostate cancer-associated DNA sequence #82.
XX      Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW      gene therapy; gene; ds.
XX      Mammalia.
PN      WO200230268-A2.
XX      18-APR-2002.
XX      12-OCT-2001; 2001WO-US32045.
XX      13-OCT-2000; 2000US-0687576.
PR      08-DEC-2000; 2000US-0733288.
PR      08-DEC-2000; 2000US-0733742.
PR      24-JAN-2001; 2001US-263957P.
PR      16-MAR-2001; 2001US-276791P.
PR      16-MAR-2001; 2001US-276888P.
PR      06-APR-2001; 2001US-281922P.
PR      24-APR-2001; 2001US-286214P.
PR      30-APR-2001; 2001US-084704P.
PR      04-MAY-2001; 2001US-288589P.
XX      (EOBR-) EOS BIOTECHNOLOGY INC.
XX      Gish KC, Mack DH, Wilson KE, Afar D, Heyezi P;
PI      WPI; 2002-471335/50.
XX      Detecting a prostate cancer-associated transcript in a cell in a
PT      patient, useful for diagnosing prostate cancer (PC) or screening
PT      modulators of PC, by determining if prostate cancer-associated genes
PT      are expressed in a prostate tissue
XX      Claim 22; Page 365-366; 436pp; English.
XX      The present invention relates to methods of detecting a prostate
CC      cancer-associated transcript in a cell from a patient. The method
CC      comprises contacting a biological sample from the patient with
CC      prostate cancer-associated polynucleotides (designated PC genes) that
CC      selectively hybridise to a sequence that is at least 80% identical
CC      to them. The prostate cancer-associated polynucleotide sequences
CC      are differentially expressed in prostate tumour tissue or in
CC      prostate cancer and are derived from the tissues of various
CC      organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC      The methods of the invention are useful for diagnosing and treating
CC      prostate cancer in mammals. The prostate cancer-associated genes are
CC      useful for diagnosing or treating prostate cancer, as well as for
CC      identifying modulators of prostate cancer or agents that inhibit
CC      prostate cancer. The nucleic acid sequences are particularly useful
CC      in gene therapy, as a vaccine or in antisense applications.
CC      ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC      sequences.

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XX	Sequence	3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;	
SQL	Query Match	84.8%; Score 3036; DB 24; Length 3923;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 3036; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1	ACAGAGAATAATGCAAGTGGCCGAGAGAGCTGGCATCAGAAAAACAGAGGGGAGATTGTGT	60
DB	1	ACAGAGAATAATGCAAGTGGCCGAGAGAGCTGGCATCAGAAAAACAGAGGGGAGATTGTGT	60
OY	61	GGCTGCACCGGAGGAGACAGAGAGATCTGATGTTGGAAAGAGCCGTGATGATCAAG	120
DB	61	GGCTGCACCGGAGGAGACAGAGAGATCTGATGTTGGAAAGAGCCGTGATGATCAAG	120
OY	121	GAATTACACACATATATCTAGTGTGTTCAATGAACACCAAGATAATTAATGTAAGAGCTA	180
DB	121	GAATTACACACATATATCTAGTGTGTTCAATGAACACCAAGATAATTAATGTAAGAGCTA	180
OY	181	GTCGGCTGTAGTCTCTCAGTACACAGGGCTGGATCACCATCGACGGCACTTTCTGAG	240
DB	181	GTCGGCTGTAGTCTCTCAGTACACAGGGCTGGATCACCATCGACGGCACTTTCTGAG	240
OY	241	TACTCAGTGCAGCAAGAAGACATACAGACATCTCAATGCGAGGGGTGAGAAATAGAAA	300
DB	241	TACTCAGTGCAGCAAGAAGACATACAGACATCTCAATGCGAGGGGTGAGAAATAGAAA	300
OY	301	GGCTGCACCTTATACATCTGAGGCGACACATCTGCTGAATGAGATATTAACATCAC	360
DB	301	GGCTGCACCTTATACATCTGAGGCGACACATCTGCTGAATGAGATATTAACATCAC	360
OY	361	TAGAAACAGACAGATGACATATATATGTCTAAGTAGTACATGTTTTGACATTTCCAG	420
DB	361	TAGAAACAGACAGATGACATATATATGTCTAAGTAGTACATGTTTTGACATTTCCAG	420
OY	421	CCCCCTTAATATATCCACACACAGAGAACAAAGAAAGAACACAGAGATCCCTGGGGA	480
DB	421	CCCCCTTAATATATCCACACACAGAGAACAAAGAAAGAACACAGAGATCCCTGGGGA	480
OY	481	AATGCCCGGCCCATCTTGGGTATCGATGAGCCCTGCCCTGTGCTGCTCCGCTTGT	540
DB	481	AATGCCCGGCCCATCTTGGGTATCGATGAGCCCTGCCCTGTGCTGCTCCGCTTGT	540
OY	541	GAGGAGAGACATTAAGAAATGAATGTGTTCTTAAGATGGGACAGAAAACGA	600
DB	541	GAGGAGAGACATTAAGAAATGAATGTGTTCTTAAGATGGGACAGAAAACGA	600
OY	601	TCTGTGTGATATTTATTGAACGGGATTAACAGATTGAAATGAAGTCCAAAGTGA	660
DB	601	TCTGTGTGATATTTATTGAACGGGATTAACAGATTGAAATGAAGTCCAAAGTGA	660
OY	661	CATTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCTTACAAAGCATGCAACA	720
DB	661	CATTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCTTACAAAGCATGCAACA	720
OY	721	AACAAAATGGAATCTGTGATGACATGAGCGCAAGCTGGGAGAGATTAACACGGG	780
DB	721	AACAAAATGGAATCTGTGATGACATGAGCGCAAGCTGGGAGAGATTAACACGGG	780
OY	781	GCAGAGGATCAGATTTGGCCCTGCTGCTAAACTGCGCTTATTAACCAAACTATTC	840
DB	781	GCAGAGGATCAGATTTGGCCCTGCTGCTAAACTGCGCTTATTAACCAAACTATTC	840
OY	841	ATATTTTAAACCTCAAAACAAAGCTTTGTAATATGATCTCTACGGTCTCTTGGG	900
DB	841	ATATTTTAAACCTCAAAACAAAGCTTTGTAATATGATCTCTACGGTCTCTTGGG	900
OY	901	CCCAACATTTCTCATATATTCACGACACATCTATTTTAATATTAATTTCCAGATCTGA	960
DB	901	CCCAACATTTCTCATATATTCACGACACATCTATTTTAATATTAATTTCCAGATCTGA	960
OY	961	CTGTGACCTTTCTACGTAGATAATACATTACATTTTGTTAAGACCCCTTGCTT	1020
DB	961	CTGTGACCTTTCTACGTAGATAATACATTACATTTTGTTAAGACCCCTTGCTT	1020
OY	1021	GCTGCCATATATATGATGACGTGTTTTCTTAAGAGTGTCTGGCCAGGGGATCTGTG	1080
DB	1021	GCTGCCATATATATGATGACGTGTTTTCTTAAGAGTGTCTGGCCAGGGGATCTGTG	1080
OY	1081	AACAGCTGGGAAGCATCTCAAGATCTTTCAGAGGTTTACTTACTACACACAGCATGA	1140
DB	1081	AACAGCTGGGAAGCATCTCAAGATCTTTCAGAGGTTTACTTACTACACACAGCATGA	1140
OY	1141	TCATTACGAGATGATTTCTTAATCAATATATCTCTAGTGTCTTGGCCATCTGAAT	1200
DB	1141	TCATTACGAGATGATTTCTTAATCAATATATCTCTAGTGTCTTGGCCATCTGAAT	1200
OY	1201	TCATTTCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGATTCATTCATTAATATCA	1260
DB	1201	TCATTTCCACTTTTGTGCCATCTCTCAAGACCTCAAAATGATTCATTCATTAATATCA	1260
OY	1261	GGATTAACCTTTTTTTTTTAACCTGGAGAAATTCATATGACGATATGGGAATTTA	1320
DB	1261	GGATTAACCTTTTTTTTTTAACCTGGAGAAATTCATATGACGATATGGGAATTTA	1320
OY	1321	ATTACATATTTTGTGTTTCCAGTACGAAAGATGACTATAGTCTTTATCCCTCCCTTGT	1380
DB	1321	ATTACATATTTTGTGTTTCCAGTACGAAAGATGACTATAGTCTTTATCCCTCCCTTGT	1380
OY	1381	GATTTTCTCCAGTATTAAGTTAAATGCTTAGCGCTGTACTGAGGCTGTATACAGAC	1440
DB	1381	GATTTTCTCCAGTATTAAGTTAAATGCTTAGCGCTGTACTGAGGCTGTATACAGAC	1440
OY	1441	AGCCTCTCCCATCCCTCCACACCTTATCTGATCACCATCAACCCCTCCCATACACCT	1500
DB	1441	AGCCTCTCCCATCCCTCCACACCTTATCTGATCACCATCAACCCCTCCCATACACCT	1500
OY	1501	AAACAAAATCTTAATCTGTAATCTCTGAACATGTACAGACATACATTAATCTCTGCT	1560
DB	1501	AAACAAAATCTTAATCTGTAATCTCTGAACATGTACAGACATACATTAATCTCTGCT	1560
OY	1561	GAGAAAGCTCTCTGCTCTCTTAATCTGAGATGATGAAGTTTGAATGAATGACTA	1620
DB	1561	GAGAAAGCTCTCTGCTCTCTTAATCTGAGATGATGAAGTTTGAATGAATGACTA	1620
OY	1621	TCTTACTTCATGCAAAAGAGGACATATGATGATTAATTAATGAATGCAAGGCCACAGA	1680
DB	1621	TCTTACTTCATGCAAAAGAGGACATATGATGATTAATTAATGAATGCAAGGCCACAGA	1680
OY	1681	CTAAAAGTATTTGATTAATGAAGTTTACATTAATTAATGAATGCAAGGCCACAGA	1740
DB	1681	CTAAAAGTATTTGATTAATGAAGTTTACATTAATTAATGAATGCAAGGCCACAGA	1740
OY	1741	GGGAAATGTTTATGGGGACGTTTGTAAAGCTGGGATGTGAAGCAAGGACGAACTCA	1800
DB	1741	GGGAAATGTTTATGGGGACGTTTGTAAAGCTGGGATGTGAAGCAAGGACGAACTCA	1800
OY	1801	TAGTATCTTATATATATTAATCTTCAATCTCTATCTATCAATATCCAAACAGCTTTT	1860
DB	1801	TAGTATCTTATATATATTAATCTTCAATCTCTATCTATCAATATCCAAACAGCTTTT	1860
OY	1861	CACGAATTCATGAGAGGCAAAATCCCAAGGTAACTTTTACATTTTCAATGAGTGC	1920
DB	1861	CACGAATTCATGAGAGGCAAAATCCCAAGGTAACTTTTACATTTTCAATGAGTGC	1920
OY	1921	GCTTTAAATTTTGGCAAAATCATCTGTCTCAATCTCAAACTTTGAGATGTGTTGCC	1980
DB	1921	GCTTTAAATTTTGGCAAAATCATCTGTCTCAATCTCAAACTTTGAGATGTGTTGCC	1980
OY	1981	TTGTAGTTAATTTGAAGAAATAGGGCACTTTGTGAGCCACTTTAGGGTTCATCTGGC	2040
DB	1981	TTGTAGTTAATTTGAAGAAATAGGGCACTTTGTGAGCCACTTTAGGGTTCATCTGGC	2040
OY	2041	AATTAAGAAATTTACAAAGAGCTACTCAGACACATTTTGAAGAGCTCTGTGTGTGT	2100
DB	2041	AATTAAGAAATTTACAAAGAGCTACTCAGACACATTTTGAAGAGCTCTGTGTGTGT	2100


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Db      2101 GGTGTGTGTGAGTGTACATGCCAAAGTGGCTCTCTCTGTGACCCATTTATTTACAGAC 2160
QY      2161 TTTAAAACAGACAGTTTTCGAATGACATGAGCGCCAAAGATGATACACACATAT 2220
Db      2161 TTTAAAACAGACAGTTTTCGAATGACATGAGCGCCAAAGATGATACACACATAT 2220
QY      2221 CTCATTATCTCCAGTAAATGTGATTAATGTCAATCTGTAAATATAAAGTTTGAC 2280
Db      2221 CTCATTATCTCCAGTAAATGTGATTAATGTCAATCTGTAAATATAAAGTTTGAC 2280
QY      2281 TTACAAAAGACAGCTGGAATGACACACAAATATGATTAATCTAACCTTACCATCA 2340
Db      2281 TTACAAAAGACAGCTGGAATGACACACAAATATGATTAATCTAACCTTACCATCA 2340
QY      2341 GGTACACACTGCTTACATATTTGTGTAAAGCAGCTGGCATTGTGGGTTCTCTTAAC 2400
Db      2341 GGTACACACTGCTTACATATTTGTGTAAAGCAGCTGGCATTGTGGGTTCTCTTAAC 2400
QY      2401 AAAATACCTTGATTAAGTCTCAGCTGGGCTGTGCATCAGGGGTTTGAATAATTCAA 2460
Db      2401 AAAATACCTTGATTAAGTCTCAGCTGGGCTGTGCATCAGGGGTTTGAATAATTCAA 2460
QY      2461 TTCTCAGCAGAAAGCAGAAATTTGAATCCCTCATCTTTTGAATCATTTACAGGTTG 2520
Db      2461 TTCTCAGCAGAAAGCAGAAATTTGAATCCCTCATCTTTTGAATCATTTACAGGTTG 2520
QY      2521 GAGAGATTCACAGACGCTCAGCTGCTTTCATTAATGCTCTGACCTGCTCTTTG 2580
Db      2521 GAGAGATTCACAGACGCTCAGCTGCTTTCATTAATGCTCTGACCTGCTCTTTG 2580
QY      2581 TGTTCATGATAGTCCATTAATTAATTTATCTTTGAAGTGCATAGAGAGATA 2640
Db      2581 TGTTCATGATAGTCCATTAATTAATTTATCTTTGAAGTGCATAGAGAGATA 2640
QY      2641 TAAGAACTCTGAGTATCAACATTAGGATTCAAAGAAATTTAGATTAAAGCTCACA 2700
Db      2641 TAAGAACTCTGAGTATCAACATTAGGATTCAAAGAAATTTAGATTAAAGCTCACA 2700
QY      2701 CTGGTCAAAAGAACCAAGATACAAAGAACTGTGAGCTGTCAATCGCCCATCTCTGTA 2760
Db      2701 CTGGTCAAAAGAACCAAGATACAAAGAACTGTGAGCTGTCAATCGCCCATCTCTGTA 2760
QY      2761 GCCAACCAACAGACAGACCCACGATGTCTGAGATCTTAAATCAAGAAACAGTG 2820
Db      2761 GCCAACCAACAGACAGACCCACGATGTCTGAGATCTTAAATCAAGAAACAGTG 2820
QY      2821 TCATGAGTTGAATTCCTATTATGAGATCTAGCTTCTGGCATCTCTGCTCTCTT 2880
Db      2821 TCATGAGTTGAATTCCTATTATGAGATCTAGCTTCTGGCATCTCTGCTCTCTT 2880
QY      2881 GACACATATTAAGCTTCTAGCTTGTGCTTCACAGACTTTATCTTTCTCCACACATGCC 2940
Db      2881 GACACATATTAAGCTTCTAGCTTGTGCTTCACAGACTTTATCTTTCTCCACACATGCC 2940
QY      2941 TTACCAATCTCTCTCTGCTGTGCTTGTGACTTCCACAGAATTTCAACGACTCT 3000
Db      2941 TTACCAATCTCTCTCTGCTGTGCTTGTGACTTCCACAGAATTTCAACGACTCT 3000
QY      3001 CAAGTCTTTTCTTCATCCCAACCACTAAGCTGAAT 3036
Db      3001 CAAGTCTTTTCTTCATCCCAACCACTAAGCTGAAT 3036

```

RESULT 6
 ACAS9834
 ID ACAS9834 standard; cDNA: 3923 BP.
 AC ACAS9834;
 XX
 XX 10-JUN-2003 (first entry)
 DE Prostate cancer therapy associated cDNA #545.

```

XX      XX      Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW      KW      immunogen; cancer; prostate specific antigen; PSA;
KW      KW      prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW      KW      PSMa; gene; ss.
XX      XX      Homo sapiens.
XX      OS      US2002192763-A1.
XX      PD      19-DEC-2002.
XX      XX      29-JUN-2001; 2001US-0895793.
XX      XX      17-APR-2000; 2000US-157455P.
XX      PR      04-OCT-2000; 2000US-0679272.
XX      PR      28-MAR-2001; 2001US-0822827.
XX      XX      (XUJ/) XU J.
XX      PA      (DILL/) DILLON D C.
XX      PA      (MITC/) MITCHAM J L.
XX      PA      (HARL/) HARLOCKER S L.
XX      PA      (JIAN/) JIANG Y.
XX      PA      (KALO/) KALOS M D.
XX      PA      (FANG/) FANGER G R.
XX      PA      (RETT/) RETTER M W.
XX      PA      (STOL/) STOLK J A.
XX      PA      (DAYC/) DAY C H.
XX      PA      (VEDV/) VEDVICK T S.
XX      PA      (CART/) CARTER D.
XX      PA      (LISX/) LI S X.
XX      PA      (WANG/) WANG A.
XX      PA      (SKEI/) SKEIKY Y A W.
XX      PA      (HEPL/) HEPLER W T.
XX      PA      (HEND/) HENDERSON R A.
XX      PA      (HURA/) HURAI J.
XX      PA      (MCNE/) MCNEILL P D.
XX      PA      (HOUN/) HOUGHTON R L.
XX      PA      (DBAS/) Y DE BASSOLS C V.
XX      PA      (FOYT/) FOY T M.
XX      PI      XU J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX      PI      Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX      PI      Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hurai J;
XX      PI      McNeill PD, Houghton RL, Y De Bassols CV, Foy TM.
XX      DR      WPI: 2003-352711/33.
XX      XX      New fusion protein comprising prostate-specific polypeptides, or its
XX      PT      immunogenic portions, useful for diagnosing, preventing and/or treating
XX      PT      cancer, particularly prostate cancer
XX      PS      Example 16: SEQ ID NO 690; 85bp; English.
XX      XX      The invention describes a fusion protein comprising at least one amino
XX      CC      acid sequence of immunogenic portions of any of the 3 sequences not
XX      CC      defined in the specification, or sequences having at least 70 or 90 %
XX      CC      sequence identity to any one of the 35 sequences defined in the USPTO
XX      CC      web site, which is encoded by any of the 4 nucleotide sequences not
XX      CC      defined in the specification. The fusion protein, composition and
XX      CC      methods are useful for diagnosing, preventing and/or treating cancer,
XX      CC      particularly prostate cancer. The proteins are useful as markers to
XX      CC      indicate the presence or absence of cancer. This sequence
XX      CC      represents a prostate cancer therapy associated cDNA.
XX      CC      Note: The sequence data for this patent did not form part of the
XX      CC      printed specification, but was obtained in electronic format directly
XX      CC      from the US patent office at
XX      CC      seqdata.uspto.gov/sequence.html?DocID=US20020192763.
XX      SQ      Sequence 3923 BP; 1157 A; 840 C; 740 G; 1186 T; 0 other;

```

Query Match 84.8%; Score 3036; DB 25; Length 3923;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	ACAGAGAAATAGCAAGTGGCGAGAGCTGGCATCAGAAAAACAGAGGGGAGATTGTGT	60	
Dd	1	ACAGAGAAATAGCAAGTGGCGAGAGCTGGCATCAGAAAAACAGAGGGGAGATTGTGT	60	
Qy	61	GGCTGACGCCAGGAGAGACCAAGAAATCTGCAATGGTGGAAAGACATGATGATACAG	120	
Dd	61	GGCTGACGCCAGGAGAGACCAAGAAATCTGCAATGGTGGAAAGACATGATGATACAG	120	
Qy	121	GAATTACAAACATATCTAGTGTGTTCAATGAACACCAAGATAAATAGTAAGAGCTA	180	
Dd	121	GAATTACAAACATATCTAGTGTGTTCAATGAACACCAAGATAAATAGTAAGAGCTA	180	
Qy	181	GTCCGTGTGAGTCTCTCAGTGCACACAGGGCTGGATCACCATGCAGCGCATTTCTGAG	240	
Dd	181	GTCCGTGTGAGTCTCTCAGTGCACACAGGGCTGGATCACCATGCAGCGCATTTCTGAG	240	
Qy	241	TACTCAGTGCAGCAAGAAAGACTACAGACATCTCAATGSCAGGGGTGAGAAATAGAAA	300	
Dd	241	TACTCAGTGCAGCAAGAAAGACTACAGACATCTCAATGSCAGGGGTGAGAAATAGAAA	300	
Qy	301	GGCTGCTGACTTTTACATCTGAGGGCACACATCTGCTGAANTGGAGTAATTAACATCAC	360	
Dd	301	GGCTGCTGACTTTTACATCTGAGGGCACACATCTGCTGAANTGGAGTAATTAACATCAC	360	
Qy	361	TAGAAGACGACAGATGACAAATATATGTCTAAGTAGACATGTTTTGACATTTCCAG	420	
Dd	361	TAGAAGACGACAGATGACAAATATATGTCTAAGTAGACATGTTTTGACATTTCCAG	420	
Qy	421	CCCCCTTAAATATCCACACACAGAAAGCAAAAGAAAGAACACAGAGATCCCTGGGAGA	480	
Dd	421	CCCCCTTAAATATCCACACACAGAAAGCAAAAGAAAGAACACAGAGATCCCTGGGAGA	480	
Qy	481	AATGCCGCCGCCATCTTGGGTGATCGATGAGCTGCCCTGTGCTGCTGCCGCTGT	540	
Dd	481	AATGCCGCCGCCATCTTGGGTGATCGATGAGCTGCCCTGTGCTGCTGCCGCTGT	540	
Qy	541	GAGGAGAGGACATTGAAATGAAATGATGTGTTCTTAAAGATGGCGAGAAACAGA	600	
Dd	541	GAGGAGAGGACATTGAAATGAAATGATGTGTTCTTAAAGATGGCGAGAAACAGA	600	
Qy	601	TCCGTGTGTGATTTTATTTGAACGGGATTACAGATTTGAAATGAAGTCCAAAGTAG	660	
Dd	601	TCCGTGTGTGATTTTATTTGAACGGGATTACAGATTTGAAATGAAGTCCAAAGTAG	660	
Qy	661	CATTACCAATGAGAGGAAACAGACGAGAAATCTTGTGCTTACACAGACATGCAACA	720	
Dd	661	CATTACCAATGAGAGGAAACAGACGAGAAATCTTGTGCTTACACAGACATGCAACA	720	
Qy	721	AACAAATGGAATCTGTGATGACATGAGCGACCAAGCTGGGAGGAGATACCAACGGG	780	
Dd	721	AACAAATGGAATCTGTGATGACATGAGCGACCAAGCTGGGAGGAGATACCAACGGG	780	
Qy	781	GCAGAGGCTGAGATTTGGGCCCTGTGCCCTTAACCTGGCTGATTAACCAATCATTTTC	840	
Dd	781	GCAGAGGCTGAGATTTGGGCCCTGTGCCCTTAACCTGGCTGATTAACCAATCATTTTC	840	
Qy	841	ATATTTTAAACCTCAAAACAAAGCTGTGTAATATGATCTGACGGTCTCTTGGG	900	
Dd	841	ATATTTTAAACCTCAAAACAAAGCTGTGTAATATGATCTGACGGTCTCTTGGG	900	
Qy	901	CCCAACATTTCTCCATATATCCAGCACACATCATTTTAAATTTAGTTCCAGATCTGTA	960	
Dd	901	CCCAACATTTCTCCATATATCCAGCACACATCATTTTAAATTTAGTTCCAGATCTGTA	960	
Qy	961	CTGAGACCTTTCTACCTGATAGATTAACATTTACTCATTTTGTAAAGACCTTCGTGT	1020	
Dd	961	CTGAGACCTTTCTACCTGATAGATTAACATTTACTCATTTTGTAAAGACCTTCGTGT	1020	
Qy	1021	GCTGCTAATATGATGACTGCTGTTTTTCCTAAGAGAGTGTCTGGCCAGGGGATCTGTG	1080	
Dd	1021	GCTGCTAATATGATGACTGCTGTTTTTCCTAAGAGAGTGTCTGGCCAGGGGATCTGTG	1080	

Qy	1081	AACAGCTGGGAGCATCTCAAGATCTTCCAGGGTATACTACTACACAGACATGA	1140	
Dd	1081	AACAGCTGGGAGCATCTCAAGATCTTCCAGGGTATACTACTACACAGACATGA	1140	
Qy	1141	TCATTACGAGAGTGAATATATCAATCAATCATCTCAGTGTCTTTGCCATCTGAAT	1200	
Dd	1141	TCATTACGAGAGTGAATATATCAATCAATCATCTCAGTGTCTTTGCCATCTGAAT	1200	
Qy	1201	TCATTGCCACTTTTGTGCCCATCTCTCAAGACCTCAAAATGTCAATTCATTAATACCA	1260	
Dd	1201	TCATTGCCACTTTTGTGCCCATCTCTCAAGACCTCAAAATGTCAATTCATTAATACCA	1260	
Qy	1261	GGATTAACCTTTTAACTGGAATAATTCATATGATGACAGCTATGGGAATTTA	1320	
Dd	1261	GGATTAACCTTTTAACTGGAATAATTCATATGATGACAGCTATGGGAATTTA	1320	
Qy	1321	ATTAACATATTTTGTTCAGTGCAGAAAGATGACTAAGTCTTTATCCCTCCCTTGT	1380	
Dd	1321	ATTAACATATTTTGTTCAGTGCAGAAAGATGACTAAGTCTTTATCCCTCCCTTGT	1380	
Qy	1381	GATTTTTCAGATTAAGTTAAATGCTTAGCCTGTGACTGAGGCTGATACAGAC	1440	
Dd	1381	GATTTTTCAGATTAAGTTAAATGCTTAGCCTGTGACTGAGGCTGATACAGAC	1440	
Qy	1441	AGCCTTCGCCATCCCTCCAGCCTTATCTGTCATACACATCAACCCCTCCATACACCT	1500	
Dd	1441	AGCCTTCGCCATCCCTCCAGCCTTATCTGTCATACACATCAACCCCTCCATACACCT	1500	
Qy	1501	AAACAAATCTTAATCTGTAATCTCTGTAACATGTCAGACATACATTAATCTCTGCT	1560	
Dd	1501	AAACAAATCTTAATCTGTAATCTCTGTAACATGTCAGACATACATTAATCTCTGCT	1560	
Qy	1561	GAGAAGCTCTCTGTCCTTAAATCTAGAAATATGAAAGTTTGAATAGTTGACTA	1620	
Dd	1561	GAGAAGCTCTCTGTCCTTAAATCTAGAAATATGAAAGTTTGAATAGTTGACTA	1620	
Qy	1621	TCTTACTTCATGCAAGAGGACACATATGAGATTCATCTATCAGATGACAGCAATA	1680	
Dd	1621	TCTTACTTCATGCAAGAGGACACATATGAGATTCATCTATCAGATGACAGCAATA	1680	
Qy	1681	CTAAAGGTATATTTGATTAAGATTTTACATTAATTAATGAAGTCAAGAGCCACAGA	1740	
Dd	1681	CTAAAGGTATATTTGATTAAGATTTTACATTAATTAATGAAGTCAAGAGCCACAGA	1740	
Qy	1741	GGGAATGTTTATGGGGACGTTTGTAAAGCCCTGGGATGTGAAGCAAGGCAAGCTCA	1800	
Dd	1741	GGGAATGTTTATGGGGACGTTTGTAAAGCCCTGGGATGTGAAGCAAGGCAAGCTCA	1800	
Qy	1801	TAGTATCTTATATATATACTTCAATTTCTCTATCTATGCAATATCCAAAGCTTTT	1860	
Dd	1801	TAGTATCTTATATATATACTTCAATTTCTCTATCTATGCAATATCCAAAGCTTTT	1860	
Qy	1861	CACGAATTCATGAGAGGCAAAATCCCAAGGTAACTTTATCCATTTCAATGGAGATGC	1920	
Dd	1861	CACGAATTCATGAGAGGCAAAATCCCAAGGTAACTTTATCCATTTCAATGGAGATGC	1920	
Qy	1921	GCTTTAGAAATTTGGCAATCATCTGCTCAATATGCAACTTTGAGATGTGTTGTC	1980	
Dd	1921	GCTTTAGAAATTTGGCAATCATCTGCTCAATATGCAACTTTGAGATGTGTTGTC	1980	
Qy	1981	TTGTAGTTAATTTGAAAGAAATAGGGCACTCTTGTGAGCCACTTTAGGGTTCACCTGGC	2040	
Dd	1981	TTGTAGTTAATTTGAAAGAAATAGGGCACTCTTGTGAGCCACTTTAGGGTTCACCTGGC	2040	
Qy	2041	AATTAAGATTTTAAAGAGCTACTCAGAGACCAATTTGTAAGAGCTCTGTGTGTGTGT	2100	
Dd	2041	AATTAAGATTTTAAAGAGCTACTCAGAGACCAATTTGTAAGAGCTCTGTGTGTGTGT	2100	
Qy	2101	GTTGTGTGTGAGAGTGCATGSCAAAGTGTGSCCTCTCTCTTACACCATTAATTTCAAG	2160	
Dd	2101	GTTGTGTGTGAGAGTGCATGSCAAAGTGTGSCCTCTCTCTTACACCATTAATTTCAAG	2160	

OS	Homo sapiens.	Location/Qualifiers
XX	Key	379..534
XX	CD5	/*tag= a
XX	polyA_signal	/product= "PCa3 protein variant 1"
XX		2019..2024
XX		/*tag= b
XX	MO9845420-A1.	
XX	15-OCT-1998.	
XX	09-APR-1998;	98WO-CA00346.
XX	10-APR-1997;	97US-0041836.
XX	(DIAG-) DIAGNOCURE INC.	
XX	Bussemakers MJG;	
XX	WPI: 1998-568347/48.	
XX	P-PSDB: AAW/9736.	
XX	New nucleic acid encoding prostate cancer antigen 3 - for diagnosis, prevention and treatment of prostatic cancer	
XX	Claim 3; Fig 2B-2J; 11pp; English.	
XX	The present sequence represents the prostate cancer antigen (PCa3)	
XX	CC cDNA splice variant 1 sequence comprising of exons 1, 2, 3, 4a and	
XX	CC 4b of the PCa3 gene. The PCa3 cDNA splice variant 1 sequence,	
XX	CC isolated from a human primary prostatic tumour tissue cDNA library,	
XX	CC was found in approximately 3% of the cDNA clones isolated. The	
XX	CC invention claims for PCa3 cDNA variants and the proteins they encode.	
XX	CC The invention also claims for antibodies against PCa3 protein. The	
XX	CC antibodies are claimed to be useful for detecting PCa3 protein in	
XX	CC immunoassay tests, for diagnosing, assessing and prognosing of	
XX	CC prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin	
XX	CC or radioisotope, and nucleic acids antisense to PCa3 cDNA are claimed	
XX	CC to be useful for treating PC, while determining elevated levels of	
XX	CC PCa3 (as RNA or protein) is useful for detecting a predisposition	
XX	CC to development of PC, e.g. in prenatal tests. Detecting PCa3 protein	
XX	CC allows differentiation between malignant and benign prostatic disease,	
XX	CC and the level of PCa3 expression allows correlation with the grade of	
XX	CC tumour. PCa3 protein and its fragments are also claimed to be useful	
XX	CC in vaccines for preventing PC; in drug screens for identifying	
XX	CC specific (ant)agonists (potentially useful therapeutically) and for	
XX	CC studying protein-DNA interactions.	
XX	Sequence 2037 BP: 622 A; 426 C; 406 G; 575 T; 8 other;	
XX	Query Match 45.5%; Score 1629; DB 19; Length 2037;	
XX	Best Local Similarity 99.6%; Pred. No. 0;	
XX	Matches 2029; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	
XX	23 AGAAGCTGGCATTGAGAAAAACAGAGGGGAATTTGTGTGCTGCAGCCGAGGAGACAG 82	
XX	1 AGAAGCTGGCATTGAGAAAAACAGAGGGGAATTTGTGTGCTGCAGCCGAGGAGACAG 60	
XX	83 GAAAGATTGGATGGTGGGAGAGCACTGATGATTCAGAGGAATTAACAACATATTAAGTAC 142	
XX	61 GAAAGATTGGATGGTGGGAGAGCACTGATGATTCAGAGGAATTAACAACATATTAAGTAC 120	
XX	143 TGTTCATGTAACACCAAGATAAATAAGTAAGAGAGTACGCGCTGTGACTCTCCACAGT 202	
XX	121 TGTTCATGTAACACCAAGATAAATAAGTAAGAGAGTACGCGCTGTGACTCTCCACAGT 180	
XX	203 GACACAGGGCTGCATCACCATTGCAGCGCACTTTCTGAGTACTAGTGCACGAAAGAAAGA 262	
XX	181 GACACAGGGCTGCATCACCATTGCAGCGCACTTTCTGAGTACTAGTGCACGAAAGAAAGA 240	

QY 263 CTACAGACATCTCAATGGCGAGGGGTGAGAAATAGAAAGGCTGCTGACTTACCATCTGA 322
DB 241 CTACAGACATCTCAATGGCGAGGGGTGAGAAATAGAAAGGCTGCTGACTTACCATCTGA 300
QY 323 GGCCACACATCTGGCTGAATGGAGTAAATTAACATCATCTAGAAAGAGAAAGTGCATA 382
DB 301 GGCCACACATCTGGCTGAATGGAGTAAATTAACATCATCTAGAAAGAGAAAGTGCATA 360
QY 383 TAATGTCTTAAGTAGTACATGTTTTGACATTTCCACCCCTTTAAATATCCACACACA 442
DB 361 TAATGTCTTAAGTAGTACATGTTTTGACATTTCCACCCCTTTAAATATCCACACACA 420
QY 443 CAGAGAGCAAAAAGGAAGCAGAGATCCCTGGAGAAATGCCGCCGCATCTTGGG 480
DB 421 CAGAGAGCAAAAAGGAAGCAGAGATCCCTGGAGAAATGCCGCCGCATCTTGGG 480
QY 503 TCATGATGAGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 562
DB 481 TCATGATGAGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 563 AATTGATGCTGCTCTTAAGAGATGGGAGAAACAGATCCTGTTGTGATATTTATTTG 622
DB 541 AATTGATGCTGCTCTTAAGAGATGGGAGAAACAGATCCTGTTGTGATATTTATTTG 600
QY 623 AAGCGATTACAGATTTGAATGAAGTACAAAGTACATTTACCAATGAGAGAAAACA 682
DB 601 AAGCGATTACAGATTTGAATGAAGTACAAAGTACATTTACCAATGAGAGAAAACA 660
QY 683 GACGAGAAATCTTGATGCTTCAACAGATGCAACAAACAAATGGAATAGTGTGATG 742
DB 661 GACGAGAAATCTTGATGCTTCAACAGATGCAACAAACAAATGGAATAGTGTGATG 720
QY 743 ACATGAGGACCCAAAGCTGGGGAGAGATTAACACAGGGGACAGAGGTCAGATTTCTGCC 802
DB 721 ACATGAGGACCCAAAGCTGGGGAGAGATTAACACAGGGGACAGAGGTCAGATTTCTGCC 780
QY 803 CTGCTGCTTAAGCTGGCTCATTAACCAATTCATTTCTATCTTAACCTCAAAACAA 862
DB 781 CTGCTGCTTAAGCTGGCTCATTAACCAATTCATTTCTATCTTAACCTCAAAACAA 840
QY 863 AGCTGTGTATATCTGATCTCTACAGGTTCTTCCGCGCCAACTTCCTCATATATCA 922
DB 841 AGCTGTGTATATCTGATCTCTACAGGTTCTTCCGCGCCAACTTCCTCATATATCA 900
QY 923 GCCACACTATTTTATATTTAGTTCACAGATCTGTGACCTTTTACACTGTAG 982
DB 901 GCCACACTATTTTATATTTAGTTCACAGATCTGTGACCTTTTACACTGTAG 960
QY 983 AATAACATTTACTATTTTGTCAAAAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1042
DB 961 AATAACATTTACTATTTTGTCAAAAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1043 GTTTTTCCTTAAGAGTGTCTGGCCAGGGGATCTGTAAACAGGCTGGGAGACATCTCAA 1102
DB 1021 GTTTTTCCTTAAGAGTGTCTGGCCAGGGGATCTGTAAACAGGCTGGGAGACATCTCAA 1080
QY 1103 GATCTTTCAGGGTTATCTACTAGACACACAGCATGATCATTAACGAGTGAATATCTA 1162
DB 1081 GATCTTTCAGGGTTATCTACTAGACACACAGCATGATCATTAACGAGTGAATATCTA 1140
QY 1163 ATCAACATTCATCCCTCAGTGTCTTGCCCATCTGAAATTCATTTTCCACTTTTGCCCA 1222
DB 1141 ATCAACATTCATCCCTCAGTGTCTTGCCCATCTGAAATTCATTTTCCACTTTTGCCCA 1200
QY 1223 TTCTCAAGACCTCAAAATGTCATTCATTAATATCACAGATTAACCTTTTATTAAC 1282
DB 1201 TTCTCAAGACCTCAAAATGTCATTCATTAATATCACAGATTAACCTTTTATTAAC 1260
QY 1283 TGAAGAATTCATATGTTACATGACGCTATGGGAAATTAATTAATTTTGTTCAGT 1342
DB 1261 TGAAGAATTCATATGTTACATGACGCTATGGGAAATTAATTAATTTTGTTCAGT 1320
QY 1343 GCAAAAGTACTAGTCTTATCTCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1402

DB 1321 GCAAAAGTACTAGTCTTATCTCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1403 TAAATGCTTGACCTGTAGAGGCTGTATACACAGACGCTCCCATCCCTCCAGC 1462
DB 1381 TAAATGCTTGACCTGTAGAGGCTGTATACACAGACGCTCCCATCCCTCCAGC 1440
QY 1463 CTATCTGCTCATACCATCAACCCCTCCCATACCACTGAACAAATATCACTTGAAT 1522
DB 1441 CTATCTGCTCATACCATCAACCCCTCCCATATYSACCTAAACAAATATCACTTGAAT 1500
QY 1523 CTTGACATGTCAGGACATACATTTATCTTCTGCTGCTGAGAGCTCTTCTGCTCTT 1582
DB 1501 CTTGACATGTCAGGACATACATTTATCTTCTGCTGCTGAGAGCTCTTCTGCTCTT 1560
QY 1583 AAATCTAGATGATGAATGAATTTGAATGAATGCTCTTCACTGATGGAAGAGG 1642
DB 1561 AAATCTAGATGATGAATGAATTTGAATGAATGCTCTTCACTGATGGAAGAGG 1620
QY 1643 ACACATATGATTCATCATCATGAGACAGCAAAATCTAAAGTGAATTTGATTA 1702
DB 1621 ACACATATGATTCATCATCATGAGACAGCAAAATCTAAAGTGAATTTGATTA 1680
QY 1703 AGAGTTGATTAATATATATGAATGCAAGACCCACAGAGGAAATGTTATGGGACGTT 1762
DB 1681 AGAGTTGATTAATATATATGAATGCAAGACCCACAGAGGAAATGTTATGGGACGTT 1740
QY 1763 TGTAAAGCTGGGATGTGAAGCAAGGCGAGGACCTCATATCTTATATATATCTT 1822
DB 1741 TGTAAAGCTGGGATGTGAAGCAAGGCGAGGACCTCATATCTTATATATATCTT 1800
QY 1823 CATTTCTATCTATCATCAATATCAACAAGCTTTTACAGAAATTCATGACGTCAA 1882
DB 1801 CATTTCTATCTATCATCAATATCAACAAGCTTTTACAGAAATTCATGACGTCAA 1860
QY 1883 TCCCAAGGTAACCTTATCATTTTCAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTG 1942
DB 1861 TCCCAAGGTAACCTTATCATTTTCAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTG 1920
QY 1943 TACTGTGCTATCTCAACTTTGAGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2002
DB 1921 TACTGTGCTATCTCAACTTTGAGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
QY 2003 GGGCACTCTTGTGAGCCACTTTAGGGTTCACCTCGGCAATTAAGAAATTTACAAGA 2059
DB 1981 GGGCACTCTTGTGAGCCACTTTAGGGTTCACCTCGGCAATTAAGAAATTTACAAGA 2037

RESULT 8
AAV62428 standard; cDNA; 1872 BP.
AAV62428;
AC AAV62428;
XX 30-DEC-1998 (first entry)
XX DE Prostate cancer antigen (PCA3) cDNA splice variant 2.
XX KW Prostate cancer antigen cDNA splice variant 2; PCA3; prostatic cancer;
XX PC; ds.
XX OS Homo sapiens.
XX OS W09845420-A1.
XX PN W09845420-A1.
XX PD 15-OCT-1998.
XX PF 09-APR-1998; 98WO-CA00346.
XX PR 10-APR-1997; 97US-0041836.
XX PA (DIAG-) DIAGNOCURE INC.
XX

PI Bussemakers MJG;
XX
DR MPI; 1998-568347/48.
XX
PT New nucleic acid encoding prostate cancer antigen 3 - for diagnosis,
PT prevention and treatment of prostatic cancer
XX
PS
XX Claim 4: Pages 76-77; 111pp; English.
XX
CC The present sequence represents the prostate cancer antigen (PCA3)
CC cDNA splice variant 2 sequence comprising of exons 1, 3, 4a and
CC 4b of the PCA3 gene. The PCA3 cDNA splice variant 2 sequence,
CC isolated from a human primary prostatic tumour tissue cDNA library,
CC was found in approximately 65% of the cDNA clones isolated. The
CC invention claims for PCA3 cDNA variants and the proteins they encode.
CC The invention also claims for antibodies against PCA3 protein. The
CC antibodies are claimed to be useful for detecting PCA3 protein in
CC immunoassay tests, for diagnosing, assessing and prognosing of
CC prostatic cancer (PC). Antibodies, optionally coupled to a cytotoxin
CC or radioisotope, and nucleic acids antisense to PCA3 cDNA are claimed
CC to be useful for treating PC, while determining elevated levels of
CC PCA3 (as RNA or protein) is useful for detecting a predisposition
CC to development of PC, e.g. in prenatal tests. Detecting PCA3 protein
CC allows differentiation between malignant and benign prostatic disease,
CC and the level of PCA3 expression allows correlation with the grade of
CC tumour. PCA3 protein and its fragments are also claimed to be useful
CC in vaccines for preventing PC; in drug screens for identifying
CC specific (ant)agonists (potentially useful therapeutically) and for
CC studying protein-DNA interactions.
XX
SQ Sequence 1872 BP; 567 A; 389 C; 369 G; 539 T; 8 other;
Query Match 38.2%; Score 1367; DB 19; Length 1872;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1/67; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATG 344
DB 98 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATG 157
QY 345 AGTATATTACATCTAGTAACAGCAAGTGCATTTATGTCTTAAGTAGACATGT 404
DB 158 AGTATATTACATCTAGTAACAGCAAGTGCATTTATGTCTTAAGTAGACATGT 217
QY 405 TTTTGACATTTTCACGCCCTTTAAATATCCACACACAGCAAGCAAAAGAAAGCAC 464
DB 218 TTTTGACATTTTCACGCCCTTTAAATATCCACACACAGCAAGCAAAAGAAAGCAC 277
QY 465 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTATCGATGAGCCCTG 524
DB 278 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGGTATCGATGAGCCCTG 337
QY 525 GCCTGGTCCCGCTTGGAGGAAAGACATTAGAAATGAATTGATGTCTTAAAGGA 584
DB 338 GCCTGGTCCCGCTTGGAGGAAAGACATTAGAAATGAATTGATGTCTTAAAGGA 397
QY 585 TGGGCGAGAAACAGATCCGTGTGTGATATTATTTGAACGGGATTTACAGATTTGAAT 644
DB 398 TGGGCGAGAAACAGATCCGTGTGTGATATTATTTGAACGGGATTTACAGATTTGAAT 457
QY 645 GAAGTCACAAAGTAGACATTACCAATGAGAGGAAACAGACGAGAAATCTTGATGGCTT 704
DB 458 GAAGTCACAAAGTAGACATTACCAATGAGAGGAAACAGACGAGAAATCTTGATGGCTT 517
QY 705 CACAAACATGCAACAAACAAATGGAATACGTGTGATGACATGAGCAGCAAGCTGGGG 764
DB 518 CACAAACATGCAACAAACAAATGGAATACGTGTGATGACATGAGCAGCAAGCTGGGG 577
QY 765 AGGAGATTAACCAAGGGGAGAGGAGATTCGTGCGCTGCTAAACCTGTGGCTTC 824
DB 578 AGGAGATTAACCAAGGGGAGAGGAGATTCGTGCGCTGCTAAACCTGTGGCTTC 637
QY 825 ATTAACCAATTCATTCTATTTCTAACCTCAAAACAAAGCTGTGTAAATATCTGATCTC 884

DB 638 ATTAACCAATTCATTCTATTTCTAACCCCAAAACAAAGCTGTGTAAATATCTGATCTC 697
QY 885 TACGGTTCCTTCTGGGGCCCAACATTTCTCCATATATCCAGCCACATCTTTTAATATT 944
DB 698 TACGGTTCCTTCTGGGGCCCAACATTTCTCCATATATCCAGCCACATCTTTTAATATT 757
QY 945 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGATATACATATACATTTGTTC 1004
DB 758 AGTTCCAGATCTGTACTGTGACCTTCTACACTGTAGATATACATATACATTTGTTC 817
QY 1005 AAAGACCTTCGTGTTGCTGCCATATATGAGCTGATGTTTCTTAAGAGAGTCTTCG 1064
DB 818 AAAGACCTTCGTGTTGCTGCCATATATGAGCTGATGTTTCTTAAGAGAGTCTTCG 877
QY 1065 GCCCAGGAGATCTGTAAACAGCTGGGAAAGCATCTCAAGATCTTCCAGGATTAATCTTA 1124
DB 878 GCCCAGGAGATCTGTAAACAGCTGGGAAAGCATCTCAAGATCTTCCAGGATTAATCTTA 937
QY 1125 CTAGCACACAGATGATCATTTAGGAGTGAATATCTAAATCAACATCATCTCAGTGTCT 1184
DB 938 CTAGCACACAGATGATCATTTAGGAGTGAATATCTAAATCAACATCATCTCAGTGTCT 997
QY 1185 TTGCCCATCTGAATTCATTTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCA 1244
DB 998 TTGCCCATCTGAATTCATTTTCCACTTTTGTGCCATTTCTCAAGACCTCAAAATGTCA 1057
QY 1245 TTCCATTAATATACAGAGATTAACCTTTTAACTCGGAAGATTCATATGTACATG 1304
DB 1058 TTCCATTAATATACAGAGATTAACCTTTTAACTCGGAAGATTCATATGTACATG 1117
QY 1305 CAGCTATGGGAATTTAATTAACATATTTGTTTCCAGTCCAAAGATGACATGCTCTTA 1364
DB 1118 CAGCTATGGGAATTTAATTAACATATTTGTTTCCAGTCCAAAGATGACATGCTCTTA 1177
QY 1365 TTCCCTCCCTTTGTTGATTTTTCACATATAAAGTTAAATGCTTAGCCTGTACTG 1424
DB 1178 TTCCCTCCCTTTGTTGATTTTTCACATATAAAGTTAAATGCTTAGCCTGTACTG 1237
QY 1425 AGGCTATATACACACAGCTCCGCCATCCCGCCGCTTATCTGTCATACACATCAAC 1484
DB 1238 AGGCTATATACACACAGCTCCGCCATCCCGCCGCTTATCTGTCATACACATCAAC 1297
QY 1485 CCCTCCCATATCACCTTAACAAATCTAATCTTAATCTTGAATGTCAGACATAC 1544
DB 1298 CCCTCCCATATYACCTTAACAAATCTAATCTTGAATGTCAGACATAC 1357
QY 1545 ATTATTCCTTCTGAGAGAGCTCTTCTGTCTTAAATCTAAGATGATGAAGTT 1604
DB 1358 ATTATTCCTTCTGAGAGAGCTCTTCTGTCTTAAATCTAAGATGATGAAGTT 1417
QY 1605 TTGAATTAAGTGCATCTTACTTTCATGCAAAAGAGGACATATGACATTCATCATCA 1664
DB 1418 TTGAATTAAGTGCATCTTACTTTCATGCAAAAGAGGACATATGACATTCATCATCA 1477
QY 1665 CATGAGACAGCAATCTAATAAGTAAATTTGATTTAAGAGTTAGATAAATATATGA 1724
DB 1478 CATGAGACAGCAATCTAATAAGTAAATTTGATTTAAGAGTTAGATAAATATATGA 1537
QY 1725 ATGCAAGAGCCACAGAGGAAAGTTATGGGGACGTTTGTAAAGCTGGAGTGAAGCA 1784
DB 1538 ATGCAAGAGCCACAGAGGAAAGTTATGGGGACGTTTGTAAAGCTGGAGTGAAGCA 1597
QY 1785 AAGGACAGGAACTCATAGATCTTATATATATATCTTACTTCTATCTCATATCAAA 1844
DB 1598 AAGGACAGGAACTCATAGATCTTATATATATATATCTTACTTCTATCTCATATCAAA 1657
QY 1845 TATCCAACAAGCTTTTCAAGATTCATGACAGTCAAAATCCCAAGAGTAACCTTATCC 1904
DB 1658 TATCCAACAAGCTTTTCAAGATTCATGACAGTCAAAATCCCAAGAGTAACCTTATCC 1717
QY 1905 ATTTCATGAGTGGCTTGTAGAAATTTGGCAAAATCATATGCTGATCTTATCTCAACTT 1964

QY	1425	AGGCTGTAATACAG - CAAAGCCTCTCCCATCCATCCCTCAGCCCTTAATCTGTGATCACCATCA	1483
Db	2453	AGGCTGTAATACAGCCACAGCCTCTCCCATCCCTCAGCCCTTAATCTGTGATCACCATCA	2512
QY	1484	CCCCCTCCATACACACTAAACAAATATCAATCTTAATCTCTGTGACATGTCAGACATA	1543
Db	2513	CCCCCTCCAT - GCACCTTAACAAATATCAATCTTAATCTCTGTGACATGTCAGAC - CAT	2570
QY	1544	CATTATTTCTTTCTGCTGAGAGAGCTCTTCTCTCTTAATCTAGAAATGATTAAGT	1603
Db	2571	CATTATTTCTTTCTGCTGAGAGAGCTCTTCTCTCTTAATCTAGAAATGATTAAGT	2630
QY	1604	TTTGTAATTAAGTTGACATCTACTCTCATCTGCAAAAGAGGACACATATGAGATTCATATC	1663
Db	2631	TTTGTAATTAAGTTGACATCTACTCTCATCTGCAAAAGAGGACACATATGAGATTCATATC	2690
QY	1664	ACATGAGACAGACAAATACTAAAGCTGTAATTTGATTATTAAGAGTTTAGATTAATATATGA	1723
Db	2691	ACATGAGACAGACAAATACTAAAGCTGTAATTTGATTATTAAGAGTTTAGATTAATATATGA	2750
QY	1724	AATGCAAGACCCACAGAGGGAATGTTATGGGGACACTTTGTAAAGCTGGGATGTGAAGC	1783
Db	2751	AATGCAAGACCCACAGAGGGAATGTTATGGGGACACTTTGTAAAGCTGGGATGTGAAGC	2810
QY	1784	AAAGGCGGGAACCTCATAGATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATC	1843
Db	2811	AAAGGCGGGAACCTCATAGATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATC	2870
QY	1844	ATATCCAAACAAGCTTTTTCACAGAAATTCATGCAAGTGCACAAATCCCAAGGTAACTTATTC	1903
Db	2871	ATATCCAAACAAGCTTTTTCACAGAAATTCATGCAAGTGCACAAATCCCAAGGTAACTTATTC	2930
QY	1904	CATTTCATGGTGAATGGGCTTTAGAAATTTTGGCAATCATCTGTCACTTATTCGAAT	1963
Db	2931	CATTTCATGGTGAATGGGCTTTAGAAATTTTGGCAATCATCTGTCACTTATTCGAAT	2990
QY	1964	TTGAGATGTGTTTGTCTCTGTAGTTAATTTGAAAGAAATAGGGCACTCTTGAGGACACTT	2023
Db	2991	TTGAGATGTGTTTGTCTCTGTAGTTAATTTGAAAGAAATAGGGCACTCTTGAGGACACTT	3050
QY	2024	TAGGGTTCACCTCTGSCAATTAAGAAATTTTCAAGAGAC	2061
Db	3051	TAGGGTTCACCTCTGSCAATTAAGAAATTTTCAAGAGAC	3088
RESULT 10			
AAS63896 standard; cDNA; 3112 BP.			
AC	AAS63896:		
XX	29-JAN-2002 (first entry)		
DT	Human prostate cDNA sequence #430.		
DE	Human, prostate cancer; ss; cytosolic; immunostimulant; tumour.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	WO200173032-A2.		
PN	04-OCT-2001.		
PD	27-MAR-2001; 2001WO-US09919.		
XX	27-MAR-2001; 2000US-0516857.		
PR	09-MAY-2000; 2000US-0568100.		
PR	12-MAY-2000; 2000US-0570737.		
PR	13-JUN-2000; 2000US-0593793.		
PR	27-JUN-2000; 2000US-0605783.		
PR	10-AUG-2000; 2000US-0616215.		
PR	29-AUG-2000; 2000US-0651236.		

PR		06-SEP-2000:	2000US-0657279,
PR		02-OCT-2000:	2000US-0679426,
PR		10-OCT-2000:	2000US-0685166.
XX			
PA	(CORI -)	CORIXA CORP.	
XX			
PI	Xu J., Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;		
PI	Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick JS, Carter D;		
PI	Li SX, Wang A, Skelky IAW, Hepler WT, Henderson RA;		
XX			
XX	WPI: 2001-639232/73.		
DR			
XX			
PT	New human prostate-specific polypeptides and polynucleotides useful for		
PI	the diagnosis and treatment of cancer, especially prostate cancer -		
PS	Claim 1; Page 384-385; 579pp; English.		
XX			
CC	The invention relates to isolated prostate-specific		
CC	polynucleotides, polypeptides, fusion proteins of the polypeptides,		
CC	antibodies raised against the polypeptides (or antigenic epitopes		
CC	derived from them) and antigen presenting cells expressing the		
CC	polypeptides. The antibodies are useful for detecting the presence of		
CC	cancer, especially prostate cancer. The polypeptides, polynucleotides and		
CC	the antigen-presenting cells are useful for stimulating and/or expanding		
CC	T cells specific for a tumour protein, and for inhibiting the development		
CC	of cancer especially for a tumour protein. Compositions comprising the		
CC	polynucleotide and/or polypeptide are useful for stimulating an immune		
CC	response, and for treating cancer. The oligonucleotide is useful for		
CC	detecting cancer. The present sequence is a prostate specific		
CC	polynucleotide of the invention.		
SQ	Sequence 3112 BP; 975 A; 587 C; 624 G; 926 T; 0 other;		
Query Match	38.1%; Score 1364; DB 22; Length 3112;		
Best Local Similarity	99.8%; Pred. No. 0;		
Matches 1774; Conservative	0; Mismatches 1; Indels 3; Gaps 3;		
OY	285 GGTGAGAAATTAAGAAAGCGTGGCTACTTACCATTGTGAGGCACACATCTGTTGAATAAG	344	
Dd			
	1313 GGTCGAGAATTAAGAAAGCGTGGCTACTTACCATTGTGAGGCACACATCTGTTGAATAAG	1377	
OY	345 AGATTAATTAACTCACTAGAAAACAGCAAGATGACAATTAATGTTCTAAGTAGCATGT	404	
Dd			
	1373 AGATAATTAACATCACTAGAAAACAGCAAGATGACAATTAATGTTCTAAGTAGCATGT	1432	
OY	405 TTTTGACATTTTCCAGCCCCCTTTAAATTTCCACACACACAGAGAACAAAAAGAACAC	464	
Dd			
	1433 TTTTGACATTTTCCAGCCCCCTTTAAATTTCCACACACACAGAGAACAAAAAGAACAC	1492	
OY	465 AGACATCCCTGGAGAAATGCGCGGCCCACTCTGGGTCATTCGATGAGCCCGCCCTGT	524	
Dd			
	1493 AGAGATCCCTGGAGAAATGCGCGGCCCACTCTGGGTCATTCGATGAGCCCGCCCTGT	1552	
OY	525 GCCTGTCGCCCTTGTGAGGAGGAGACATTAGAAAATGAATTGATGTCTTCTTAAAGA	584	
Dd			
	1553 GCCTGTCGCCCTTGTGAGGAGGAGACATTAGAAAATGAATTGATGTCTTCTTAAAGA	1612	
OY	585 TGCGCAGAGAAACAGATCTCTTGTGGATATTATTATTGAACGGGATTACAGATTGAAAT	644	
Dd			
	1613 TGCGCAGAGAAACAGATCTCTTGTGGATATTATTATTGAACGGGATTACAGATTGAAAT	1672	
OY	645 GAAGTCACAAGTGGAGCTTACCAATGAGAGAAAAACAGAGAGAAAAATCTGATGGCT	704	
Dd			
	1673 GAAGTCACAAGTGGAGCTTACCAATGAGAGAAAAACAGAGAGAAAAATCTTGTATGGCTT	1733	
OY	705 CACAAGACATSCAACAAACAAATGGAATTACTGTGATGACATGAGAGCACCAAGCTGGGG	764	
Dd			
	1733 CACAAGACATSCAACAAACAAATGGAATTACTGTGATGACATGAGAGCACCAAGCTGGGG	1792	
OY	765 AGGAGATTAACACAGGGGCGAGAGGGTCAGGATTTTGCGCCCTGCTTAACTGTGCTTC	824	
Dd			
	1793 AGGAGATTAACACAGGGGCGAGAGGGTCAGGATTTTGCGCCCTGCTTAACTGTGCTTC	1852	

QY 825 ATACCAATCATTTTCATATTTCTAACCTCAAAAACAAAGCTGTGTAATATCTGATCTC 884
Db 1853 ATAAACCAATCATTTTCATATTTCTAACCTCAAAAACAAAGCTGTGTAATATCTGATCTC 1912
QY 885 TAGCGTCTCTGGGCCCAACATCTCCATATATCCAGCCACCTACTTTTAAATATTT 944
Db 1913 TAGCGTCTCTGGGCCCAACATCTCCATATATCCAGCCACCTACTTTTAAATATTT 1972
QY 945 AGTTCACAGATCTGACTGTGACCTTTCTACACTGTAGAAATACATTTACTATTTTGTTC 1004
Db 1973 AGTTCACAGATCTGACTGTGACCTTTCTACACTGTAGAAATACATTTACTATTTTGTTC 2032
QY 1005 AAAGACCTTGCTGTGCTGCTTAATATGATGACTACTGTGTTTCTTAAGAGTGTCTG 1064
Db 2033 AAAGACCTTGCTGTGCTGCTTAATATGATGACTACTGTGTTTCTTAAGAGTGTCTG 2092
QY 1065 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTATACCTTA 1124
Db 2093 GCCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTATACCTTA 2152
QY 1125 CTAGCACACAGCATGATCATTAAGAGTGAATATCTATCAACATCATCTCAGTGTCT 1184
Db 2153 CTAGCACACAGCATGATCATTAAGAGTGAATATCTATCAACATCATCTCAGTGTCT 2212
QY 1185 TTGCCCATACAGAAATTTATTTCCACTTTTGTGCCCATCTCAAGACTCTCAAAATGTCA 1244
Db 2213 TTGCCCATACAGAAATTTATTTCCACTTTTGTGCCCATCTCAAGACTCTCAAAATGTCA 2272
QY 1245 TTCCATTAATATACAGAGATTAATCTTTTAACTTTTAACTGGGAAGATTAATGTAACATG 1304
Db 2273 TTCCATTAATATACAGAGATTAATCTTTTAACTTTTAACTGGGAAGATTAATGTAACATG 2332
QY 1305 CAGCTATGGAAATTAATTAATATTTTGTTCAGTGAAGATGAATGATGCTTTTA 1364
Db 2333 CAGCTATGGAAATTAATTAATATTTTGTTCAGTGAAGATGAATGATGCTTTTA 2392
QY 1365 TCCCTCCCTTTGTTGATTTTTTTTCCAGTATTAAGTAAATGCTTACTG 1424
Db 2393 TCCCTCCCTTTGTTGATTTTTTTTCCAGTATTAAGTAAATGCTTACTG 2452
QY 1425 AGGCTGTATACAG-CACAGCCTTCCCATCCCTCCAGCCTTATGTCATCACCATAA 1483
Db 2453 AGGCTGTATACAGCAGCAGCCTCTCCCATCTCCAGCCTTATGTCATCACCATAA 2512
QY 1484 CCCCTCCCATACCATTAACAAATTAATCTGTAATTCCTTGAACATGTCAGACATA 1543
Db 2513 CCCCTCCCAT-GCACCTTAACAAATTAATCTGTAATTCCTTGAACATGTCAGG-CATA 2570
QY 1544 CATATTCCTCTGCTGAGAGGCTCTCTCTCTCTTAATCTAGAATGTAAGT 1603
Db 2571 CATATTCCTCTGCTGAGAGGCTCTCTCTCTCTTAATCTAGAATGTAAGT 2630
QY 1604 TTGAAATAGTTGACTATCTTACTTCATGCAAGAGGAGACATATGAGATTCTATC 1663
Db 2631 TTGAAATAGTTGACTATCTTACTTCATGCAAGAGGAGACATATGAGATTCTATC 2690
QY 1664 ACATGAGACAGCAAAATTAATAAGTGTATTAATTAAGAGTTTAAATATATATGA 1723
Db 2691 ACATGAGACAGCAAAATTAATAAGTGTATTAATTAAGAGTTTAAATATATATGA 2750
QY 1724 AATCAAGAGCCACAGAGGAGATGTTATGGGACGCTTTAAAGCCGGGATGGAAGC 1783
Db 2751 AATCAAGAGCCACAGAGGAGATGTTATGGGACGCTTTTAAGCCGGGATGGAAGC 2810
QY 1784 AAAGCAGGGAACCTCATATGATCTTATATATATATCTTACTTCTATCTATCA 1843
Db 2811 AAAGCAGGGAACCTCATATGATCTTATATATATATCTTACTTCTATCTATCA 2870
QY 1844 ATATCCAAACAGCTTTTACAGAAATTCATGCAAGTGAATCCCAAGATTAACCTTATVC 1903
Db 2871 ATATCCAAACAGCTTTTACAGAAATTCATGCAAGTGAATCCCAAGATTAACCTTATVC 2930
QY 1904 CATTCAATGATGAGCTTGAAGATTTTGGCAAAATCATACTGTACTTATCTCAACT 1963

Db 2931 CATTCAATGATGAGCTTGAAGATTTTGGCAAAATCATACTGTCACTTATCTCAACT 2990
QY 1964 TTGAGATGCTTTGCTCTGCTGATTAATTTGAAGAAATAGGCACTTGTAGCACTT 2023
Db 2991 TTGAGATGCTTTGCTCTGCTGATTAATTTGAAGAAATAGGCACTTGTAGCACTT 3050
QY 2024 TAGGTTCACTCTGCAATTAAGAAATTTTACAAAGAGC 2061
Db 3051 TAGGTTCACTCTGCAATTAAGAAATTTTACAAAGAGC 3088

RESULT 11
AAH93803
ID AAH93803 standard; cDNA; 3112 bp.
XX
AC AAH93803;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence P710P #1.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosolic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN W0200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI: 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1: Page 382-383; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytosolic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 3112 bp; 975 A; 587 C; 624 G; 926 T; 0 other;

Query Match 38.1%; Score 1364; DB 22; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 285 GGTGAGAAATTAAGAAAGGCTCTGACTTTTACATCTGAGGCCACATCTGCAATGG 344
Db 1313 GGTGAGAAATTAAGAAAGGCTCTGACTTTTACATCTGAGGCCACATCTGCAATGG 1372

QY 345 AGATAATTACACTAGAAAGCAGATGACATATATATGTCTAAGTAGACATGG 404
|||||
Db 1373 AGATATATTACATCTAGTAACAGCAATGACATATATATGTCTAAGTAGACATGG 1432
QY 405 TTTTGACATTTTCAGCCCCCTTTAAATATCCACACACAGAGAACACAAAAGAGACAC 464
|||||
Db 1433 TTTTGACATTTTCAGCCCCCTTTAAATATCCACACACAGAGAACACAAAAGAGACAC 1492
QY 465 AAGATATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTGATGATGAGACCTTGCCTGT 524
|||||
Db 1493 AAGATATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTGATGATGAGACCTTGCCTGT 1552
QY 525 GCCTGGTCCCGCTTGGAGGAGAGACATTAGAAATGAATGATGTCTCTTAAGGA 584
|||||
Db 1553 GCCTGGTCCCGCTTGGAGGAGAGACATTAGAAATGAATGATGTCTCTTAAGGA 1612
QY 585 TGGGCGAGAAACAGATCCTGTGTGATATTTATTTGAACGGGATTACAGATTTGAAT 644
|||||
Db 1613 TGGGCGAGAAACAGATCCTGTGTGATATTTATTTGAACGGGATTACAGATTTGAAT 1672
QY 645 GAAGTCACAAAGTGAGCATTTACCAATGAGAGAAAACACAGAAATCTTGATGCTT 704
|||||
Db 1673 GAAGTCACAAAGTGAGCATTTACCAATGAGAGAAAACACAGAAATCTTGATGCTT 1732
QY 705 CACAAGACATGCACAAACAAATGGAATAGCTGTGATGACATGAGGACAGCAAGCTGGGG 764
|||||
Db 1733 CACAAGACATGCACAAACAAATGGAATAGCTGTGATGACATGAGGACAGCAAGCTGGGG 1792
QY 765 AGGAGATTAACAAGGGGAGAGGGTCAGATTCCTGGCCCTGTCTCTTAACCTGTGCTTC 824
|||||
Db 1793 AGGAGATTAACAAGGGGAGAGGGTCAGATTCCTGGCCCTGTCTCTTAACCTGTGCTTC 1852
QY 825 ATTAACCAATCATTTATATTTCTAACCTCAAAACAAAGCTGTGTAATATCTGATCTC 884
|||||
Db 1853 ATTAACCAATCATTTATATTTCTAACCTCAAAACAAAGCTGTGTAATATCTGATCTC 1912
QY 885 TAGGTTCTCTTGGGCCCCAACATCTCATATATGACGACACATCTTTTAATATTT 944
|||||
Db 1913 TAGGTTCTCTTGGGCCCCAACATCTCATATATGACGACACATCTTTTAATATTT 1972
QY 945 AGTTCCAGATCTGATCTGACCTTCTACACGTGATGATTAACATTAATCTCATTTTGTTC 1004
|||||
Db 1973 AGTTCCAGATCTGATCTGACCTTCTACACGTGATGATTAACATTAATCTCATTTTGTTC 2032
QY 1005 AAAGACCTTCTGCTGCTGCTCAATATGATGATGATCTGCTTTCTTAAGAGTGTCTG 1064
|||||
Db 2033 AAAGACCTTCTGCTGCTGCTCAATATGATGATGATCTGCTTTCTTAAGAGTGTCTG 2092
QY 1065 GCCCAGGGGATCTGTAACAGGCTGGGAGCANTCTCAAGATCTTTCAGAGGTTATACTTA 1124
|||||
Db 2093 GCCCAGGGGATCTGTAACAGGCTGGGAGCANTCTCAAGATCTTTCAGAGGTTATACTTA 2152
QY 1125 CTAGCACAGCATGATCATTTAGAGAGTAATATATTAATCAACATCATCTCAGAGTCT 1184
|||||
Db 2153 CTAGCACAGCATGATCATTTAGAGAGTAATATATTAATCAACATCATCTCAGAGTCT 2212
QY 1185 TTGGCCATATCTGAATTCATTTCCACCTTTGTGCCATCTTCAGACCTCAAAATGTCA 1244
|||||
Db 2213 TTGGCCATATCTGAATTCATTTCCACCTTTGTGCCATCTTCAGACCTCAAAATGTCA 2272
QY 1245 TTCCATTAATACAGAGATTAATCTTTTAACTGGAAGATTCAGATTTACATG 1304
|||||
Db 2273 TTCCATTAATACAGAGATTAATCTTTTAACTGGAAGATTCAGATTTACATG 2332
QY 1305 CAGCTATGGGAATTAATATATTTGTTTCCAGTCAAAAGATGATAGTCTCTTA 1364
|||||
Db 2333 CAGCTATGGGAATTAATATATTTGTTTCCAGTCAAAAGATGATAGTCTCTTA 2392
QY 1365 TCCCTCCCTTTGTTGATTTTTTCCAGTCAAAAGATGATAGTCTCTTA 1424
|||||
Db 2393 TCCCTCCCTTTGTTGATTTTTTCCAGTCAAAAGATGATAGTCTCTTA 2452

QY 1425 AGGCTGATACAG-CACAGCCTCTCCCATCCCTCAGGCTTATCTGATCACCATCA 1483
|||||
Db 2453 AGGCTGATACAGC-CACAGCCTCTCCCATCCCTCAGGCTTATCTGATCACCATCA 2512
QY 1484 CCCCTCCATACACCTTAACAAATCTAATCTGTAATCTTGAACATGTCAGACATA 1543
|||||
Db 2513 CCCCTCCAT-GCACCTTAACAAATCTAATCTGTAATCTTGAACATGTCAG-CAATA 2570
QY 1544 CATTAATCTCTGCTGAGAGGCTCTCTCTGCTCTTAATCTGAATGATGATAAG 1603
|||||
Db 2571 CATTAATCTCTGCTGAGAGGCTCTCTCTGCTCTTAATCTGAATGATGATAAG 2630
QY 1604 TTTGAATAGTTGACATATCTTACTTATGCAAGAGGACACATATGATATCATATC 1663
|||||
Db 2631 TTTGAATAGTTGACATATCTTACTTATGCAAGAGGACACATATGATATCATATC 2690
QY 1664 ACATGAGACAGCAATACTAATAAGTAAATTTGATTAAGAGTTAGATTAATATATGA 1723
|||||
Db 2691 ACATGAGACAGCAATACTAATAAGTAAATTTGATTAAGAGTTAGATTAATATATGA 2750
QY 1724 AATGCAAGGCCACAGAGGAAATGTTATGAGGACGTTTGTATGCTGGATGTGAAGC 1783
|||||
Db 2751 AATGCAAGGCCACAGAGGAAATGTTATGAGGACGTTTGTATGCTGGATGTGAAGC 2810
QY 1784 AAAGCAGGGAACCTGATAGTATCTATATATATATCTTCAATTTCTATCTATACACA 1843
|||||
Db 2811 AAAGCAGGGAACCTGATAGTATCTATATATATATCTTCAATTTCTATCTATACACA 2870
QY 1844 AATGCAAGGCCACAGAGGAAATGTTATGAGGACGTTTGTATGCTGGATGTGAAGC 1903
|||||
Db 2871 AATGCAAGGCCACAGAGGAAATGTTATGAGGACGTTTGTATGCTGGATGTGAAGC 2930
QY 1904 CATTTATGCTGATGAGGCTTTTGAATTTTGGCAATTCATCTGCTCATCTATCTAAT 1963
|||||
Db 2931 CATTTATGCTGATGAGGCTTTTGAATTTTGGCAATTCATCTGCTCATCTATCTAAT 2990
QY 1964 TTGAGATGTTGCTGCTGCTGATGATTAATGAAGAAATGAGGACCTTGTGAGCCACT 2023
|||||
Db 2991 TTGAGATGTTGCTGCTGCTGATGATTAATGAAGAAATGAGGACCTTGTGAGCCACT 3050
QY 2024 TAGGTTCACTCTGSCAATTAAGAAATTAACAAGAGC 2061
|||||
Db 3051 TAGGTTCACTCTGSCAATTAAGAAATTAACAAGAGC 3088

RESULT 12
AAH85117
ID AAH85117 standard; cDNA; 3112 BP.
XX
AC AAH85117;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence p710P #1.
XX
DE Human prostate cancer; therapy; diagnosis; cat eye syndrome;
XX
KW Chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN MO200134802-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30904.
XX
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kalos MD, Retter MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX WPI: 2001-308785/32.
XX
XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer -
XX
XX Claim 5; Page 282-283; 325pp; English.
PS
XX The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
XX Sequence 3112 BP; 975 A; 587 C; 624 G; 926 T; 0 other;

Query Match 38.1%; Score 1364; DB 22; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

OY 285 GGTGAAATGAAGAGGCTGCTGACTTACCATCTGAGCCACACATCTGCTGAATGG 344
DB 1313 GGTGAAATGAAGAGGCTGCTGACTTACCATCTGAGCCACACATCTGCTGAATGG 1372
OY 345 AGATATTTAATCACTCTAGAAACAGCAAGATGACATATATATGCTAAGTAGTGCATGT 404
DB 1373 AGATATTTAATCACTCTAGAAACAGCAAGATGACATATATATGCTAAGTAGTGCATGT 1432
OY 405 TTTTGCACATTTCCGCGCCCTTTAATATTCACACACAGCAAGATGACATATATGCTAAGTAGTGCATGT 464
DB 1433 TTTTGCACATTTCCGCGCCCTTTAATATTCACACACAGCAAGATGACATATATGCTAAGTAGTGCATGT 1492
OY 465 AGAGATCCCTGGGAAATGCGCGCGCCCATCTTGGGTCAATGATGAGCCCTGCGCTGT 524
DB 1493 AGAGATCCCTGGGAAATGCGCGCGCCCATCTTGGGTCAATGATGAGCCCTGCGCTGT 1552
OY 525 GCCTGTGCTCCGCTTGTGAGGAGACATTTAGAAATGATGATGTCTTCTTAAGA 584
DB 1553 GCCTGTGCTCCGCTTGTGAGGAGACATTTAGAAATGATGATGTCTTCTTAAGA 1612
OY 585 TGGGAGAGAAACAGATCCTGTGTGATTTTATTTGAAGGGGATTACAGATTGAAT 644
DB 1613 TGGGAGAGAAACAGATCCTGTGTGATTTTATTTGAAGGGGATTACAGATTGAAT 1672
OY 645 GAAGTCACAAAGTGAATACCAATGAGAGAAACAGAGAAATCTTGATGCTT 704
DB 1673 GAAGTCACAAAGTGAATACCAATGAGAGAAACAGAGAAATCTTGATGCTT 1732
OY 705 CACAAGACATGACAAACAAATGGAATCTGTGATGACATGAGCGACCAAGCTGGGG 764
DB 1733 CACAAGACATGACAAACAAATGGAATCTGTGATGACATGAGCGACCAAGCTGGGG 1792
OY 765 AGGAGATTAACAGGGGGAGAGGGTCTGAGGATTTGCGCCCTGCTAACTGTGCTTC 824
DB 1793 AGGAGATTAACAGGGGGAGAGGGTCTGAGGATTTGCGCCCTGCTAACTGTGCTTC 1852
OY 825 ATAACCAATCATTTTCAATTTCTAACCCCTCAAAACAAAGCTGTTAATATTCGATTC 884
DB 1853 ATAACCAATCATTTTCAATTTCTAACCCCTCAAAACAAAGCTGTTAATATTCGATTC 1912
OY 885 TAGGGTCTCTTGGGCCCAACATTTCCATATATCCAGCCACATCTTTTATATTT 944
DB 1913 TAGGGTCTCTTGGGCCCAACATTTCCATATATCCAGCCACATCTTTTATATTT 1972

OY 945 AGTCCAGAGCTGTACTGTGACCTTTCTACACTGTAGAAATTAATCTCATTTTGTTC 1004
DB 1973 AGTCCAGAGCTGTACTGTGACCTTTCTACACTGTAGAAATTAATCTCATTTTGTTC 2032
OY 1005 AAGAGCCCTGCTGTGCTGCTTATATGCTACTGCTTTTCTTAAGAGCTTCTG 1064
DB 2033 AAGAGCCCTGCTGTGCTGCTTATATGCTACTGCTTTTCTTAAGAGCTTCTG 2092
OY 1065 GCCCAGGGAGCTGTGACAGAGCTGGGAAGCATCTCAAGATCTTCCAGGGTTACTTGA 1124
DB 2093 GCCCAGGGAGCTGTGACAGAGCTGGGAAGCATCTCAAGATCTTCCAGGGTTACTTGA 2152
OY 1125 CTAGCACACAGCATGATATTAACAGAGATTAATCTAATCAACATCATCTGCTGTCT 1184
DB 2153 CTAGCACACAGCATGATATTAACAGAGATTAATCTAATCAACATCATCTGCTGTCT 2212
OY 1185 TTGCCATACGAAATTAATTTCCAGCTTTTGGCCCAATTCACAGCCCTCAAAATGCA 1244
DB 2213 TTGCCATACGAAATTAATTTCCAGCTTTTGGCCCAATTCACAGCCCTCAAAATGCA 2272
OY 1245 TTCCATTAATTCACAGATTAATCTTTTAACTGGAAGATTAATCTGTTACATG 1304
DB 2273 TTCCATTAATTCACAGATTAATCTTTTAACTGGAAGATTAATCTGTTACATG 2332
OY 1305 CAGCTATGGAATTAATTAATCATATTTGTTTCCAGTGCACAAAGATGACTAAGTCTTGA 1364
DB 2333 CAGCTATGGAATTAATTAATCATATTTGTTTCCAGTGCACAAAGATGACTAAGTCTTGA 2392
OY 1365 TCCCTCCCTGTTGTTGATTTTTCAGATAAAGTAAATTCCTAGCCCTGTACTG 1424
DB 2393 TCCCTCCCTGTTGTTGATTTTTCAGATAAAGTAAATTCCTAGCCCTGTACTG 2452
OY 1425 AGGCTGATTAACG-CACAGCCTTCCCATCCCTCCACCTTATCTGTCATCCACATCA 1483
DB 2453 AGGCTGATTAACGACACAGCCTTCCCATCCCTCCACCTTATCTGTCATCCACATCA 2512
OY 1484 CCCCTCCATACACACTTAAACAAATCTAATCTGTAATCTTCTGAACATGTCAGACATA 1543
DB 2513 CCCCTCCAT-GCACCTTAAACAAATCTAATCTGTAATCTTCTGAACATGTCAGAG-CATA 2570
OY 1544 CATTTATCTTCTGCTGAGAGAGCTTCTCTGTCCTTAAATCTAGAAATGATGAAGT 1603
DB 2571 CATTTATCTTCTGCTGAGAGAGCTTCTCTGTCCTTAAATCTAGAAATGATGAAGT 2630
OY 1604 TTTGAATTAAGTTGACTATCTTACATTCATGCAAAAGAGGACATATGAGATTCATATC 1663
DB 2631 TTTGAATTAAGTTGACTATCTTACATTCATGCAAAAGAGGACATATGAGATTCATATC 2690
OY 1664 ACATGAGACAGCAAAATTAATAAGTGAATTTGAAGTTTGAATGAATTAATATGA 1723
DB 2691 ACATGAGACAGCAAAATTAATAAGTGAATTTGAAGTTTGAATGAATTAATATGA 2750
OY 1724 AATGCAAGAGCCACAGAGGAATGTTATGAGGACGTTTGAAGCCGGGATGTAAGC 1783
DB 2751 AATGCAAGAGCCACAGAGGAATGTTATGAGGACGTTTGAAGCCGGGATGTAAGC 2810
OY 1784 AAAGCAGGGAACCTCATAGTATCTTAATATATTAATCTTCAATCTCATCTATCA 1843
DB 2811 AAAGCAGGGAACCTCATAGTATCTTAATATATTAATCTTCAATCTCATCTATCA 2870
OY 1844 ATATCCAAACAGCTTTTACAGAAATTCATGAGAGTCAAAATCCCAAAGTAACTTATC 1903
DB 2871 ATATCCAAACAGCTTTTACAGAAATTCATGAGAGTCAAAATCCCAAAGTAACTTATC 2930
OY 1904 CATTTCAATGAGTGGGCTTTAGAAATTTGGCAATCATCTGCTCATATCTCAACT 1963
DB 2931 CATTTCAATGAGTGGGCTTTAGAAATTTGGCAATCATCTGCTCATATCTCAACT 2990
OY 1964 TTGAGATGTTGTTGCTTGTAGTAAATTTGAAGAAATAGGGCACTCTTGTGAGCCACTT 2023
DB 2991 TTGAGATGTTGTTGCTTGTAGTAAATTTGAAGAAATAGGGCACTCTTGTGAGCCACTT 3050
OY 2024 TAGGGTCACTCTGGCAATTAAGAAATTTACAAAGAGC 2061

|||||
Db 3051 TAGGTTCACTCCTGCGCAATTAAGATTACAAAGAGC 3088
RESULT 13
AAH02868
ID AAH02868 standard; cDNA; 3112 BP.
XX
AC AAH02868;
XX
DT 14-JUN-2001 (first entry)
XX
DE Prostate tumour antigen cDNA sequence for P710P #1.
XX
KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
KW prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN MO200125272-A2.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000MO-US27464.
XX
PR 04-OCT-1999; 99US-0157455.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Skelky YAW, Reed SG, Cheever MA;
XX
DR MPI; 2001-245062/25.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for
XX the treatment and diagnosis of prostate cancer
XX
PS Claim 4; Page 265; 276pp; English.
XX
CC The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression of the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 3112 BP; 975 A; 587 C; 624 G; 926 T; 0 other;
Query Match 38.1%; Score 1364; DB 22; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
OY 285 GGTGAGAAATTAAGAAAGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 344
DB 1313 GGTGAGAAATTAAGAAAGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATGG 1372
OY 345 AGTAAATTAACATCATAGAAACAGCAAGATGACATATATATGCTTAAGTAGACATGT 404
DB 1373 AGTAAATTAACATCATAGAAACAGCAAGATGACATATATGCTTAAGTAGACATGT 1432
OY 405 TTTTGACATTTCCAGCCCTTTAATATTCACACACACAGAGAAGCAAAAAGAGAC 464
DB 1433 TTTTGACATTTCCAGCCCTTTAATATTCACACACACAGAGAAGCAAAAAGAGAC 1492
OY 465 AGAGATCCCTGGGAGAAATGCCGCGCCATCTTGGGTTCATGCATGAGCCCTGCT 524
DB 1493 AGAGATCCCTGGGAGAAATGCCGCGCCATCTTGGGTTCATGCATGAGCCCTGCT 1552

OY 525 GCCTGGTCCCGCTTGTGAGGAGAGACATTAGAAATGATGTTGCTTAAAGGA 584
DB 1553 GCCTGGTCCCGCTTGTGAGGAGAGACATTAGAAATGATGTTGCTTAAAGGA 1612
OY 585 TGGGACAGAAACAGATCCCTGTTGTGATATTTTGAACGGATTAAGATTGAAAT 644
DB 1613 TGGGACAGAAACAGATCCCTGTTGTGATATTTTGAACGGATTAAGATTGAAAT 1672
OY 645 GAAATCACAAGTAGACATTACCAATGAGAGAAAACAGACGAAAATCTTGATGCTT 704
DB 1673 GAAATCACAAGTAGACATTACCAATGAGAGAAAACAGACGAAAATCTTGATGCTT 1732
OY 705 CACAAGACATGCACAACAAAATGAAATGAAATCTGTGATGATGAGGACGCAAGCTGGGG 764
DB 1733 CACAAGACATGCACAACAAAATGAAATGAAATCTGTGATGATGAGGACGCAAGCTGGGG 1792
OY 765 AGGAGATTAACACAGGGGAGAGGGTACAGATTTGGCCCTGCTGCTAAACTGGCGTTC 824
DB 1793 AGGAGATTAACACAGGGGAGAGGGTACAGATTTGGCCCTGCTGCTAAACTGGCGTTC 1852
OY 825 ATTAACCAATCATTTTCATATTTCTAAACCTCAAAACAAAGCTGTGTATATCTGATCTC 884
DB 1853 ATTAACCAATCATTTTCATATTTCTAAACCTCAAAACAAAGCTGTGTATATCTGATCTC 1912
OY 885 TAGGTTCTCTTCGGGCCCAACATCTCTCATATATTCAGGACACATCTTTTAATATT 944
DB 1913 TAGGTTCTCTTCGGGCCCAACATCTCTCATATATATTCAGGACACATCTTTTAATATT 1972
OY 945 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGATGATTAACATTAATCTTGTGTC 1004
DB 1973 AGTTCCAGATCTGTACTGTGACCTTTCTACACTGATGATTAACATTAATCTTGTGTC 2032
OY 1005 AAAGACCTTTCGTTGCTGCTGCTTAATATAGTGAAGCTGTTTCTTAAGAGCTGTCG 1064
DB 2033 AAAGACCTTTCGTTGCTGCTGCTTAATATAGTGAAGCTGTTTCTTAAGAGCTGTCG 2092
OY 1065 GCCCAGGGATCTGTAAACAGGCTGGGAAGCATTCAAGATCTTCCAGGTTATCTTA 1124
DB 2093 GCCCAGGGATCTGTAAACAGGCTGGGAAGCATTCAAGATCTTCCAGGTTATCTTA 2152
OY 1125 CTAGCACACAGCATGATCATTTAGAGAGTGAATATCTTAATCAACATCATCTGATGTC 1184
DB 2153 CTAGCACACAGCATGATCATTTAGAGAGTGAATATCTTAATCAACATCATCTGATGTC 2212
OY 1185 TTGCCCATCTGAAATTCATTTCCACTTTTGTGCCATTTCAAGACCTCAAAATGTCA 1244
DB 2213 TTGCCCATCTGAAATTCATTTCCACTTTTGTGCCATTTCAAGACCTCAAAATGTCA 2272
OY 1245 TTCCATTAATATTCACAGATTAATCTTTTAACTGAGGAATTCAGATGTTACATG 1304
DB 2273 TTCCATTAATATTCACAGATTAATCTTTTAACTGAGGAATTCAGATGTTACATG 2332
OY 1305 CAGCATATGGGAATTTAATACATATTTGTTTCCAGTGCAGAAAGATGACTAAGTCCCTTA 1364
DB 2333 CAGCATATGGGAATTTAATACATATTTGTTTCCAGTGCAGAAAGATGACTAAGTCCCTTA 2392
OY 1365 TCCCTCCCTTGTGATTTTTCACATATTAAGTTAAAGTTAGCTTGAAGCTGTGATG 1424
DB 2393 TCCCTCCCTTGTGATTTTTCACATATTAAGTTAAAGTTAGCTTGAAGCTGTGATG 2452
OY 1425 AGGCTGTATACAG-CACAGCTCTGCCCATTCCTCCAGCTTATCTGATACACATCA 1483
DB 2453 AGGCTGTATACAG-CACAGCTCTGCCCATTCCTCCAGCTTATCTGATACACATCA 2512
OY 1484 CCCCTCCATACACACCTTAACAAATCTAATCTTGAATCTTGAACATGTGAGACATA 1543
DB 2513 CCCCTCCAT-AGACCTAAACAAATCTAATCTTGAATCTTGAACATGTGAG-CA 2570
OY 1544 CATTAATCTTCTGCTGAGAAAGCTTCTCTGCTTAAATCTTAAGATGATGTAAGT 1603
DB 2571 CATTAATCTTCTGCTGAGAAAGCTTCTCTGCTTAAATCTTAAGATGATGTAAGT 2630

OY	1604	TTTGAATAGCTTGACACTATTCTTCAATGCAAGAAGGGACACATATGAGATTCATCATC	1663
Db	2631	TTTTAAATAAGGTGCACATCTTACTCTTCATGCAAAAAGAGGACACATATGAGATTCATCATC	2690
OY	1664	ACATGAGACAGACAATATCTAAAACTGTAATTTGTTAATGAGATTTGATTAATATATNGA	1723
Db	2691	ACATGAGACAGACAATATCTAAAACTGTAATTTGTTAATGAGATTTGATTAATATATATNGA	2750
OY	1724	AATGCAAGAGCCACAGAGGGAATGTTATGGGCGACGTTGTAAAGCCTGGGATGTGAAGC	1783
Db	2751	AATGCAAGAGCCACAGAGGGAATGTTATGGGCGACGTTGTAAAGCCTGGGATGTGAAGC	2810
OY	1784	AAAGCGAGGGAACCTCAGTAGTCTTAAATATATATCTCAATCTCTCTATCTATACACA	1843
Db	2811	AAAGCGAGGGAACCTCAGTAGTCTTAAATATATATCTCAATCTCTCTATCTATACACA	2870
OY	1844	ATATCCAACAAGCTTTTACAGAGAAATCATGCAGTGCAGTCAAAATCCCCAAAGGTAACCTTTATC	1903
Db	2871	ATATCCAACAAGCTTTTACAGAGAAATCATGCAGTGCAGTCAAAATCCCCAAAGGTAACCTTTATC	2930
OY	1904	CATTTCATGGTGAATGGGCTTTAGAAATTTTGGCAAATCATACGTGCTACTTATCTCAACT	1963
Db	2931	CATTTCATGGTGAATGGGCTTTAGAAATTTTGGCAAATCATACGTGCTACTTATCTCAACT	2990
OY	1964	TTGAGATGTGTTTGTCCCTGTAGCTTAATFAGAAACAATPATGGGCACTCTTGAGACCCTT	2023
Db	2991	TTGAGATGTGTTTGTCCCTGTAGCTTAATFAGAAACAATPATGGGCACTCTTGAGACCCTT	3050
OY	2024	TAGGGTTCACCTCTGGCAATPAAGAAATTTTACAAAGAGC	2061
Db	3051	TAGGGTTCACCTCTGGCAATPAAGAAATTTTACAAAGAGC	3088

	RESULT 14
ID	AAF86946
AC	AAF86946 standard; cDNA; 3112 BP.
XX	AAF86946;
DT	06-JUL-2001 (first entry)
DE	Human P710P inventive antigen coding sequence SEQ ID NO: 342.
XX	
KW	Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilms' tumour gene;
XX	chromosome 11p13; zinc finger transcription factor; ss.
OS	Homo sapiens.
PN	WO200125273-A2.
PD	12-APR-2001.
PF	04-OCT-2000; 2000WO-US27465.
PR	04-OCT-1999; 99US-0157459.
PA	(CORI-) CORIXA CORP.
PI	Skeiky YAW, Xu J, Cheever MA, Reed SG;
DR	WTI; 2001-328324/34.
PT	Polypeptide comprising part of the Wilms' Tumour gene product sequence I
PT	used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT	and cancer associated with WTI -
PS	Disclosure; Page 217-218; 228pp; English.

The present invention describes compositions comprising peptides derived from the Wilms' tumour protein wti1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human wti1 proteins are provided. The human wti1 gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The

Query Match	38.1%;	Score 1364;	DB 22;	Length 3112;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1774;	Conservative	0;	Mismatches 1;	Indels 3; Gaps 3;
CC immunogenic peptides of the invention are particularly useful in the				
CC diagnosis and treatment of cancer and leukemia. The present sequence is				
CC a coding sequence used in the exemplification of the invention.				
xx				
xx				
Sequence 3112 BP: 975 A; 587 C; 624 G; 926 T; 0 other:				
QY	285	GSTGGAATTAAGAAAGGCTGCTGTCTTACCATCTGAGGGCCACACATCTGCTGAATAG	344	
Db	1313	GTTGGGAATTAAGAAAGGCTGCTGTCTTACCATCTGAGGGCCACACATCTGCTGAATAG	1372	
QY	345	AGATTAATTAACATCACTAGAAACACACAGATGACATATTAATGTCTTAAGTAGTGACATGT	404	
Db	1373	AGATTAATTAACATCACTAGAAACACACAGATGACATATTAATGTCTTAAGTAGTGACATGT	1432	
QY	405	TTTTCACATTTCCAGCCCTTTTAATATCCACACACACAGAGAGACACAAAGAACAC	464	
Db	1433	TTTTCACATTTCCAGCCCTTTTAATATCCACACACACAGAGAGACACAAAGAACAC	1492	
QY	465	AGAGATCCCTGGGAGAAATGGCCGGCCGCAATCTTGGGTCAATGAGGCTCCGCCCTGT	524	
Db	1493	AGAGATCCCTGGGAGAAATGGCCGGCCGCAATCTTGGGTCAATGAGGCTCCGCCCTGT	1552	
QY	525	GCTTGCTCCGCTGTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAAGGA	584	
Db	1553	GCTTGCTCCGCTGTGTGAGGAGAGACATTAAGAAATGAATGATGTCTTCTTAAAGGA	1612	
QY	585	TGGCGAGAAACACAGATCCTGTGTGTGATATTATTTGAACGGGATTAACAGATTTGAAT	644	
Db	1613	TGGCGAGAAACACAGATCCTGTGTGTGATATTATTTGAACGGGATTAACAGATTTGAAT	1672	
QY	645	GAAATCAAAAGTAGACATTCACATGAGAGAAACACAGAGAAATCTTGATGCTT	704	
Db	1673	GAAATCAAAAGTAGACATTCACATGAGAGAAACACAGAGAAATCTTGATGCTT	1732	
QY	705	CACAAGACATCAACAAACAAATGAGATACGTGATACATATGAGGCGCAACCTGGGG	764	
Db	1733	CACAAGACATCAACAAACAAATGAGATACGTGATACATATGAGGCGCAACCTGGGG	1792	
QY	765	AGAGATTAACACAGGGGCGAGAGGTCAGGATTCGGCCCTGCTCTTAACCTGTGCTTC	824	
Db	1793	AGAGATTAACACAGGGGCGAGAGGTCAGGATTCGGCCCTGCTCTTAACCTGTGCTTC	1852	
QY	825	ATAACCAAAATATTTCATATTTCTTAACCTTAACAAACAGCTGTTGTAATCTGATCTC	884	
Db	1853	ATAACCAAAATATTTCATATTTCTTAACCTTAACAAACAGCTGTTGTAATCTGATCTC	1912	
QY	885	TACGGTTCCTGTGGGCCCAACATTCCTCATATATCCAGCCACACTCATTTTAAATATT	944	
Db	1913	TACGGTTCCTGTGGGCCCAACATTCCTCATATATCCAGCCACACTCATTTTAAATATT	1972	
QY	945	AGTTCCAGATCTCTACTGTGACCTTTCTACACTGTAAGAAATTAACATTAATCTATTTGTTT	1004	
Db	1973	AGTTCCAGATCTCTACTGTGACCTTTCTACACTGTAAGAAATTAACATTAATCTATTTGTTT	2032	
QY	1005	AAAGACCCCTTCGTGTGCTGCTCAATATGATGACTGCTTTTCTTAAGAGGTGCTCG	1064	
Db	2033	AAAGACCCCTTCGTGTGCTGCTCAATATGATGACTGCTTTTCTTAAGAGGTGCTCG	2092	
QY	1065	GCCCAAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCAGGGGTATACTTA	1124	
Db	2093	GCCCAAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTTCAGGGGTATACTTA	2152	
QY	1125	CTACACACAGCATGATCATTTACGAGATGAATTAATCAATCAATCATCTCTAGTGTCT	1184	
Db	2153	CTACACACAGCATGATCATTTACGAGATGAATTAATCAATCAATCATCTCTAGTGTCT	2212	
QY	1185	TTGGCCATTAAGAAATTCATTTCCCACTTTTGTGGCCATTCCTCAAGACTCAAAATGTCA	1244	
Db	2213	TTGGCCATTAAGAAATTCATTTCCCACTTTTGTGGCCATTCCTCAAGACTCAAAATGTCA	2272	

QY 1245 TTCCATTATATACAGATTAACCTTTTAAACCTGGAAGATTCATGTTACATG 1304
 |||||||
 Db 2273 TTCCATTATATACAGATTAACCTTTTAAACCTGGAAGATTCATGTTACATG 2332
 |||||||
 QY 1305 CAGCTATGGAATTAATATACATATTTGTTTCCAGTCAAAAGATGATAGTCTTTA 1364
 |||||||
 Db 2333 CAGCTATGGAATTAATATACATATTTGTTTCCAGTCAAAAGATGATAGTCTTTA 2392
 |||||||
 QY 1365 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATGCTTAGCTTGTATG 1424
 |||||||
 Db 2393 TCCCTCCCTTTGTTGATTTTTCAGATTAAGTTAAATGCTTAGCTTGTATG 2452
 |||||||
 QY 1425 AGGCTGTATACAG-CACAGCCCTCCCTCCAGCTTATCTGTATACACATCA 1483
 |||||||
 Db 2453 AGGCTGTATACAGCCAGCCCTCCCTCCAGCTTATCTGTATACACATCA 2512
 |||||||
 QY 1484 CCCCTCCCTACACCTTAACAAATCTAATCTTGAATCTTGAACATGTCAGACATA 1543
 |||||||
 Db 2513 CCCCTCCCTACAT-GCAGCTTAACAAATCTAATCTTGAACATGTCAGG-CATA 2570
 |||||||
 QY 1544 CATTTATCTCTGCTGGAAGCTCTCTGCTCTTAAATCTAGAAATGATGTAAGT 1603
 |||||||
 Db 2571 CATTTATCTCTGCTGGAAGCTCTCTGCTCTTAAATCTAGAAATGATGTAAGT 2630
 |||||||
 QY 1604 TTTGATATAGTACTATCTTCTCATGCAAAAGGAGACATATGATTCATCATC 1663
 |||||||
 Db 2631 TTTGATATAGTACTATCTTCTCATGCAAAAGGAGACATATGATTCATCATC 2690
 |||||||
 QY 1664 ACATGAGACAGCAAAATCTAATAAGTATTTGATTTAAGATTTAGATTAATATATGA 1723
 |||||||
 Db 2691 ACATGAGACAGCAAAATCTAATAAGTATTTGATTTAAGATTTAGATTAATATATGA 2750
 |||||||
 QY 1724 AATGCAAGGCCACAGAGGGAATGTTTATGGGACGTTTGTAAGCTTGATGTAAGC 1783
 |||||||
 Db 2751 AATGCAAGGCCACAGAGGGAATGTTTATGGGACGTTTGTAAGCTTGATGTAAGC 2810
 |||||||
 QY 1784 AAGGAGGAGACCTCATGATCTATATATATATATCTTCTCATCTATCTATACATA 1843
 |||||||
 Db 2811 AAGGAGGAGACCTCATGATCTATATATATATATCTTCTCATCTATCTATACATA 2870
 |||||||
 QY 1844 ATATCCCAACAGCTTTTCACAGAAATTCATGACAGTGCATCCCAAGGTAACTTTATC 1903
 |||||||
 Db 2871 ATATCCCAACAGCTTTTCACAGAAATTCATGACAGTGCATCCCAAGGTAACTTTATC 2930
 |||||||
 QY 1904 CATTTTCATGCTGAGTGCCTTTAGAAATTTGGCAATCATCTGCTACTTATCTCACT 1963
 |||||||
 Db 2931 CATTTTCATGCTGAGTGCCTTTAGAAATTTGGCAATCATCTGCTACTTATCTCACT 2990
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 QY 1964 TTGAGATGCTTTGCTGCTGTTAGTTAATGAAAGAAATAGGGCAGCTGTGAGCCACTT 2023
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RESULT 15

ABL95267
 ID ABL95267 standard; cDNA; 3112 BP.

AC ABL95267;

DT 19-JUL-2002 (first entry)

XX Human P710P cDNA sequence SEQ ID NO 468.

DE Human: cancer: prostate cancer; vaccine; cytostatic; immunostimulant;
 KW gene therapy; gene; ss.
 KM
 XX Homo sapiens.
 OS
 XX

XX

PN US200202248-A1.
 XX 21-FEB-2002.
 PD 12-JAN-2001; 2001US-0759143.
 XX 25-FEB-1997; 97US-0806099.
 PF 01-AUG-1997; 97US-0904804.
 PR 09-FEB-1998; 98US-0020956.
 PR 25-FEB-1998; 98US-0030607.
 PR 14-JUL-1998; 98US-0115453.
 PR 23-SEP-1998; 98US-0159812.
 PR 15-JAN-1999; 98US-0232149.
 PR 09-APR-1999; 99US-0288946.
 PR 13-JUL-1999; 99US-0352616.
 PR 12-NOV-1999; 99US-0439313.
 PR 18-NOV-1999; 99US-0483686.
 PR 14-JAN-2000; 2000US-0483672.
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX (XUJ/) XU J.
 PA (DILL/) DILLON D. C.
 PA (MITC/) MITCHAM J. L.
 PA (HARL/) HARLOCKER S. L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M. D.
 PA (FANG/) FANGER G. R.
 PA (RETT/) RETTER M. W.
 PA (STOL/) STOLK J. A.
 PA (DAYC/) DAY C. H.
 PA (VEDV/) VEDVICK T. S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S. X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y. A. W.
 PA (HEPL/) HEPLER W. T.
 PA (HEND/) HENDERSON R. A.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
 XX
 DR WPI: 2002-255649/30.
 XX
 PT New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer
 PT
 PS Claim 1: SEQ ID NO 468; 87pp: English.
 PS
 XX The present invention provides prostate-specific coding sequences and
 CC the encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention.
 CC
 SQ Sequence 3112 BP; 975 A; 587 C; 624 G; 926 T; 0 other;
 XX
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QY	345	AGATAATTACATCTCTGGAACACGACAGATGACAAATTAAATGCTAGTACTGACACTG	404
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QY	465	AGAGATCCCTGGGAGAAATGGCCCCGGCCCATCTTGGGTTCATTCGATGAGCCTCGCCCTGT	524
Db	1493	AGAGATCCCTGGGAGAAATGGCCCCGGCCCATCTTGGGTTCATTCGATGAGCCTCGCCCTGT	1552
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QY	705	CACAAGACATGCAACAAAACAAATGGAATAGCTGTGATACATGTGAGAGCCCAACTGGGG	764
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:40:03 : Search time 205.585 Seconds
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7690.430 Million cell updates/sec

Title: US-09-402-713a-6

Perfect score: 3582

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1364	38.1	3112	4 US-09-439-313-468	Sequence 468, App
2	1364	38.1	3112	4 US-09-352-616A-468	Sequence 468, App
3	1357	37.9	2426	4 US-09-439-313-470	Sequence 470, App
4	1357	37.9	2426	4 US-09-352-616A-470	Sequence 470, App
5	1123	31.4	2229	4 US-09-439-313-469	Sequence 469, App
6	1123	31.4	2229	4 US-09-352-616A-469	Sequence 469, App
7	720	20.1	812	4 US-09-439-313-471	Sequence 471, App
8	720	20.1	812	4 US-09-352-616A-471	Sequence 471, App
9	201	5.6	718	4 US-09-439-313-313	Sequence 313, App
10	201	5.6	718	4 US-09-352-616A-313	Sequence 313, App
11	201	5.6	718	4 US-09-232-149A-313	Sequence 313, App
12	179	5.0	301	4 US-09-439-313-287	Sequence 287, App
13	179	5.0	301	4 US-09-352-616A-287	Sequence 287, App
14	179	5.0	301	4 US-09-232-149A-287	Sequence 287, App
15	127	3.5	283	4 US-09-439-313-235	Sequence 235, App
16	127	3.5	283	4 US-09-352-616A-235	Sequence 235, App
17	127	3.5	283	4 US-09-232-149A-235	Sequence 235, App
18	29	0.8	540	4 US-09-220-132-125	Sequence 125, App
19	29	0.8	1867	2 US-08-607-509-3	Sequence 3, App1
20	29	0.8	1867	2 US-08-634-642-3	Sequence 3, App1
21	29	0.8	1867	2 US-08-989-370-3	Sequence 3, App1
22	29	0.8	2169	3 US-08-806-326-5	Sequence 5, App1
23	29	0.8	3925	3 US-08-793-044-1	Sequence 1, App1
24	29	0.8	48974	3 US-08-920-422-17	Sequence 10, App1
25	28	0.8	12141	3 US-09-488-671-10	Sequence 17, App1
26	27	0.8	65	1 US-08-222-177A-116	Sequence 116, App
27	27	0.8	65	1 US-08-222-177A-421	Sequence 421, App

C	28	27	0.8	72	1	US-08-222-177A-131	Sequence 131, App
C	29	27	0.8	72	1	US-08-222-177A-427	Sequence 427, App
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C	37	27	0.8	835	4	US-09-171-209-42	Sequence 42, App1
C	38	27	0.8	1325	4	US-08-915-795-6	Sequence 6, App1
C	39	27	0.8	1526	4	US-09-495-050A-293	Sequence 293, App
C	40	27	0.8	1560	4	US-08-907-706-2	Sequence 2, App1
C	41	27	0.8	1803	4	US-09-909-595-3	Sequence 3, App1
C	42	27	0.8	1816	4	US-09-645-926A-5	Sequence 5, App1
C	43	27	0.8	2040	1	US-08-393-985-17	Sequence 17, App1
C	44	27	0.8	3000	1	US-08-393-985-3	Sequence 3, App1
C	45	27	0.8	3001	4	US-09-539-333D-167	Sequence 167, App

ALIGNMENTS

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RESULT 1
US-09-439-313-468
; Sequence 468, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Rafter, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ. ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-468

Query Match      38.1%; Score 1364; DB 4; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
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DB	1313	GGTGAGAAATTAAGAAAGGCTGCTGACTTTCACATCTGAGCCACACATCTGCGAATG	1372
QY	345	AGATTAATTAACATCAGTAAGAAAGGCTGCTGACTTTCACATCTGAGCCACACATCTGCGAATG	404
DB	1373	AGATTAATTAACATCAGTAAGAAAGGCTGCTGACTTTCACATCTGAGCCACACATCTGCGAATG	1432
QY	405	TTTTGACATTTTCAGCCCTTTAATATTCACACACAGAAAGCAAAAGAGAC	464
DB	1433	TTTTGACATTTTCAGCCCTTTAATATTCACACACAGAAAGCAAAAGAGAC	1492
QY	465	AGAGATCCCTGGAGAAATCCCGCCGCTTTGGGTCATGATGAGCGCTCGCCCTG	524
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RESULT 2
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; Sequence 468, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiaogchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-468

Query Match 38.1%; Score 1364; DB 4; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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Db 1493 AGAATCCCTGGGAGAAATGCGCGCGCATCTTGGGTATCATGATAGCTCCCTGT 1552

OY	1604	TTTGAAATTAAGTTGACACTATCTTACTTCACTGCAAAAGAGGACACATATGAGATTATCATC	1663
Db	2631	TTTTAAATTAAGTTGACACTATCTTACTTCACTGCAAAAGAGGACACATATGAGATTATCATC	2690
OY	1664	ACATGAGACACCAATATCTAAAGATGTATTTGATTATTAAGAGTTAGATTAATATATGA	1723
Db	2661	ACATGAGACACCAATATCTAAAGATGTATTTGATTATTAAGAGTTAGATTAATATATGA	2750
OY	1724	AATGCAGAGCCACAGAGGGAATGTATTAAGGGGACGTTTGTAAGCCTGGGATGTGAAGC	1783
Db	2751	AATGCAGAGCCACAGAGGGAATGTATTAAGGGGACGTTTGTAAGCCTGGGATGTGAAGC	2810
OY	1784	AAAGCGAGGGAACCTCATAGTATCTTATATATATCTTCAATTTCTATCTATCA	1843
Db	2811	AAAGCGAGGGAACCTCATAGTATCTTATATATATCTTCAATTTCTATCTATCA	2870
OY	1844	ATATCCAAACAAGCTTTTTCACAGAAATTCATGTGACAGTACCAATCCCAAGATTAACCTTATC	1903
Db	2871	ATATCCAAACAAGCTTTTTCACAGAAATTCATGTGACAGTACCAATCCCAAGATTAACCTTATC	2930
OY	1904	CATTTCATGTGATGAGTCCGCTTTAGAAATTTTGGCAATATCATCTGTCATTATCTCAACT	1963
Db	2931	CATTTCATGTGATGAGTCCGCTTTAGAAATTTTGGCAATATCATCTGTCATTATCTCAACT	2990
OY	1964	TTTGAGATGTGTTTGTCCTTGTAGTTAATTTGAAAGAAATAGGGCACTTTGTGAGCACTT	2022
Db	2991	TTTGAGATGTGTTTGTCCTTGTAGTTAATTTGAAAGAAATAGGGCACTTTGTGAGCACTT	3050
OY	2024	TAGGGTTCACCTCGCCAAATTAAGATTTTACAAAGAGC	2061
Db	3051	TAGGGTTCACCTCGCCAAATTAAGATTTTACAAAGAGC	3088
RESULT 3			
US-09-439-313-470/c			
; Sequence 470, Application US/09439313			
; Patent No. 6329505			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, David C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan Louise			
; APPLICANT: Jiang Yugu			
; APPLICANT: Reed, Steven G.			
; APPLICANT: Kalos, Michael			
; APPLICANT: Fanger, Gary			
; APPLICANT: Retter, Mark			
; APPLICANT: Solk, John			
; APPLICANT: Day, Craig			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
; FILE REFERENCE: 210121.427C9			
; CURRENT APPLICATION NUMBER: US/09/439,313			
; NUMBER OF SEQ ID NOS: 575			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 470			
; LENGTH: 2426			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-439-313-470			
Query Match			
Best Local Similarity 99.8%, Pred. No. 0;			
Matches 1767; Conservative 0; Mismatches 1; Indels 3; Gaps 3;			
OY	285	GGTGAGAATAAGAAAGGCTCTGACTTTACATCTGAGGCCACACATCTTGCTGAATGG	344
Db	1769	GGTGAGAATAAGAAAGGCTCTGACTTTACATCTGAGGCCACACATCTTGCTGAATGG	1710
OY	345	AGATATTAATCACTATGAAAGCAAGATGACATATTAATGTCTAAGTAGTACATGT	404
Db	1709	AGATATTAATCACTATGAAAGCAAGATGACATATTAATGTCTAAGTAGTACATGT	1650

QY	405	TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGCAACACAAAAGAAACAC	464
Db	1649	TTTTGCACATTTCCAGCCCTTTAAATATCCACACACAGCAACACAAAAGAAACAC	1590
QY	465	AGAGATCCCTGGGAAATAATGCCGGGCGGCATCTTGGGTCATCGATGAGCCCTGGCCGT	524
Db	1589	AGAGATCCCTGGGAAATAATGCCGGGCGGCATCTTGGGTCATCGATGAGCCCTGGCCGT	1530
QY	525	GCCTTGTCCTCGCTTGTGAGGAGAGACATTTAGAAAATGAATGATGTCTTCTTAAAGCA	584
Db	1539	GCCTTGTCCTCGCTTGTGAGGAGAGACATTTAGAAAATGAATGATGTCTTCTTAAAGCA	1470
QY	585	TGGGAGAGAAAACACATCTCTGTGGATATTATTATTGAGGGATTTCCAGATTGGAAT	644
Db	1469	TGGGAGAGAAAACACATCTCTGTGGATATTATTATTGAGGGATTTCCAGATTGGAAT	1410
QY	645	GAAGTCACAAAGTGACATTTACCAATGAGAGAAAAACAGAGAAAACTTGATGCGTT	704
Db	1409	GAAGTCACAAAGTGACATTTACCAATGAGAGAAAAACAGAGAAAACTTGATGCGTT	1350
QY	705	CACAAGACATGGCAACAAACAAATGGATACGTGTGATACATGAGGAGCCAAAGCTGGGG	764
Db	1349	CACAAGACATGGCAACAAACAAATGGATACGTGTGATACATGAGGAGCCAAAGCTGGGG	1290
QY	765	AGAGATTAACAACGGGGCAGAGGGTCAGAGATTTGCGCCCTGCTGCTTAACTGTGCGTTT	824
Db	1289	AGAGATTAACAACGGGGCAGAGGGTCAGAGATTTGCGCCCTGCTGCTTAACTGTGCGTTT	1230
QY	825	ATAACCAATCATTTCTATATTCTTAACCTCAAAAACAAAGCTGTGTAATATCGATCTC	884
Db	1229	ATAACCAATCATTTCTATATTCTTAACCTCAAAAACAAAGCTGTGTAATATCGATCTC	1170
QY	885	TACGGTCTCTTGCGCCCAACATTTCTCATATATACGCCACACATCATTTTATATTT	944
Db	1169	TACGGTCTCTTGCGCCCAACATTTCTCATATATACGCCACACATCATTTTATATTT	1110
QY	945	AGTCCCGAGATCTGTACTGTGACCTTTCTAACCTTAAATATACATTTCTCATTTGTTC	1004
Db	1109	AGTCCCGAGATCTGTACTGTGACCTTTCTAACCTTAAATATACATTTCTCATTTGTTC	1050
QY	1005	AAAGACCCCTGTGTGTGCTGCCTAATATGTAGCTACATGTTTTCCTAAGAGAGTGTGTG	1064
Db	1049	AAAGACCCCTGTGTGTGCTGCCTAATATGTAGCTACATGTTTTCCTAAGAGAGTGTGTG	990
QY	1065	GCCCAAGGGGATCTGTGAACAGGCTGGGAAGACATCTCAAGATCTTTCAGGGTTATCTTA	1124
Db	989	GCCCAAGGGGATCTGTGAACAGGCTGGGAAGACATCTCAAGATCTTTCAGGGTTATCTTA	930
QY	1125	CTAGACACACATGATCATTTACGAGAGGATTTCTAATCAATCAATCCTCAGTGTCT	1184
Db	929	CTAGACACACATGATCATTTACGAGAGGATTTCTAATCAATCAATCCTCAGTGTCT	870
QY	1185	TTGCCCATAGTGAATAATTCATTTCCACATTTGTGCCATTTCTCAAGACCTCAAAATGTCA	1244
Db	869	TTGCCCATAGTGAATAATTCATTTCCACATTTGTGCCATTTCTCAAGACCTCAAAATGTCA	810
QY	1245	TTCCATTAATATACAGAGATTAACCTTTTCTTAACTGGAAGAATTCATGTTACTG	1304
Db	809	TTCCATTAATATACAGAGATTAACCTTTTCTTAACTGGAAGAATTCATGTTACTG	750
QY	1305	CAGCTATGGAATTAATTAACATTTTGTGTTTCCAGTCAAGAAATGACTAAGTCCTTA	1364
Db	749	CAGCTATGGAATTAATTAACATTTTGTGTTTCCAGTCAAGAAATGACTAAGTCCTTA	690
QY	1365	TCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAAGTTAAATGCTTAGCCTGTACTG	1424
Db	689	TCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAAGTTAAATGCTTAGCCTGTACTG	630
QY	1425	AGGCTGTAATTAAG-CACAGCCTCTGCCCATCTCCACGCTTATCTGTCAACATCA	1483
Db	629	AGGCTGTAATTAAGCACAAGCCTCTGCCCATCTCCACGCTTATCTGTCAACATCA	570

QY	1484	CCCCCCCCATACACACTTAACAAACAAATCTAACTTGTAATTCCTTGAACTATGACAGACTA	15433
Db	569	CCCCCCTCAT -GCACCTTAACCAAAATCTAACTTGTAATTCCTTGAACTATGACAG -CATTA	512
QY	1544	CATTATTCCTTCTGCGCTGAGAAGCCTCTCTTGCTCTTAAATCATGAAATGTAAGAAT	16030
Db	511	CATTATTCCTTCTGCGCTGAGAAGCCTCTCTTGCTCTTAAATCATGAAATGTAAGAAT	452
QY	1604	TTTGAAATTAAGTTGACTATCTACTTTCATGACAAGAAGGACACATATGATTCATCATC	16633
Db	451	TTTGAAATTAAGTTGACTATCTACTTTCATGACAAGAAGGACACATATGATTCATCATC	392
QY	1664	ACATGAGACACACCAATTAATAAAAGTGAATTTGATTAATAAGTTTGAATTAATATATGA	17233
Db	391	ACATGAGACACACCAATTAATAAAAGTGAATTTGATTAATAAGTTTGAATTAATATATGA	332
QY	1724	AATGCAGAAAGCCACAGAGGAATGTTTATGGGCAACGTTTGAAGCCCTGGGATGTGAAGC	17833
Db	331	AATGCAGAAAGCCACAGAGGAATGTTTATGGGCAACGTTTGAAGCCCTGGGATGTGAAGC	272
QY	1784	AAAGGCAGGAACCTCATAGTATCTTAATATTAATTAATCTTCAATTCCTATCTATACACA	18433
Db	271	AAAGGCAGGAACCTCATAGTATCTTAATATTAATTAATTAATCTTCAATTCCTATCTATACACA	212
QY	1844	ATATCCAAACAAGCTTTTACAGAAATTCATGAGTGCAGAAATCCCAAAAGTAAACCTTATTC	19033
Db	211	ATATCCAAACAAGCTTTTACAGAAATTCATGAGTGCAGAAATCCCAAAAGTAAACCTTATTC	152
QY	1904	CATTTCAGTGAAGTGCCTTTAGAAATTTTGGCAAAATCATCTGCTCACTATCTCAACT	19633
Db	151	CATTTCAGTGAAGTGCCTTTAGAAATTTTGGCAAAATCATCTGCTCACTATCTCAACT	92
QY	1964	TTTGAGATGTGTTGTCTCTTGAATTAATTTGAAGAAATATAGGGCACTCTGTGAGCCACTT	20233
Db	91	TTTGAGATGTGTTGTCTCTTGAATTAATTTGAAGAAATATAGGGCACTCTGTGAGCCACTT	32
QY	2024	TAGGGTTCACCTCTGGCAATTAAGAAATTTAC	2054
Db	31	TAGGGTTCACCTCTGGCAATTAAGAAATTTAC	1

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1  RESULT 4
2  US-09-352-616A-470/c
3  Sequence 470, Application US/09352616A
4  Patent No. 6395378
5  GENERAL INFORMATION:
6  APPLICANT: Dillon, Davin C.
7  APPLICANT: Hallocker, Susan Louise
8  APPLICANT: Jiang, Yuqi
9  APPLICANT: Xu, JIANGCHUN
10 APPLICANT: Mitcham, Jennifer Lynn
11 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOT
12 FILE REFERENCE: 210121.42708
13 CURRENT APPLICATION NUMBER: US/09/352.616A
14 NUMBER OF SEQ ID NOS: 472
15 SOFTWARE: FastSeq for Windows Version 3.0.
16 SEQ ID NO 470
17 LENGTH: 2426
18 TYPE: DNA
19 ORGANISM: Homo sapiens
20 US-09-352-616A-470

```

Query Match 37.98; Score 1357; DB 4; Length 2426;

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Best local similarity  55.08,  Freq. NO: 0;
Matches 1767;  Conservative  0;  Mismatches  1;  Indels  3;  Gaps  3;

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OY	285	GGTGAGAAATTAAGAAAGCGCTGCACATTACCATCTGGGCCACACATCTGCTGAATATGG	344
Dd	1769	GGTGAGAANTTAAGAAAGCGCTGCACATTACCATCTGGGCCACACATCTGCTGAATATGG	1710
OY	345	AGATAAATTAACATCCTAGAAAACGACAAGATGACAAATATAATTCCTAAGTAGTGCATGT	404

Db	1709	AGATATATTAACATCTACTAGAAACAGCAAGATGACAAATTAATATGTCATAAGTAGTCATCT	1655
OY	405	TTTTGCACATTTCCAGCCCTTTAAATATCCACACACACAGAGAACACAAAAGGAAGCAC	464
Db	1649	TTTTGCACAAATTTCCAGCCCTTTAAATATATCCACACACACAGAGAACACAAAAGGAAGCAC	1590
OY	465	AGAAATCCCTGGGAGAAATGCCCGCGCCACTCTTGSGTCATCGATGAGCTCGCCCTGT	524
Db	1589	AGAAATCCCTGGGAGAAATGCCCGCGCCACTCTTGSGTCATCGATGAGCTCGCCCTGT	1530
OY	525	GCCGTGTCGCCCTGTGAGGGAAGACATTAAGAAATGAATGAATGATGATGTCCTCTTAAGAG	584
Db	1529	GCCGTGTCGCCCTGTGAGGGAAGACATTAAGAAATGAATGAATGATGATGTCCTCTTAAGAG	1470
OY	585	TGGGACAGAAAACAGATCTGTTGTGATATTTATTTGMAAGGGATTAACAATTTGAAAT	644
Db	1469	TGGGACAGAAAACAGATCTGTTGTGATATTTATTTGMAAGGGATTAACAATTTGAAAT	1410
OY	645	GAAGTCACAAAGTAGCATTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCTT	704
Db	1409	GAAGTCACAAAGTAGCATTACCAATGAGAGAAAACAGACGAGAAAATCTTGATGCTT	1350
OY	705	CACAAGCATGCAACAAAAGAAATGAAATCTGTGATGATGACATGAGGCGCAAGCTGGGG	764
Db	1349	CACAAGCATGCAACAAAAGAAATGAAATCTGTGATGATGACATGAGGCGCAAGCTGGGG	1290
OY	765	AGGAGATTAACACGGGGGAGAGGATCAGAGATTTGGCCCTGCGCTAAATCTGTCCTTC	824
Db	1289	AGGAGATTAACACGGGGGAGAGGATCAGAGATTTGGCCCTGCGCTAAATCTGTCCTTC	1230
OY	825	ATAAACCAATCATTTATTTCTAATCCCTCAAAACAAAGCTGTTGTAATATCTGATCTC	884
Db	1229	ATAAACCAATCATTTATTTCTAATCCCTCAAAACAAAGCTGTTGTAATATCTGATCTC	1170
OY	885	TACGGTCCCTCTGGGCCCAACATCTCCATATATATCCAGCCACACTCATTTTAAATATTT	944
Db	1169	TACGGTCCCTCTGGGCCCAACATCTCCATATATATCCAGCCACACTCATTTTAAATATTT	1110
OY	945	AGTTCCAGATCTGTACTGTACCTTTCTACAGTGTAGAAATACATATCTCATTTTGTTC	1004
Db	1109	AGTTCCAGATCTGTACTGTACCTTTCTACAGTGTAGAAATACATATCTCATTTTGTTC	1055
OY	1005	AAAGACCCCTTGCTGTGCTGCCATAATATGATGACTGATGTTTTTCTAAGAGATGTTCTG	1064
Db	1049	AAAGACCCCTTGCTGTGCTGCCATAATATGATGACTGATGTTTTTCTAAGAGATGTTCTG	990
OY	1065	GCCCAAGGGATCTGTGAACAGGCTGGGAGAGCATCTCAAGATCTTCCAGGGTATACTTA	1124
Db	989	GCCCAAGGGATCTGTGAACAGGCTGGGAGAGCATCTCAAGATCTTCCAGGGTATACTTA	930
OY	1125	CTACACACACATGATCATTAAGGAGATTAATCTAATACATCATCTCCAGTGTCT	1184
Db	929	CTACACACACATGATCATTAAGGAGATTAATCTAATACATCATCTCCAGTGTCT	870
OY	1185	TTGGCCATCTGAAATTCATTTCCACATTTTGTGCCATTTCTCAAGACCTCAAAATGTCA	1244
Db	869	TTGGCCATCTGAAATTCATTTCCACATTTTGTGCCATTTCTCAAGACCTCAAAATGTCA	810
OY	1245	TTCCATTAATATCACAGATTAACCTTTTTTTAACTGGAAGATTCATGTTACATG	1304
Db	809	TTCCATTAATATCACAGATTAACCTTTTTTTAACTGGAAGATTCATGTTACATG	750
OY	1305	CAGCATGAGGAATTAATTAACATATTTTGTTCOAGTGCAAAAGTGTCTAAGCCCTTA	1364
Db	749	CAGCATGAGGAATTAATTAACATATTTTGTTCOAGTGCAAAAGTGTCTAAGCCCTTA	690
OY	1365	TCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAAGTTAAATGCTTAAGCCTGTACTG	1424
Db	689	TCCCTCCCTTTGTTGATTTTTTTTCCAGTATAAAGTTAAATGCTTAAGCCTGTACTG	630
OY	1425	AGCGTATATACAG-CACAGCCTGTCCCATCTCCAGCCTTATCTGTATCATACCATCA	1483

Db	629	AGGCTGTAATACAGCACAAGCCTCTCCCATCCCTCCACGCTTATCTGTCAATCACCATCA	570
Qy	1484	CCCCCTCCCATACCACTTAACAAAATCTTAAGTTGTAATTTCTTGAACATGTGCAGACATA	1543
Db	569	CCCCCTCCCAT -GCACCTTAACAAAATCTTAAGTTGTAATTTCTTGAACATGTGCAGG -CATA	512
Qy	1544	CATTATTCCTCTCTGCTGAGAAAGCTCTTCTCTCTTAAATCTAGAAATGATGTAAAGT	1604
Db	511	CATTATTCCTCTCTGCTGAGAAAGCTCTTCTCTCTTAAATCTAGAAATGATGTAAAGT	452
Qy	1604	TTTGAATTAAGTTGACTATCTTACTTTCATGACAAAGAGGAGACATATAGATTCATCTC	1663
Db	451	TTTGAATTAAGTTGACTATCTTACTTTCATGACAAAGAGGAGACATATAGATTCATCTC	392
Qy	391	ACATGAGACAGCAAAATACTAAAGTGTAAATTTGATTTATTAAGATTTAGATTAATATATGA	1723
Db	1664	ACATGAGACAGCAAAATACTAAAGTGTAAATTTGATTTATTAAGATTTAGATTAATATATGA	1723
Qy	1724	AATGCAGAGCCACAGAGGGAATGTTTATGGGGCAGCTTTTGAACCTGGAGTGTGAAGC	1783
Db	331	AATGCAGAGCCACAGAGGGAATGTTTATGGGGCAGCTTTTGAAGCCGGGATGTGAAGC	272
Qy	1784	AAAGGACAGGAACCCATAGTATCTTATATATATATACCTCAATTCCTATCTATCCACA	1843
Db	271	AAAGGACAGGAACCCATAGTATCTTATATATATATACCTCAATTCCTATCTATCCACA	212
Qy	1844	ATATCCAAAGAGCTTTTCCACAGAAATTCATGCAGTGCAAATCCCAAGAGTAACCTTTATC	1903
Db	211	ATATCCAAAGAGCTTTTCCACAGAAATTCATGCAGTGCAAATCCCAAGAGTAACCTTTATC	152
Qy	1904	CATTTCATGTGTAGTGGCGCTTTAGAAATTTGGCAATCATACTGGTCACTTATCTCAACT	1963
Db	151	CATTTCATGTGTAGTGGCGCTTTAGAAATTTGGCAATCATACTGGTCACTTATCTCAACT	92
Qy	1964	TTTGAATTAAGTTGACTATCTTACTTTCATGACAAAGAGGAGACATATAGATTCATCTC	2023
Db	91	TTTGAATTAAGTTGACTATCTTACTTTCATGACAAAGAGGAGACATATAGATTCATCTC	32
Qy	2024	TAGGTTCCACTCTGCGCAATTAAGAAATTTAC	2054
Db	31	TAGGTTCCACTCTGCGCAATTAAGAAATTTAC	1
RESULT 5			
US-09-439-313-469/c			
: Sequence 469, Application US/09439313			
: Patent No. 6329505			
: GENERAL INFORMATION:			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Dillon, Davin C.			
: APPLICANT: Mitcham, Jennifer L.			
: APPLICANT: Harlocker, Susan Louise			
: APPLICANT: Jiang Yuxui			
: APPLICANT: Reed, Steven G.			
: APPLICANT: Kalos, Michael			
: APPLICANT: Fanger, Gary			
: APPLICANT: Retter, Mark			
: APPLICANT: Solk, John			
: APPLICANT: Day, Craig			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
: FILE REFERENCE: 210121.427C9			
: CURRENT APPLICATION NUMBER: US/09/439,313			
: CURRENT FILING DATE: 1999-11-12			
: NUMBER OF SEQ ID NOS: 575			
: SOFTWARE: FastSeq for Windows Version 3.0			
: SEQ ID NO 469			
: LENGTH: 2229			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: US-09-439-313-469			
Query Match			

		Best Local Similarity	99.7%; Pred. No. 0;	Matches 1773; Conservative 0; Mismatches 1; Indels 5; Gaps 5;
OY	285	GGTGAATAATGAAGAGCTGCTGACCTTACCATGTGAGGCGACACATCTGCTGAAAAGG	344	
Db	1775	GGTGAATAATGAAGAGCTGCTGACCTTACCATGTGAGGCGACACATCTGCTGAAAAGG	1716	
OY	345	AGATTAATTAACATCACTAGAAAACAGACAGATGACATATTAATGTCTAGTAGTGCATGT	404	
Db	1715	AGATTAATTAACATCACTAGAAAACAGACAGATGACATATTAATGTCTAGTAGTGCATGT	1656	
OY	405	TTTGGCACAATTTCCAGCCCCCTTTAAATATCCACACACACAGAGACACAAAAGAACAC	464	
Db	1655	TTTGGCACAATTTCCAGCCCCCTTTAAATATCCACACACACAGAGACACAAAAGAACAC	1596	
OY	465	AGAGATCCCTGGGAGAAATGCCGCGCCCATCTTGGGTCAATCATGAGCCCTCGCCCTGT	524	
Db	1595	AGAGATCCCTGGGAGAAATGCCGCGCCCATCTTGGGTCAATCATGAGCCCTCGCCCTGT	1536	
OY	525	GCTGTGCTCCGCTGTGTAGGAGAGACATTAAGAAATGAATGTGTCTCTTAAAGGA	584	
Db	1535	GCTGTGCTCCGCTGTGTAGGAGAGACATTAAGAAATGAATGTGTCTCTTAAAGGA	1476	
OY	585	TGGGAGGAAAAAGATCCTGTGTGATTTATTTGAAGGGGATTACAGATTGGAAT	644	
Db	1475	TGGGAGGAAAAAGATCCTGTGTGATTTATTTGAAGGGGATTACAGATTGGAAT	1416	
OY	645	GAATGACAAAGTGAAGATTAACATGAGAGAAAAACAGAGAAAAATCTTGATGCTT	704	
Db	1415	GAATGACAAAGTGAAGATTAACATGAGAGAAAAACAGAGAAAAATCTTGATGCTT	1356	
OY	705	CACAAGACATGCAACAAACAAATGGAATTAATGATGATGATGAGGAGCCAGCTGGGG	764	
Db	1355	CACAAGACATGCAACAAACAAATGGAATTAATGATGATGATGAGGAGCCAGCTGGGG	1296	
OY	765	AGAGATTAACACAGGGGAGAGGCTGAGATTTGCGCCCTGCTGCTAACCTGTCGCTTC	824	
Db	1295	AGAGATTAACACAGGGGAGAGGCTGAGATTTGCGCCCTGCTGCTAACCTGTCGCTTC	1236	
OY	825	ATAACCAATCATTTTCAATTTTCTAACCCCTCAAAACAAAGCTGTTGAATATCTGATCTC	884	
Db	1235	ATAACCAATCATTTTCAATTTTCTAACCCCTCAAAACAAAGCTGTTGAATATCTGATCTC	1176	
OY	885	TACGGTTCCTTCTGGGCGCAACATTTCTCATATATCCAGCACACTCAATTTTAATATTT	944	
Db	1175	TACGGTTCCTTCTGGGCGCAACATTTCTCATATATCCAGCACACTCAATTTTAATATTT	1116	
OY	945	AGTTCACAGATCTGACTGTACCTTTCTACACTGTAGATTAACATTCATTTTGTTC	1004	
Db	1115	AGTTCACAGATCTGACTGTACCTTTCTACACTGTAGATTAACATTCATTTTGTTC	1056	
OY	1005	AAAGACCTTCTGCTGCTTAATATATGACTGACTGTTTTCTTAAGAGAGTGTCTG	1064	
Db	1055	AAAGACCTTCTGCTGCTTAATATATGACTGACTGTTTTCTTAAGAGAGTGTCTG	996	
OY	1065	GCCAGAGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGCTTAATCTTA	1124	
Db	995	GCCAGAGGATCTGTGAACAGGCTGGAGACATCTCAAGATCTTCCAGGCTTAATCTTA	936	
OY	1125	CTAGACACAGACATGATTAAGGAGATTAATCTAATTAACATCTCTCTGCTGCT	1184	
Db	935	CTAGACACAGACATGATTAAGGAGATTAATCTAATTAACATCTCTCTGCTGCT	876	
OY	1185	TTGGCCACTACTGAATTCATTTCCACTTTTGTGCCCTTCTCAAGAGCTCAAAATGTCA	1244	
Db	875	TTGGCCACTACTGAATTCATTTCCACTTTTGTGCCCTTCTCAAGAGCTCAAAATGTCA	816	
OY	1245	TTTCATTAAATATCAGAGATTAATCTTTTAACTGGAAGAAATTCATGTTACATG	1304	
Db	815	TTTCATTAAATATCAGAGATTAAC-TTTTAACTGGAAGAAATTCATGTTACATG	757	
OY	1305	CAGCTATGGGAATTAATTAATTTTGTCTTCCAGTGCAAAATGACTAAGTCTTTA	1364	

Db	756	CAGCTATGGGAATTAATTAATTAATTTTGTCTTCCAGTGCAAAAGATGACTAAGTCTTTA	697	
OY	1365	TCCCTCCCTTTGTTGATTTTTTTCAGATAATAAGTTAAATGCTTACGCTTGACTG	1424	
Db	696	TCCCTCCCTTTGTTGATTTTTTTCAGATAATAAGTTAAATGCTTACGCTTGACTG	637	
OY	1425	AGGCTATTAACAG-CACAGCTCTCCCATCCCTCCACAGCTTATCTCATCACCATCA	1483	
Db	636	AGGCTATTAACAGCACAGAGCTCTCCCATCCCTCCACAGCTTATCTCATCACCATCA	577	
OY	1484	CCCCCTCCATACACACTTAAACAAATCTAATCTTGAATCTTGAACATGTGACAGACTA	1543	
Db	576	CCCCCTCCAT-GCACCTTAAACAAATCTAATCTTGAATCTTGAACATGTGACAG-CA	519	
OY	1544	CATTATTCCTTCTGCTGAGAGGCTCTCTCTTGTCTCTTAATCTAGAAATGTAATG	1603	
Db	518	CATTATTCCTTCTGCTGAGAGGCTCTCTCTTGTCTCTTAATCTAGAAATGTAATG	459	
OY	1604	TTTGAATTAAGTTGACTATCTTACTTATGCAAAAGAGGACATATGAGATTGATCATC	1663	
Db	458	TTTGAATTAAGTTGACTATCTTACTTATGCAAAAGAGGACATATGAGATTGATCATC	399	
OY	1664	ACATGAGACAGAAATTAATAAGGTAATTTGATTAAGAGTTAGATTAATATATGA	1723	
Db	398	ACATGAGACAGAAATTAATAAGGTAATTTGATTAAGAGTTAGATTAATATATGA	340	
OY	1724	AATGCAAGAGCCACAGAGGAAATGTTATGGGCGCAGTTGTAAGCCTGGAGATGGAAGC	1783	
Db	339	AATGCAAGAGCCACAGAGGAAATGTTATGGGCGCAGTTGTAAGCCTGGAGATGGAAGC	280	
OY	1784	AAAGCAGGAACTCATATGATCTTAATTAATTAATTAATTAATTAATTAATTAATTA	1843	
Db	279	AAAGCAGGAACTCATATGATCTTAATTAATTAATTAATTAATTAATTAATTAATTA	220	
OY	1844	ATATCCAAACAGCTTTTACAGAAATTCATGAGAGCAAAATCCCAAGCTAACCTTTATC	1903	
Db	219	ATATCCAAACAGCTTTTACAGAAATTCATGAGAGCAAAATCCCAAGCTAACCTTTATC	160	
OY	1904	CATTTCATGATGAGTGCCTTTAGAAATTTGGCAAAATCATCTGCTACTTATCTCACT	1963	
Db	159	CATTTCATGATGAGTGCCTTTAGAAATTTGGCAAAATCATCTGCTACTTATCTCACT	100	
OY	1964	TTGAGATGTGTTTGTCTTGTAGTTAATTAAGAAATAGGGCACTGTGAGCCACTT	2023	
Db	99	TTGAGATGTGTTTGTCTTGTAGTTAATTAAGAAATAGGGCACTGTGAGCCACTT	40	
OY	2024	TAGGTTCACTCTCGCAATTAAGATTTTACAAAGAGCT	2062	
Db	39	TAGGTTCACTCTCGCAATTAAGATTTTACAAAGAGCT	1	

RESULT 6
 US-09-352-616A-469/C
 ; Sequence 469, Application US/09352616A
 ; Patent No. 6395278
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang, Yuhui
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Mitcham, Jennifer Lynn
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; FILE REFERENCE: 210121.427C8
 ; CURRENT APPLICATION NUMBER: US/09/352,616A
 ; CURRENT FILING DATE: 1999-07-13
 ; NUMBER OF SEQ ID NOS: 472
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 469
 ; LENGTH: 2229
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-352-616A-469

Query Match 31.4%; Score 1123; DB 4; Length 2229;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1773; Conservative 0; Mismatches 1; Indels 5; Gaps 5;

285 GGTGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATG 344
 1775 GGTGAAATTAAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGCTGAATG 1716
 345 AGATAATTAACATCTAGTAAGACAGCAATGATATATGCTTAAGTAGTACATG 404
 1715 AGATAATTAACATCTAGTAAGACAGCAATGATATATGCTTAAGTAGTACATG 1656
 405 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGGAGGACAAAAGAGAC 464
 1655 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGGAGGACAAAAGAGAC 1596
 465 AGAGATCCCTGGGAGAAATGCCGGCCCATCTTGCTCATCGATGAGCCCTGCT 524
 1595 AGAGATCCCTGGGAGAAATGCCGGCCCATCTTGCTCATCGATGAGCCCTGCT 1536
 525 GCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
 1535 GCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1476
 585 TGGGAGAGAAACAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 644
 1475 TGGGAGAGAAACAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1416
 645 GAATGCACAAATGAGCATTTACCAATGAGAGGAAACAGACGAAATCTTGATGCT 704
 1415 GAATGCACAAATGAGCATTTACCAATGAGAGGAAACAGACGAAATCTTGATGCT 1356
 705 CACAGACATGCAACAAATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764
 1355 CACAGACATGCAACAAATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1296
 765 AGAGATTAACACAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
 1295 AGAGATTAACACAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1236
 825 ATACCAAAATCATTTCAATTTCTTAACCTCAAAACAAAGCTGTTGTAATCTGATCT 884
 1235 ATACCAAAATCATTTCAATTTCTTAACCTCAAAACAAAGCTGTTGTAATCTGATCT 1176
 885 TAGGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944
 1175 TAGGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1116
 945 AGTTCCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004
 1115 AGTTCCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1056
 1005 AAAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1064
 1055 AAAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996
 1065 GCCCAGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1124
 995 GCCCAGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 936
 1125 CTAGCACACAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1184
 935 CTAGCACACAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876
 1185 TTGCCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1244
 875 TTGCCATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816
 1245 TTGCATTAATACAGGATTAACCTTTTAACTGGAAGATTAAGTGTACAG 1304
 815 TTGCATTAATACAGGATTAACCTTTTAACTGGAAGATTAAGTGTACAG 757

1305 CAGCTATGGGAATTTAATACATATTTGTTTCCAGTGCAGAAAGATGACTAAGTCTTTA 1364
 756 CAGCTATGGGAATTTAATACATATTTGTTTCCAGTGCAGAAAGATGACTAAGTCTTTA 697
 1365 TCCCTCCCTTTGTTGATTTTTCAGATATAAGTTAAATGCTTACCTTGTACTG 1424
 696 TCCCTCCCTTTGTTGATTTTTCAGATATAAGTTAAATGCTTACCTTGTACTG 637
 1425 AGGCTATATACAG-CACAGCCTTCCCTCCATCCCTCCAGCCTTATCTGTATCATCCATCA 1483
 636 AGGCTATATACAGCAGCAGCCTTCCCTCCATCCCTCCAGCCTTATCTGTATCATCCATCA 577
 1484 CCCCCTCCATACACCTTAAACAAATCTAATCTGATTTCTGATGACATGCTGAGACATA 1543
 576 CCCCCTCCAT-AGACCTTAAACAAATCTAATCTGATTTCTGATGACATGCTGAGC-CA 519
 1544 CATTTATCTTCTGCTGCTGAGAAAGCTTCTGCTGCTTAAATCTGAAATGATGTAAGT 1603
 518 CATTTATCTTCTGCTGCTGAGAAAGCTTCTGCTGCTTAAATCTGAAATGATGTAAGT 459
 1604 TTTGATTAAGTTCATATCTTACTTACTGCAAAAGAGGACACATATGATGATGATGATG 1663
 458 TTTGATTAAGTTCATATCTTACTTACTGCAAAAGAGGACACATATGATGATGATGATG 399
 1664 ACATGAGACAGCAAAATCTAATAAGTATGATTAAGATTAAGATTAATATATGTA 1723
 398 ACATGAGACAGCAAAATCTAATAAGTATGATTAAGATTAAGATTAATATATGTA 340
 1724 AATGCAAGACCCAGAGGAAATGTTTATGAGGACAGCTTGTATAGCCTGGAGTGTAGC 1783
 339 AATGCAAGACCCAGAGGAAATGTTTATGAGGACAGCTTGTATAGCCTGGAGTGTAGC 280
 1784 AAAGGAGGAAACCTATGATCTTATTAATATCTTACTTACTTACTTACTTACTTACTT 1843
 279 AAAGGAGGAAACCTATGATCTTATTAATATCTTACTTACTTACTTACTTACTTACTT 220
 1844 ATATCCAAAGCTTTTCAAGAAATCATGACAGTGAATATCCCAAGGATTAACCTTATC 1903
 219 ATATCCAAAGCTTTTCAAGAAATCATGACAGTGAATATCCCAAGGATTAACCTTATC 160
 1904 CATTTATGCTGCTGCTGCTTGAATTTTGGCAATCATCTGCTTATCTAATCTAATCT 1963
 159 CATTTATGCTGCTGCTGCTTGAATTTTGGCAATCATCTGCTTATCTAATCTAATCT 100
 1964 TTGAGATGTTGTTGCTGCTGCTGATTAATGAAGAAATGAGGACCTTGTGAGCAGCT 2023
 99 TTGAGATGTTGTTGCTGCTGCTGATTAATGAAGAAATGAGGACCTTGTGAGCAGCT 40
 2024 TAGGTTCACTCCTGCAATTAAGAAATTTACAAGAGCT 2062
 39 TAGGTTCACTCCTGCAATTAAGAAATTTACAAGAGCT 1

RESULT 7
 US-09-439-313-471/C
 ; Sequence 471, Application US/09439313
 ; Patent No. 6329505
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang Yugu
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Solk, John
 ; APPLICANT: Day, Craig
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C9
 ; CURRENT APPLICATION NUMBER: US/09/439, 313

;; CURRENT FILING DATE: 1999-11-12
;; NUMBER OF SEQ ID NOS: 575
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 471
;; LENGTH: 812
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-439-313-471

Query Match 20.1%; Score 720; DB 4; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGTGGAATTAAGAAAGGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATGG 344
DB 720 GGTGGAATTAAGAAAGGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATGG 661
QY 345 AGATTAATTAACATCTAGAAACAGCAAGATGACATTAATGTCTAAGTAGTGACATGT 404
DB 660 AGATTAATTAACATCTAGAAACAGCAAGATGACATTAATGTCTAAGTAGTGACATGT 601
QY 405 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGAGCACAAGAAAGAACAC 464
DB 600 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGAGCACAAGAAAGAACAC 541
QY 465 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATCGATGAGCCCTGCCCTGT 524
DB 540 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATCGATGAGCCCTGCCCTGT 481
QY 525 GCTGTGTCCTGCTGTGAGGAGAGACATTTAGAAATGAATGATGTCTCTTAAGAAG 584
DB 480 GCTGTGTCCTGCTGTGAGGAGAGACATTTAGAAATGAATGATGTCTCTTAAGAAG 421
QY 585 TGGGAGGAGAAACAGATCTGTGTGATATTTTGAACGGGATTCAGATTGGAAT 644
DB 420 TGGGAGGAGAAACAGATCTGTGTGATATTTTGAACGGGATTCAGATTGGAAT 361
QY 645 GAAGTCACAAAGTGACATTTACCAATGAGAGAGAAACAGAGAGAAATCTTGATGCTT 704
DB 360 GAAGTCACAAAGTGACATTTACCAATGAGAGAGAAACAGAGAGAAATCTTGATGCTT 301
QY 705 CACAAGACATGCAACAAACAAATGGAATGATGATGATGATGATGATGATGATGATG 764
DB 300 CACAAGACATGCAACAAACAAATGGAATGATGATGATGATGATGATGATGATGATG 241
QY 765 AGGAGATTAACCAAGGGGAGAGGGTCAGAGATTTGGCCCTGCTGCTAACTGTGCTTC 824
DB 240 AGGAGATTAACCAAGGGGAGAGGGTCAGAGATTTGGCCCTGCTGCTAACTGTGCTTC 181
QY 825 ATAACCAAAATATTTCATATTTCTAACCCTCAAAAAGCTGTTGTAATATCTGATCTC 884
DB 180 ATAACCAAAATATTTCATATTTCTAACCCTCAAAAAGCTGTTGTAATATCTGATCTC 121
QY 885 TACGGTTCCTTCTGGGCCCAACATTTCCATATATCCAGCCACACTCTTTTAAATATT 944
DB 120 TACGGTTCCTTCTGGGCCCAACATTTCCATATATCCAGCCACACTCTTTTAAATATT 61
QY 945 AGTTCCAGATCTGATGACCTTTCTACACTGTAGAAATACATTACTATTTGTTC 1004
DB 60 AGTTCCAGATCTGATGACCTTTCTACACTGTAGAAATACATTACTATTTGTTC 1

RESULT 8
US-09-352-616A-471/c
; Sequence 471, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jianshun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

;; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
;; FILE REFERENCE: 210121.427C8
;; CURRENT APPLICATION NUMBER: US/09/352,616A
;; CURRENT FILING DATE: 1999-07-13
;; NUMBER OF SEQ ID NOS: 472
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 471
;; LENGTH: 812
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-352-616A-471

Query Match 20.1%; Score 720; DB 4; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 GGTGGAATTAAGAAAGGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATGG 344
DB 720 GGTGGAATTAAGAAAGGCTGCTGCTTACCATCTGAGGCCACACATCTGCTGAATGG 661
QY 345 AGATTAATTAACATCTAGAAACAGCAAGATGACATTAATGTCTAAGTAGTGACATGT 404
DB 660 AGATTAATTAACATCTAGAAACAGCAAGATGACATTAATGTCTAAGTAGTGACATGT 601
QY 405 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGAGCACAAGAAAGAACAC 464
DB 600 TTTTGACATTTCCAGCCCTTTTAATATCCACACACAGAGAGCACAAGAAAGAACAC 541
QY 465 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATCGATGAGCCCTGCCCTGT 524
DB 540 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATCGATGAGCCCTGCCCTGT 481
QY 525 GCTGTGTCCTGCTGTGAGGAGAGACATTTAGAAATGAATGATGTCTCTTAAGAAG 584
DB 480 GCTGTGTCCTGCTGTGAGGAGAGACATTTAGAAATGAATGATGTCTCTTAAGAAG 421
QY 585 TGGGAGGAGAAACAGATCTGTGTGATATTTTGAACGGGATTCAGATTGGAAT 644
DB 420 TGGGAGGAGAAACAGATCTGTGTGATATTTTGAACGGGATTCAGATTGGAAT 361
QY 645 GAAGTCACAAAGTGACATTTACCAATGAGAGAGAAACAGAGAGAAATCTTGATGCTT 704
DB 360 GAAGTCACAAAGTGACATTTACCAATGAGAGAGAAACAGAGAGAAATCTTGATGCTT 301
QY 705 CACAAGACATGCAACAAACAAATGGAATGATGATGATGATGATGATGATGATGATG 764
DB 300 CACAAGACATGCAACAAACAAATGGAATGATGATGATGATGATGATGATGATGATG 241
QY 765 AGGAGATTAACCAAGGGGAGAGGGTCAGAGATTTGGCCCTGCTGCTAACTGTGCTTC 824
DB 240 AGGAGATTAACCAAGGGGAGAGGGTCAGAGATTTGGCCCTGCTGCTAACTGTGCTTC 181
QY 825 ATAACCAAAATATTTCATATTTCTAACCCTCAAAAAGCTGTTGTAATATCTGATCTC 884
DB 180 ATAACCAAAATATTTCATATTTCTAACCCTCAAAAAGCTGTTGTAATATCTGATCTC 121
QY 885 TACGGTTCCTTCTGGGCCCAACATTTCCATATATCCAGCCACACTCTTTTAAATATT 944
DB 120 TACGGTTCCTTCTGGGCCCAACATTTCCATATATCCAGCCACACTCTTTTAAATATT 61
QY 945 AGTTCCAGATCTGATGACCTTTCTACACTGTAGAAATACATTACTATTTGTTC 1004
DB 60 AGTTCCAGATCTGATGACCTTTCTACACTGTAGAAATACATTACTATTTGTTC 1

RESULT 9
US-09-439-313-313
; Sequence 313, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

```

; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-313

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Query Match          5.6%; Score 201; DB 4; Length 718;
Best Local Similarity 99.3%; Pred. No. 1e-84;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 344
DB 73 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 132
QY 345 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 404
DB 133 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 192
QY 405 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGACAAAAGAGAC 464
DB 193 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGACAAAAGAGAC 252
QY 465 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGTTCATGATGAGCCTGCGCCTGT 524
DB 253 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGTTCATGATGAGCCTGCGCCTGT 312
QY 525 GCCTGCTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGTATGTCTTCTTAAGGA 584
DB 313 GCCTGCTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGTATGTCTTCTTAAGGA 372
QY 585 TGG 587
DB 373 TGG 375

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RESULT 10
US-09-352-616A-313
; Sequence 313, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718

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; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-313

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Query Match          5.6%; Score 201; DB 4; Length 718;
Best Local Similarity 99.3%; Pred. No. 1e-84;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 344
DB 73 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 132
QY 345 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 404
DB 133 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 192
QY 405 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGACAAAAGAGAC 464
DB 193 TTTTGACATTTCCAGCCCTTTAAATATCCACACACAGAGACAAAAGAGAC 252
QY 465 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGTTCATGATGAGCCTGCGCCTGT 524
DB 253 AGAGATCCCTGGGAGAAATGCCCGGCCCATCTTGGTTCATGATGAGCCTGCGCCTGT 312
QY 525 GCCTGCTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGTATGTCTTCTTAAGGA 584
DB 313 GCCTGCTCCCGCTTGTGAGGGAAGACATTAGAAATGAATGTATGTCTTCTTAAGGA 372
QY 585 TGG 587
DB 373 TGG 375

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RESULT 11
US-09-232-149A-313
; Sequence 313, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(718)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-313

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Query Match          5.6%; Score 201; DB 4; Length 718;
Best Local Similarity 99.3%; Pred. No. 1e-84;
Matches 301; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 285 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 344
DB 73 GGTGAGAAATTAAGAAAGGCTGCTGACTTACATCTGAGGCCACACATCTGCTGAATGG 132
QY 345 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 404
DB 133 AGATTAATTAACATCACTAGAAACAGCAAGATGACATATATATCTTAAGTAGACATGT 192

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Db 181 GGGCAGAGGGTCAGATCTGGCCCTGCGCTAAACGTGCGTTCATTAACCAATCATT 122
QY 839 TCATATTTCTAACCCCAACCAAGCTGTGTAATATCTGATCTACG 888
Db 121 TCATATTTCTAACCCCAACCAAGCTGTGTAATATCTGATCTACG 72

RESULT 15

US-09-439-313-235
; Sequence 235, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 235
; LENGTH: 283
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-235

Query Match

3.5%; Score 127; DB 4; Length 283;
Best Local Similarity 100.0%; Pred.No. 6.5e-50;

Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 157 TGTTCATGGATAGTCCAAATAAATGTTATCTTGAAGTATGATGCTCATAGAGAGATA 216
QY 2641 TAAGAACTCTGAGTGATATCAACATTAGGAGATCAAGAAATATTAGATTAAAGCTCACA 2700
Db 217 TAAGAACTCTGAGTGATATCAACATTAGGAGATCAAGAAATATTAGATTAAAGCTCACA 276
QY 2701 CTGGTCA 2707
Db 277 CTGGTCA 283

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- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3036	84.8	3923	9 US-09-759-143-690	Sequence 690, App
2	3036	84.8	3923	9 US-09-780-669-690	Sequence 690, App
3	3036	84.8	3923	9 US-09-822-827-690	Sequence 690, App
4	3036	84.8	3923	10 US-09-895-793-690	Sequence 690, App
5	3036	84.8	3923	10 US-09-895-814-690	Sequence 690, App
6	3036	84.8	3923	12 US-10-144-678A-690	Sequence 690, App
7	3036	84.8	3923	13 US-10-012-896-690	Sequence 690, App
8	3036	84.8	3923	14 US-10-205-823-316	Sequence 316, App
9	1364	38.1	3112	9 US-09-759-143-468	Sequence 468, App
10	1364	38.1	3112	9 US-09-780-669-468	Sequence 468, App
11	1364	38.1	3112	9 US-09-822-827-468	Sequence 468, App
12	1364	38.1	3112	10 US-09-895-793-468	Sequence 468, App
13	1364	38.1	3112	10 US-09-895-814-468	Sequence 468, App
14	1364	38.1	3112	12 US-10-144-678A-468	Sequence 468, App
15	1364	38.1	3112	13 US-10-012-896-468	Sequence 468, App
16	1364	38.1	3112	14 US-10-010-940-468	Sequence 468, App

c 17	1357	37.9	2426	9 US-09-759-143-470	Sequence 470, App
c 18	1357	37.9	2426	9 US-09-780-669-470	Sequence 470, App
c 19	1357	37.9	2426	9 US-09-822-827-470	Sequence 470, App
c 20	1357	37.9	2426	10 US-09-895-793-470	Sequence 470, App
c 21	1357	37.9	2426	10 US-09-895-814-470	Sequence 470, App
c 22	1357	37.9	2426	12 US-10-144-678A-470	Sequence 470, App
c 23	1357	37.9	2426	13 US-10-012-896-470	Sequence 470, App
c 24	1357	37.9	2426	14 US-10-010-940-470	Sequence 470, App
c 25	1357	37.9	2426	14 US-10-205-823-448	Sequence 448, App
c 26	1123	31.4	2229	9 US-09-759-143-469	Sequence 469, App
c 27	1123	31.4	2229	9 US-09-780-669-469	Sequence 469, App
c 28	1123	31.4	2229	9 US-09-822-827-469	Sequence 469, App
c 29	1123	31.4	2229	10 US-09-895-793-469	Sequence 469, App
c 30	1123	31.4	2229	10 US-09-895-814-469	Sequence 469, App
c 31	1123	31.4	2229	12 US-10-144-678A-469	Sequence 469, App
c 32	1123	31.4	2229	13 US-10-012-896-469	Sequence 469, App
c 33	1123	31.4	2229	14 US-10-010-940-469	Sequence 469, App
c 34	738	20.6	876	11 US-09-957-708-3	Sequence 3, Appl1
c 35	720	20.1	812	9 US-09-759-143-471	Sequence 471, App
c 36	720	20.1	812	9 US-09-780-669-471	Sequence 471, App
c 37	720	20.1	812	9 US-09-822-827-471	Sequence 471, App
c 38	720	20.1	812	10 US-09-895-793-471	Sequence 471, App
c 39	720	20.1	812	10 US-09-895-814-471	Sequence 471, App
c 40	720	20.1	812	12 US-10-144-678A-471	Sequence 471, App
c 41	720	20.1	812	13 US-10-012-896-471	Sequence 471, App
c 42	720	20.1	812	14 US-10-010-940-471	Sequence 471, App
c 43	524	14.6	684	8 US-08-926-626-7	Sequence 7, Appl1
c 44	524	14.6	684	12 US-10-191-252-7	Sequence 7, Appl1
c 45	473	13.2	597	12 US-10-195-730-46	Sequence 46, Appl1

ALIGNMENTS

RESULT 1
US-09-759-143-690
Sequence 690, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo saplen
US-09-759-143-690
Query Match 84.8%; Score 3036; DB 9; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ACAGAAAGAAATATGCAATGTCGAGACAACTGGCATATGAAAAACAGAGGGAGATTTGTGT	60
Db	1	ACAGAAAGAAATATGCAATGTCGAGACAACTGGCATATGAAAAACAGAGGGAGATTTGTGT	60
QY	61	GGCTCAGCCCGAGGGAGACACAGGAAGATCTGCATGTGSGAAGGACCTGATGATPACAG	120
Db	61	GGCTCAGCCCGAGGGAGACACAGGAAGATCTGCATGTGSGAAGGACCTGATGATPACAG	120
QY	121	GAATTACAAACATATTAATAGTGTCTTAAATGAAACCAAGATAAATTAAGTGAAGAGCTA	180
Db	121	GAATTACAAACATATTAATAGTGTCTTAAATGAAACCAAGATAAATTAAGTGAAGAGCTA	180
QY	181	GTCGCGCTGTGAGTCTCTTCAGTGTACACAGGGCTGGATATCAATGAGCGCACTTCTGAG	240
Db	181	GTCGCGCTGTGAGTCTCTTCAGTGTACACAGGGCTGGATATCAATGAGCGCACTTCTGAG	240
QY	241	TACTAGTAGCAGCAAGAAGAAAGACTGTACACATCTCAATGGCAGGGGTGAGAAATPAGAAA	300
Db	241	TACTAGTAGCAGCAAGAAGAAAGACTGTACACATCTCAATGGCAGGGGTGAGAAATPAGAAA	300
QY	301	GGCTGCTACATTTTACCATCTGAGGCGCACACATCTGCTGAAATGGAGATTAATTAACATCAC	360
Db	301	GGCTGCTACATTTTACCATCTGAGGCGCACACATCTGCTGAAATGGAGATTAATTAACATCAC	360
QY	361	TAGAAACAGCAAGATGACAAATTAATATGCTAAGTAGTACATGTTTTTGGACATTTCCAG	420
Db	361	TAGAAACAGCAAGATGACAAATTAATATGCTAAGTAGTACATGTTTTTGGACATTTCCAG	420
QY	421	CCCTCTTAAATATCCACACACACAGGAGCAACAAAGAGACACAGACATCCCTGGGAGA	480
Db	421	CCCTCTTAAATATCCACACACACAGGAGCAACAAAGAGACACAGACATCCCTGGGAGA	480
QY	481	AATGCGCGCGCCGCAATCTTGGGTCAATGAGCCCTGCGCTGTGCTCCGCTGT	540
Db	481	AATGCGCGCGCCGCAATCTTGGGTCAATGAGCCCTGCGCTGTGCTCCGCTGT	540
QY	541	GAGGAGAGACATTTGAAAAATGAATGTATGTTCTTTAAAGATGGCGAGAAAACAGA	600
Db	541	GAGGAGAGACATTTGAAAAATGAATGTATGTTCTTTAAAGATGGCGAGAAAACAGA	600
QY	601	TCCCTTTGTGATTTATTTGAACGGGATTAACAGATTTGAAATGAATGAACTCAACAAAGTAG	660
Db	601	TCCCTTTGTGATTTATTTGAACGGGATTTAAGATTTGAAATGAATGAACTCAACAAAGTAG	660
QY	661	CATTACCAATGAGAGAAACAGACAGCAAAAAATCTGTGATGGCTTCACAAAGCATGCAACA	720
Db	661	CATTACCAATGAGAGAAACAGACAGCAAAAAATCTGTGATGGCTTCACAAAGCATGCAACA	720
QY	721	AACAAATATGAAATCTGTGATGACATGAGCCAGCCAGCTGGGGAGAGATTAACACAGGG	780
Db	721	AACAAATATGAAATCTGTGATGACATGAGCCAGCCAGCTGGGGAGAGATTAACACAGGG	780
QY	781	GCAGAGGGTCAAGANTCTGGCGCGTGCCTAAACTGTGCTTCAATACCAAAATCATTTTC	840
Db	781	GCAGAGGGTCAAGANTCTGGCGCGTGCCTAAACTGTGCTTCAATACCAAAATCATTTTC	840
QY	841	ATATTTCTAACCCTCCAAAACAAAGCTGTGTTAAATCTGATCTCAGCGTTCTCTTGGG	900
Db	841	ATATTTCTAACCCTCCAAAACAAAGCTGTGTTAAATCTGATCTCAGCGTTCTCTTGGG	900
QY	901	CCCAACATTTCTCATATATTCAGCCACACATCATTTTAAATTTAGTTCCAGATCTGTA	960
Db	901	CCCAACATTTCTCATATATTCAGCCACACATCATTTTAAATTTAGTTCCAGATCTGTA	960
QY	961	CTGTGACCTTCTACACTGTAGAAATTAACATTACATTTTGTCAAAAGACCTTCGTGT	1020
Db	961	CTGTGACCTTCTACACTGTAGAAATTAACATTACATTTTGTCAAAAGACCTTCGTGT	1020
QY	1021	GCTGCTATATATGATGACTGTTTTTCCTAAGAGAGTGTCTGGCCACAGGAGATCTGTG	1080
Db	1021	GCTGCTATATATGATGACTGTTTTTCCTAAGAGAGTGTCTGTGCCACAGGAGATCTGTG	1080
QY	1081	AACAGGCTGGAGACATCTCAAGATCTTTCCAGGGTTATACTTCTAGCACACAGCATGA	1140

Dp	1081	AACAGCGTGGGAAGCATCTCAAGATCTTCCAGGGTTTACTTACTACACACAGCAGA	1140
Qy	1141	TCATTACGGAGGAAATTATCTAATCAATCAATCCCTGATGTCCTTGGCCATACGAAAT	1200
Dp	1141	TCATTACGGAGGAAATTATCTAATCAATCAATCCCTGATGTCCTTGGCCATACGAAAT	1200
Qy	1201	TCATTGCCACTTTTGTGTGCCCAATTCACAAGACCTCCAAAATGTCATTCCATTAAATACACA	1260
Dp	1201	TCATTGCCACTTTTGTGTGCCCAATTCACAAGACCTCCAAAATGTCATTCCATTAAATACACA	1260
Qy	1261	GGATTAACTTTTTTTTTTAACCTGGAGAAATTCAAATGTTACATGACGTATGGAAATTTA	1320
Dp	1261	GGATTAACTTTTTTTTTTAACCTGGAGAAATTCAAATGTTACATGACGTATGGAAATTTA	1320
Qy	1321	ATTACATATTTTGTGTTTCCAGTGCACAAATAGCATAGACCTTTATACCTCCCTTGTGTT	1380
Dp	1321	ATTACATATTTTGTGTTTCCAGTGCACAAATAGCATAGACCTTTATACCTCCCTTGTGTT	1380
Qy	1381	GATTTTTTTTCCAGTATAAAGTTAAATGCTTAAGCTTGTACTGAGGCTGTATACAGCAC	1440
Dp	1381	GATTTTTTTTCCAGTATAAAGTTAAATGCTTAAGCTTGTACTGAGGCTGTATACAGCAC	1440
Qy	1441	AGCCCTCCCAATCCCTCCAGCCTTATCTGTATCATACCATCAACCCCTCCCATACCACT	1500
Dp	1441	AGCCCTCCCAATCCCTCCAGCCTTATCTGTATCATACCATCAACCCCTCCCATACCACT	1500
Qy	1501	AAACAAAATCTAATCTGTAAATTCCTTGAACATGTCAGACATATTAATTCCTTCTGCT	1560
Dp	1501	AAACAAAATCTAATCTGTAAATTCCTTGAACATGTCAGACATATTAATTCCTTCTGCT	1560
Qy	1561	GAGAGCTCTTCTCTGTCCTTAAATCTAGAATGATGTAAAGTTTGAATAAAGTTGACTA	1620
Dp	1561	GAGAGCTCTTCTCTGTCCTTAAATCTAGAATGATGTAAAGTTTGAATAAAGTTGACTA	1620
Qy	1621	TCTTACTTCATGCAAGAAGGAGACATATGAGATTCTATCATATGACATGACAGCAATA	1680
Dp	1621	TCTTACTTCATGCAAGAAGGAGACATATGAGATTCTATCATATGACATGACAGCAATA	1680
Qy	1681	CTAAAGGATATTTGATTATTAAGGTTTACGTTAAATTAATGAATGCAAGACACAGA	1740
Dp	1681	CTAAAGGATATTTGATTATTAAGGTTTACGTTAAATTAATGAATGCAAGACACAGA	1740
Qy	1741	GGGAATGTTTATGGGGCAGTTTGTAACTCGGAGTGTGAAGCAAGGACAGGAACTCA	1800
Dp	1741	GGGAATGTTTATGGGGCAGTTTGTAACTCGGAGTGTGAAGCAAGGACAGGAACTCA	1800
Qy	1801	TAGTATCTTAATATATATATATCTTCAATTCCTATCTCTATCAATATCCAAAGACTTTT	1860
Dp	1801	TAGTATCTTAATATATATATATCTTCAATTCCTATCTCTATCAATATCCAAAGACTTTT	1860
Qy	1861	CACGAAATTCAGTGCAGTCAATATCCCAAGGTAACTTTTCATTTCAATGATGATGAC	1920
Dp	1861	CACGAAATTCAGTGCAGTCAATATCCCAAGGTAACTTTTCATTTCAATGATGATGAC	1920
Qy	1921	GCTTATGAAATTTTGGCAATATATATCTGTCACCTATATCTCAACTTTGAGATGTTTTC	1980
Dp	1921	GCTTATGAAATTTTGGCAATATATATCTGTCACCTATATCTCAACTTTGAGATGTTTTC	1980
Qy	1981	TTGTATGTTAAATGAAAGAAATAGGGACCTTGTGAGGACCACTTTAGGGTTCACCTCGGC	2040
Dp	1981	TTGTATGTTAAATGAAAGAAATAGGGACCTTGTGAGGACCACTTTAGGGTTCACCTCGGC	2040
Qy	2041	AATTAAGAAATTTACAAGAGCTACTGACGACCAATTTGTTAAGACCTGTGTGTGTGTGT	2100
Dp	2041	AATTAAGAAATTTACAAGAGCTACTGACGACCAATTTGTTAAGACCTGTGTGTGTGTGT	2100
Qy	2101	GT	2160
Dp	2101	GT	2160
Qy	2161	TTAAACCAAGCATGTTTCAATGGACATATGACCTGCCAATGATGTATCAACCACTAT	2220
Dp	2161	TTAAACCAAGCATGTTTCAATGGACATATGACCTGCCAATGATGTATCAACCACTAT	2220

[illegible]

D	b	1741	GGCAATGTTATG	GGGCGACGTTTGTA	AGCTGGGATGTG	TAAGCAAAAGCGAGGAACCTCA	1800
Q	y	1801	TAGTATCTTAT	ATAATACTTCAT	TTCTATCTCTAT	CACAAATATCCAAACAGCTTTT	1860
D	b	1801	TAGTATCTTAT	ATAATACTTCAT	TTCTATCTCTAT	CACAAATATCCAAACAGCTTTT	1860
Q	y	1861	CACAGATTCAG	CAGTGC	AAATCCCAAAGGTAA	ACTTTATCATATGTAAGTGC	1920
D	b	1861	CACAGATTCAG	CAGTGC	AAATCCCAAAGGTAA	ACTTTATCATATGTAAGTGC	1920
Q	y	1921	GCCTTGAATTT	GGCAATAC	TAGTGCAT	TTATCCAACTTGAATGTGTC	1980
D	b	1921	GCCTTGAATTT	GGCAATAC	TAGTGCAT	TTATCCAACTTGAATGTGTC	1980
Q	y	1981	TTGAGTAAAT	GAAAGAAAT	ATAGGGCACT	TTTATAGGTTACCTCCG	2040
D	b	1981	TTGAGTAAAT	GAAAGAAAT	ATAGGGCACT	TTTATAGGTTACCTCCG	2040
Q	y	2041	AAATAAGAAAT	TTTCAAAAG	ACTCTAGACCA	AGTTGTAAAGACTCTGTGTGTGT	2100
D	b	2041	AAATAAGAAAT	TTTCAAAAG	ACTCTAGACCA	AGTTGTAAAGACTCTGTGTGTGT	2100
Q	y	2101	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGTGTGTGTGTGTGT	2160
D	b	2101	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGTGTGTGTGTGTGT	2160
Q	y	2161	TTAAACAC	ATGTTTCAAA	ATGAGCTAT	AGCTGCAATGATATCACACATAT	2220
D	b	2161	TTAAACAC	ATGTTTCAAA	ATGAGCTAT	AGCTGCAATGATATCACACATAT	2220
Q	y	2221	CTCATTAAT	TTTCCAGTA	ATATGTAT	GTATCTGTAAATATTTTAAAGGTTTGAC	2280
D	b	2221	CTCATTAAT	TTTCCAGTA	ATATGTAT	GTATCTGTAAATATTTTAAAGGTTTGAC	2280
Q	y	2281	TTTCAACAA	AGACCTGGA	ATATGTAT	GTATCTGTAAATATTTTAAAGGTTTGAC	2340
D	b	2281	TTTCAACAA	AGACCTGGA	ATATGTAT	GTATCTGTAAATATTTTAAAGGTTTGAC	2340
Q	y	2341	GCTACAC	ATGCTTGA	CATATAT	TTTGTAAACACCTGCAATTTGTGGTCTCTTAAAG	2400
D	b	2341	GCTACAC	ATGCTTGA	CATATAT	TTTGTAAACACCTGCAATTTGTGGTCTCTTAAAG	2400
Q	y	2401	AAATAC	TTTGCAT	TAAAGT	CTCAGCTGAGGCTGTGCATCAGGCGTTTGAGAATATTTCAA	2460
D	b	2401	AAATAC	TTTGCAT	TAAAGT	CTCAGCTGAGGCTGTGCATCAGGCGTTTGAGAATATTTCAA	2460
Q	y	2461	TTTCTCAG	CAGACCGA	ATTTGAAT	TTTCCCTCATCTTTTATAGAAATCATTTTACAGGTTTG	2520
D	b	2461	TTTCTCAG	CAGACCGA	ATTTGAAT	TTTCCCTCATCTTTTATAGAAATCATTTTACAGGTTTG	2520
Q	y	2521	GAGAGAT	TCAGAC	CTCAGGCT	TTTCTCATATATGTCTGAAATCTTGTGCCCTCTTGT	2580
D	b	2521	GAGAGAT	TCAGAC	CTCAGGCT	TTTCTCATATATGTCTGAAATCTTGTGCCCTCTTGT	2580
Q	y	2581	TGTTTCA	TGATTC	CAATTAAT	TATTTATCTTTTGAACATGATCTATAGAGAGATA	2640
D	b	2581	TGTTTCA	TGATTC	CAATTAAT	TATTTATCTTTTGAACATGATCTATAGAGAGATA	2640
Q	y	2641	TAAAGAT	CTGAT	GTATTA	CAACATTTAGAGATTTTAAAGTTTAACTCACA	2700
D	b	2641	TAAAGAT	CTGAT	GTATTA	CAACATTTAGAGATTTTAAAGTTTAACTCACA	2700
Q	y	2701	CTGCTCA	AAAAAGAA	CCAAAT	CAAGAACTGTGAGCTGATCCCTCACTCTGTGA	2760
D	b	2701	CTGCTCA	AAAAAGAA	CCAAAT	CAAGAACTGTGAGCTGATCCCTCACTCTGTGA	2760
Q	y	2761	GCACAA	CAACCA	AGCAGCA	CCCAAGCATGTCTGAGATCTTAAATCAAGAAACAGGTG	2820
D	b	2761	GCACAA	CAACCA	AGCAGCA	CCCAAGCATGTCTGAGATCTTAAATCAAGAAACAGGTG	2820
Q	y	2821	TCATG	AGTTGA	ATTTCT	TATATGATGTCTGAGCTGTGCGCATCTCTGCTCTCTT	2880
D	b	2821	TCATG	AGTTGA	ATTTCT	TATATGATGTCTGAGCTGTGCGCATCTCTGCTCTCTT	2880

[illegible]

RESULT 3

```

US-09-822-827-690
: Sequence 690, Application US/09822827
: Patent No. US20020081680A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.534C1
: CURRENT APPLICATION NUMBER: US/09/822.827
: CURRENT FILING DATE: 2001-03-28
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 690
: LENGTH: 3923
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-822-827-690

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Query Match	84.8%;	Score 3036;	DB 9;	Length 3923;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3036;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1	ACACAAGAAATAGCAAGTCCGACAAAGTGGCATCAGAAAAACAGAGGGAGATTTCGT	60
Db	1	ACAGAAGAAATAGCAAGTCCGACAAAGTGGCATCAGAAAAACAGAGGGAGATTTCGT	60
OY	61	GGCTGCAGCCGAGGAGACACAGGAAGATCTGCATGGTGGGAAGACCCTGATGATACAGAG	120
Db	61	GGCTGCAGCCGAGGAGACACAGGAAGATCTGCATGGTGGGAAGACCCTGATGATACAGAG	120
OY	121	GAATTACACACATATCTACTTATGTGTTCATATGAACACCAAAATTAATTAAGTGAAGAGCTA	180
Db	121	GAATTACACACATATCTACTTATGTGTTCATATGAACACCAAAATTAATTAAGTGAAGAGCTA	180
OY	181	GTCCGCTGTGATGTCTCCTCACTGACACACAGGGCTGGATCACCATGCAGCGCACTTCTGAG	240
Db	181	GTCCGCTGTGATGTCTCCTCACTGACACACAGGGCTGGATCACCATGCAGCGCACTTCTGAG	240
OY	241	TACTCAGTGCACGCAAGAAAGACTACAGACATCTTCATATGGCAGGGGTGAGAAATPAGAAA	300
Db	241	TACTCAGTGCACGCAAGAAAGACTACAGACATCTTCATATGGCAGGGGTGAGAAATPAGAAA	300
OY	301	GGCTGCTGACTTATCCATCTGAGGCCACACATCTGCTGAATGGAGATTAATTAACATCAC	360
Db	301	GGCTGCTGACTTATCCATCTGAGGCCACACATCTGCTGAATGGAGATTAATTAACATCAC	360
OY	361	TAGAAACAGCAAGATGACAAATATATGTCTTAAGTAGTGCATGTTTTTGCACATTTCCAG	420
Db	361	TAGAAACAGCAAGATGACAAATATATGTCTTAAGTAGTGCATGTTTTTGCACATTTCCAG	420
OY	421	CCCCCTTTAAATATCACACACACAGGAAGCAAAAGAACACACAGAGATCCCGGGGAGA	480
Db	421	CCCCCTTTAAATATCACACACACAGGAAGCAAAAGAACACACAGAGATCCCGGGGAGA	480
OY	481	AATGCCCGCGCCGACATCTTTGGGTATCATGATGAGCCTCGCCCTGTGCTCGCGCTTGT	540
Db	481	AATGCCCGCGCCGACATCTTTGGGTATCATGATGAGCCTCGCCCTGTGCTCGCGCTTGT	540

QY	541	GAGGAGAGACATTAGAAAAATGATGTGTCCTTAAAGATGGGACAGAAAACAGA	600
Dd	541	GAGGAAAGACATTAGAAAAATGATGTGTCCTTAAAGATGGGACAGAAAACAGA	600
QY	601	TCCTGTTCGATATTTATTTGAAACGGGATTACAGATTTGAAATGAAGTCCAAAGTGAG	660
Dd	601	TCCTGTTCGATATTTATTTGAAACGGGATTACAGATTTGAAATGAAGTCCAAAGTGAG	660
QY	661	CATTACCAATGAGAGAAAACAGACGAGAAAATCTGATGGCTTCACAGACATGCAACA	720
Dd	661	CATTACCAATGAGAGAAAACAGACGAGAAAATCTGATGGCTTCACAGACATGCAACA	720
QY	721	AACAAATGGATATCTGTGATGACATGACGACCAAGCTGGGAGAGATAACACGGG	780
Dd	721	AACAAATGGATATCTGTGATGACATGACGACCAAGCTGGGAGAGATAACACGGG	780
QY	781	GCAGAGGGTCAGGATTCGGCCCGTGGCCAAACTGGCTGATATACCAAAATCATTTTC	840
Dd	781	GCAGAGGGTCAGGATTCGGCCCGTGGCCAAACTGGCTGATATACCAAAATCATTTTC	840
QY	841	ATATTTCAACCCCTCAAAACAAACGCTGTGTGAATATGATCTCTACGGTTCCTTCGGG	900
Dd	841	ATATTTCAACCCCTCAAAACAAACGCTGTGTGAATATGATCTCTACGGTTCCTTCGGG	900
QY	901	CCCAACATCTCCATATATCCAGCCACATCTATTTTAATATTTAGTTCCACAGATCTGTA	960
Dd	901	CCCAACATCTCCATATATCCAGCCACATCTATTTTAATATTTAGTTCCACAGATCTGTA	960
QY	961	CTGGACCCCTTCTACACGTAGAAATACATTTGCTTTCGAAAGACCCTTCGGTGT	1020
Dd	961	CTGGACCCCTTCTACACGTAGAAATACATTTGCTTTCGAAAGACCCTTCGGTGT	1020
QY	1021	GCCTGCTAATATGATGCTGACTGTGTTCCTAAGAGATGGTCTCGCCAGGAGATCTGTG	1080
Dd	1021	GCCTGCTAATATGATGCTGACTGTGTTCCTAAGAGATGGTCTCGCCAGGAGATCTGTG	1080
QY	1081	AACAGGCTGGAGACATCTCAAGATCTTTCAGGGTATACTTCTACACACAGCATGA	1140
Dd	1081	AACAGGCTGGAGACATCTCAAGATCTTTCAGGGTATACTTCTACACACAGCATGA	1140
QY	1141	TCATTAGGAGATGAATATCTAATACACATCATCTCAAGTCTTTCGGCCCTACTCGAAT	1200
Dd	1141	TCATTAGGAGATGAATATCTAATACACATCATCTCAAGTCTTTCGGCCCTACTCGAAT	1200
QY	1201	TCATTTCCCATTTTGTGCCCCATCTCAAGACCTCAAAATGTCATTCATTAATATACAA	1260
Dd	1201	TCATTTCCCATTTTGTGCCCCATCTCAAGACCTCAAAATGTCATTCATTAATATACAA	1260
QY	1261	GGATTTACCTTTTTTTTTAACCTGGAGAAATTCATGTTACATCAGCTATGGAAATTTA	1320
Dd	1261	GGATTTACCTTTTTTTTTAACCTGGAGAAATTCATGTTACATCAGCTATGGAAATTTA	1320
QY	1321	ATTACATATTTTGTTCOCATGCAAGAGATACATAGTCTTATTCCTCCCTTGTGTT	1380
Dd	1321	ATTACATATTTTGTTCOCATGCAAGAGATACATAGTCTTATTCCTCCCTTGTGTT	1380
QY	1381	GATTTTTTTTCAGATATTAAGTATTAAGTCTTACGCTTGTAAGGCTGTATACAGAC	1440
Dd	1381	GATTTTTTTTCAGATATTAAGTATTAAGTCTTACGCTTGTAAGGCTGTATACAGAC	1440
QY	1441	AGCCTCTCCCATCCCTCCAGCCTTATCTGTGATCACCATCAACCCCTCCCATACACT	1500
Dd	1441	AGCCTCTCCCATCCCTCCAGCCTTATCTGTGATCACCATCAACCCCTCCCATACACT	1500
QY	1501	AAACAAAATCTAATCTGTATTTCTTGAACATGTGCAGACATACATTAATTCCTTCGCT	1560
Dd	1501	AAACAAAATCTAATCTGTATTTCTTGAACATGTGCAGACATACATTAATTCCTTCGCT	1560
QY	1561	GAGAGGCTCTCTGCTGCTTAAATCAGAAATGATGAAAGTTTGAATAGTGTGACTA	1620
Dd	1561	GAGAGGCTCTCTGCTGCTTAAATCAGAAATGATGAAAGTTTGAATAGTGTGACTA	1620
QY	1621	TCTTACTTCATGACAAAGAGGACACATATAGATTATCATCTCATGACATGACACAAATA	1680

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Db 1621 TCTTACCTTCATGCAAGAAGGACACATATGAGATTTCATCATCATGAGACAGCAATA 1680
Oy 1681 CTAAGAAGTATTTGATTTATAGAGTTTATGATAATATATGAATGCAAGACACAGA 1740
Db 1681 CTAAGAAGTATTTGATTTATAGAGTTTATGATAATATATGAATGCAAGACACAGA 1740
Oy 1741 GGGAAATGTTATGSGGACGTTTGTAAAGCTGGAGTGTGAACCAAGGAGGAACTCA 1800
Db 1741 GGGAAATGTTATGSGGACGTTTGTAAAGCTGGAGTGTGAACCAAGGAGGAACTCA 1800
Oy 1801 TAGTATCTTAT 1860
Db 1801 TAGTATCTTAT 1860
Oy 1861 CACAGAATTCATGACGTCGAATCCCAAGGTAACCTTTATCCATTTTCATGAGTGC 1920
Db 1861 CACAGAATTCATGACGTCGAATCCCAAGGTAACCTTTATCCATTTTCATGAGTGC 1920
Oy 1921 GCTTTAGAAATTTGGCAAAATCATCTGCTCACTATATCTCAACTTTGAGATGTGTTC 1980
Db 1921 GCTTTAGAAATTTGGCAAAATCATCTGCTCACTATATCTCAACTTTGAGATGTGTTC 1980
Oy 1981 TTGTAGTAAATTTGAAGAATAGGGCACTCTGTGAGCACTTTAGGGTTCACTCTGGC 2040
Db 1981 TTGTAGTAAATTTGAAGAATAGGGCACTCTGTGAGCACTTTAGGGTTCACTCTGGC 2040
Oy 2041 AATAAGAAATTTACAAAGAGCTACACAGACAGTGTGTAAGAGCTGTGTGTGTGT 2100
Db 2041 AATAAGAAATTTACAAAGAGCTACACAGACAGTGTGTAAGAGCTGTGTGTGTGT 2100
Oy 2101 GT 2160
Db 2101 GT 2160
Oy 2161 TTAATAACAAGCATGTTTCAATGGCACTATGAGTGTGCAATGATGATGATGATGAT 2220
Db 2161 TTAATAACAAGCATGTTTCAATGGCACTATGAGTGTGCAATGATGATGATGATGAT 2220
Oy 2221 CTCATTTATCTCCAGTAATGTGATTAATGTGATCTGTGTGTGTGTGTGTGTGTGT 2280
Db 2221 CTCATTTATCTCCAGTAATGTGATTAATGTGATCTGTGTGTGTGTGTGTGTGTGT 2280
Oy 2281 TTCAAAAAGAGCGTGGAAATGAGCAACCAATATGATTAATCTTACCTCTACATCA 2340
Db 2281 TTCAAAAAGAGCGTGGAAATGAGCAACCAATATGATTAATCTTACCTCTACATCA 2340
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Db 2341 GCTACACACTGCTTGACATATATTTGTGTGAAGACACTGCAATTTGTGGTCTCTTAAGC 2400
Oy 2401 AAAATTTCTTGCAATTAAGTCTGAGCTGGGCTGTGCATCAGGCGGTTTGAGAAATTTCA 2460
Db 2401 AAAATTTCTTGCAATTAAGTCTGAGCTGGGCTGTGCATCAGGCGGTTTGAGAAATTTCA 2460
Oy 2461 TTCTCAGAGAGGACAGAAATTTGAATTCCTTCATCTTTTGAAGAAATTTGCAAGGTTTG 2520
Db 2461 TTCTCAGAGAGGACAGAAATTTGAATTCCTTCATCTTTTGAAGAAATTTGCAAGGTTTG 2520
Oy 2521 GAGAGAGTTTACAGAGCTGAGTCTTCACTAATGTCTGGAAGTTCTGTCCCTCTTTG 2580
Db 2521 GAGAGAGTTTACAGAGCTGAGTCTTCACTAATGTCTGGAAGTTCTGTCCCTCTTTG 2580
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Db 2581 TGTTCATGATAGTCCAAATAATATGTTATCTTTGAAGTATGCTCTCAATAGAGATA 2640
Oy 2641 TAAGAACTGAGAGATATCAACATTTAGAGATTTCAAGAAATTTAATTTAAGTCTACA 2700
Db 2641 TAAGAACTGAGAGATATCAACATTTAGAGATTTCAAGAAATTTAATTTAAGTCTACA 2700
Oy 2701 CTGCTCAAAAGAAACCAAGATACAAAGAACTGAGTGTCTGCTCTCTGTA 2760
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Db 2701 CTGCTCAAAAGAAACCAAGATACAAAGAACTGAGTGTCTGCTCTCTGTA 2760
Oy 2761 GCCACACCAACAGCAGAGGACCCAGCATGTCTGAGATCTTAAATCAAGAAACAGTG 2820
Db 2761 GCCACACCAACAGCAGAGGACCCAGCATGTCTGAGATCTTAAATCAAGAAACAGTG 2820
Oy 2821 TCATGAGTTGAATTCCTTATTTATGATGATGATGATGATGATGATGATGATGATGAT 2880
Db 2821 TCATGAGTTGAATTCCTTATTTATGATGATGATGATGATGATGATGATGATGATGAT 2880
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Db 2881 GACACATATATAGCTTCTAGCTTCTGCTTCCAGACATTTATCTTTTCCAAACATGCG 2940
Oy 2941 TTACCAATCT 3000
Db 2941 TTACCAATCT 3000
Oy 3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036
Db 3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036

RESULT 4
US-09-895-793-690
; Sequence 690, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 690
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-690
Query Match 84.8%; Score 3036; DB 10; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ACAGAGAAATATGCAAGTCCCGAGAGACTGGCATCAGAAAAACAGAGGAGATTGTGT 60
Oy 61 GCGTCGACGCGAGGACAGCAAGATGCAATGATGGGAGAGAGCTGATGATACAGAG 120
|||||

Db 61 GGCCTGAGCCGAGGAGACAGGAAAGTCTGCATGGTGGGAAGGACCTGATGATACAG 120
OY 121 GAATTACACATATATCTAGTGTTCATGACACCAAGATAATTAAGTGAAGCTA 180
Db 121 GAATTACACATATATCTAGTGTTCATGACACCAAGATAATTAAGTGAAGCTA 180
OY 181 GTCCGCTGTGAGTCTCCCTCAGTACAGAGGGCTGATGATCAGATCGAGGCACTTCTGAG 240
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OY 301 GGCTGTGACTTACCATCTGAGGCGCACATCTGCTGAATGAGATATTAACATCAC 360
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OY 361 TGAAGAACAGAGATGACATATATATGTCTAAGTACATGATGTTTTCACATTTCCAG 420
Db 361 TGAAGAACAGAGATGACATATATATGTCTAAGTACATGATGTTTTCACATTTCCAG 420
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Db 541 GAGGGAAGGACATTGAGAAATGATGATGTCTTCTTAAGAGTGGGAGAGAAACAG 600
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Db 601 TCTCTGTGTGATATTTATTTGACGGGATTACAGATTTGAAATGATGATGAG 660
OY 661 CATTTACCAATGAGAGAAACAGAGAGAAATCTGATGGCTTCAAGACATGTAACA 720
Db 661 CATTTACCAATGAGAGAAACAGAGAGAAATCTGATGGCTTCAAGACATGTAACA 720
OY 721 AACAAATGGAATACTGTGATGACATGAGGACGCAAGCTGGGAGAGATTAACAGGG 780
Db 721 AACAAATGGAATACTGTGATGACATGAGGACGCAAGCTGGGAGAGATTAACAGGG 780
OY 781 GCAGAGGTCAGGATCTGGCCCTGCTCTTAACTGTGCTTCAATACCAAAATCTTTC 840
Db 781 GCAGAGGTCAGGATCTGGCCCTGCTCTTAACTGTGCTTCAATACCAAAATCTTTC 840
OY 841 ATATTTCTAACCCCTCAAAACAAAGCTGTGTAATATCTGATCTACGCTTCCCTGGG 900
Db 841 ATATTTCTAACCCCTCAAAACAAAGCTGTGTAATATCTGATCTACGCTTCCCTGGG 900
OY 901 CCCAATCTCTCATATATCCAGCCACACTCATTTTAAATTTAGTTCCAGATCTGA 960
Db 901 CCCAATCTCTCATATATCCAGCCACACTCATTTTAAATTTAGTTCCAGATCTGA 960
OY 961 CTGTGACCTTTTCTACACTGATAGATTAATCTCAATTTTGTTCAAAGACCTTCTGTT 1020
Db 961 CTGTGACCTTTTCTACACTGATAGATTAATCTCAATTTTGTTCAAAGACCTTCTGTT 1020
OY 1021 GGTGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 GGTGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
OY 1081 AACAGGCTGGAGAGATCTCAAGATCTTCCAGGGTATATCTTACTAGACACAGCATGA 1140
Db 1081 AACAGGCTGGAGAGATCTCAAGATCTTCCAGGGTATATCTTACTAGACACAGCATGA 1140
OY 1141 TCATTTACGAGATGATATTAATCAACATCATCTCAGTGTCTTGGCCCATACTGAAT 1200
Db 1141 TCATTTACGAGATGATATTAATCAACATCATCTCAGTGTCTTGGCCCATACTGAAT 1200

OY 1201 TCATTTCCACATTTTGTGCCATCTCAAGACCTCAAAATGTCATTCATTAATATAC 1260
Db 1201 TCATTTCCACATTTTGTGCCATCTCAAGACCTCAAAATGTCATTCATTAATATAC 1260
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Db 1321 ATTACATATTTTGTTCAGTGCAGAAAGATGACTAAGTCTTATCTCTCCCTTGT 1380
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Db 1381 GATTTTTTCCAGTAAAGTAAATGTTTACCTTGTACGAGGCTGATACAGCAC 1440
OY 1441 AGCCTCTCCCATCCCTCCAGCCTTATCTGTATCATCAACCCCTCCATACCACT 1500
Db 1441 AGCCTCTCCCATCCCTCCAGCCTTATCTGTATCATCAACCCCTCCATACCACT 1500
OY 1501 AAACAAATCTAATCTGTAATCTTGAACATGTGAGACATACATTAATCTTCTGCT 1560
Db 1501 AAACAAATCTAATCTGTAATCTTGAACATGTGAGACATACATTAATCTTCTGCT 1560
OY 1561 GAGAACCTCTCTCTCTTAAATCTGAAATGATGAAAGTTTGAATTAAGTACAT 1620
Db 1561 GAGAACCTCTCTCTCTTAAATCTGAAATGATGAAAGTTTGAATTAAGTACAT 1620
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Db 1621 TCTTACTTATGCAAGAGGACACATATGAGATTCATCATGACAGCAAAAT 1680
OY 1681 CTAAAGTGTAAATTTATTAAGATTTAAGATTTAATATATGAAATGCAAGACACAG 1740
Db 1681 CTAAAGTGTAAATTTATTAAGATTTAAGATTTAATATATGAAATGCAAGACACAG 1740
OY 1741 GGGATGTTTATGGGACAGTGTGAAGCTGGAGTGAAGCAAGGAGGAGACCTCA 1800
Db 1741 GGGATGTTTATGGGACAGTGTGAAGCTGGAGTGAAGCAAGGAGGAGACCTCA 1800
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OY 1861 CACAGATTCATGACGATGCAATCCCAAGGTAACCTTTATTCATTTATGCTGATGC 1920
Db 1861 CACAGATTCATGACGATGCAATCCCAAGGTAACCTTTATTCATTTATGCTGATGC 1920
OY 1921 GCTTGAATTTTGGCAATCATGCTGATCTATCTCAACTTTGATGATGTTGTGC 1980
Db 1921 GCTTGAATTTTGGCAATCATGCTGATCTATCTCAACTTTGATGATGTTGTGC 1980
OY 1981 TTGTAGTTAATGAAAGAAATAGGCACTCTTGTGAGCACTTTAGGTTCACTCTGGC 2040
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Db 2041 AATAAGATTTTCAAGAGCTTCTGAGACGAGTTTGAAGGCTGTGTGTGTGTGTGT 2100
OY 2101 GTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2160
Db 2101 GTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2160
OY 2161 TTAAGAACAGCATGTTTCAATAGGACATGAGCTGCCAATGATGATACACCATAT 2220
Db 2161 TTAAGAACAGCATGTTTCAATAGGACATGAGCTGCCAATGATGATACACCATAT 2220
OY 2221 CTCATATCTCTCCAGTAAATGATATATGATGATGATGATGATGATGATGATGATG 2280
Db 2221 CTCATATCTCTCCAGTAAATGATATATGATGATGATGATGATGATGATGATGATG 2280

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Db 2281 TTCACAAAAGCAGTGGAAATGAGACACACAAATATGCAATTAATCTAACCTCCFACCAATCA 2340
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Db 2341 GCTACACAGCTGTTGACATATATGTTAGAGACACCTGCGANTTGTGGTCTCTTAAGC 2400
QY 2401 AAAATACTTGGATTAGTCTCAGCTGGGGCTGTGCATCAGCGGCTTTAGAGAAATATCA 2460
Db 2401 AAAATACTTGGATTAGTCTCAGCTGGGGCTGTGCATCAGCGGCTTTAGAGAAATATCA 2460
QY 2461 TTTCACAGCAGAGCCAGAAATTTGAATTCCTTCATCTTTTAGAAATCATTTACCGAGTTG 2520
Db 2461 TTTCACAGCAGAGCCAGAAATTTGAATTCCTTCATCTTTTAGAAATCATTTACCGAGTTG 2520
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Db 2521 GAGAGGATTCAGACAGCTCAGGTGCTTCAATATGCTCGAATTCCTGACCTGCTTGG 2580
QY 2581 TGTTCATGATAGTCCAAATTAATATGTTATCTTTGAACATGATGCTCATAGAGAGATA 2640
Db 2581 TGTTCATGATAGTCCAAATTAATATGTTATCTTTGAACATGATGCTCATAGAGAGATA 2640
QY 2641 TAAAGACTCTGAGTATATCAACATTTAGGATTTCAAGAAATATTTAGATTTAGCTACA 2700
Db 2641 TAAAGACTCTGAGTATATCAACATTTAGGATTTCAAGAAATATTTAGATTTAGCTACA 2700
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Db 2761 GCCACAAACCAAGAGAGACCCAAAGCATGCTGAGATCTTAAATCAAGAAACCAAGT 2820
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QY 2881 GACACATATATGACTTACGCTTGTGCTCCAGCATTTTATCTTTTCCAAACATCGC 2940
Db 2881 GACACATATATGACTTACGCTTGTGCTCCAGCATTTTATCTTTTCCAAACATCGC 2940
QY 2941 TTACCAATCCCTCTCTGCTGTGTTGCTTTGGACTTCCCAAGAAATTTCAAGACTCT 3000
Db 2941 TTACCAATCCCTCTCTGCTGTGTTGCTTTGGACTTCCCAAGAAATTTCAAGACTCT 3000
QY 3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036
Db 3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036

RESULT 5

US-09-895-814-690
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895.814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 690
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-690
Query Match 84.8%; Score 3036; DB 10; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGAGAAATAGCAAGTCCGAGAGCTGCATCAGAAAAACAGAGGGAGATTGTGT 60
Db 1 ACAGAGAAATAGCAAGTCCGAGAGCTGCATCAGAAAAACAGAGGGAGATTGTGT 60
QY 61 GCGTCAGCCGAGGAGACCGAAGATCTGATGCGGAGAGACCTGATGATACAGAG 120
Db 61 GCGTCAGCCGAGGAGACCGAAGATCTGATGCGGAGAGACCTGATGATACAGAG 120
QY 121 GAATTACACACATATCTTATGTTTCAATGAACACCAAGATAAATAGTAAGACTA 180
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QY 181 GTCCGTGTGAGTCTCTCAATGACACAGAGCTGATCAGCATGAGGCACTTCTGAG 240
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QY 421 CCCCTTAAATATCACACACACAGAAAGCAAAAGAGACAGAGATCCCTGGGAGA 480
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QY 541 GAGGGAAGGACATTAGAAATGAATGATGTCTTAAAGATGGGCGAGAAACAGA 600
Db 541 GAGGGAAGGACATTAGAAATGAATGATGTCTTAAAGATGGGCGAGAAACAGA 600
QY 601 TCCGTGTGGATTTATTTGAAGGAGATTTAGATTTGAATGAAGTACAAAGTGAG 660
Db 601 TCCGTGTGGATTTATTTGAAGGAGATTTAGATTTGAATGAAGTACAAAGTGAG 660
QY 661 CATTAACATGAGAGAAACAGACGAAATCTTGATGCTTCAACAGATGCAACA 720
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QY 721 AACAAATGGAATCTGTGATGACATGAGCGACCAAGCTGGGAGAGATTAACACGGG 780

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Db 721 AACAAATGGAATGATGATGACATGAGGACGCCAAGCTGGGAGAGATACCAACGCG 780
OY 781 GGAGAGGGGACAGATTCGCGCCCTGCTCTAAACGTGGCGTTCCATACCAATCATTTTC 840
Db 781 GGAGAGGGGACAGATTCGCGCCCTGCTCTAAACGTGGCGTTCCATACCAATCATTTTC 840
OY 841 ATATTTCTAACCCCTCAAAACAAAGCTGTGTATATCTGATCTCTAGGCTTCCTGCG 900
Db 841 ATATTTCTAACCCCTCAAAACAAAGCTGTGTATATCTGATCTCTAGGCTTCCTGCG 900
OY 901 CCCAATTCCTCCATATATCCAGCCACACTATTTTAAATATTAGTCCAGATCTGTA 960
Db 901 CCCAATTCCTCCATATATCCAGCCACACTATTTTAAATATTAGTCCAGATCTGTA 960
OY 961 CTGTGACCTTTCTACACGTGATGATTAATCTACTCTATTTGTTCAAAGACCCCTGCT 1020
Db 961 CTGTGACCTTTCTACACGTGATGATTAATCTACTCTATTTGTTCAAAGACCCCTGCT 1020
OY 1021 GCTGCCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 GCTGCCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
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Db 1081 AACAGGCTGGAGACATCTCAAGATCTTCCAGGGTTATCTTACTAGACACAGCATGA 1140
OY 1141 TCATTAACGAGATGATTAATCTATATCAATCATCTCTAGTGTCTTGGCCATATCTAAT 1200
Db 1141 TCATTAACGAGATGATTAATCTATATCAATCATCTCTAGTGTCTTGGCCATATCTAAT 1200
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OY 1261 GGATTAACCTTTTAACTGGAAGATTCATGTATCATATGACATGAGGAATTTA 1320
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OY 1621 TCTTACTTCATGCAAGAGGACACATATGAGATTCATCATCATGAGACGCAATA 1680
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OY 1681 CTAAAGTGTATTTGATATATAGAGTTAGATTAATATATGAATGCAAGGCGCACA 1740
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OY 1741 GGGAAATGTTATGAGGACGTTTGTAAAGCTGGAGTGTAGACCAAGGAGGAACTCA 1800
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Db 1801 TAGTATCTTATATATATATCTTCTATCTCTATCATCAATATCCAAAGCTTTT 1860

Db 1801 TAGTATCTTATATATATATCTTCTATCTCTATCATCAATATCCAAAGCTTTT 1860
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OY 1981 TTGTAGTATATGAAAGAAATAGGACATCTTGTAGCCACTTTAGGTTCACTCCTGCG 2040
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Db 2041 AATTAAGATTTTACAAAGAGCTCTAGAGCCAGTTTAAAGGCTCTGTGTGTGTGT 2100
OY 2101 GT 2160
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OY 2161 TTTAAACAAAGCATGTTTCAATGACATATGACATGACATGATGATGATGATGATG 2220
Db 2161 TTTAAACAAAGCATGTTTCAATGACATATGACATGACATGATGATGATGATGATG 2220
OY 2221 CTCTATTTCTCCAGTAATGATATATATGATGATGATGATGATGATGATGATGAT 2280
Db 2221 CTCTATTTCTCCAGTAATGATATATATGATGATGATGATGATGATGATGATGAT 2280
OY 2281 TTCACAAAGAGCATGTAATGGAATGACACACATATGATGATGATGATGATGATGAT 2340
Db 2281 TTCACAAAGAGCATGTAATGGAATGACACACATATGATGATGATGATGATGATGAT 2340
OY 2341 GCTACACACTGCTTGACATATATGTTAGAGACACTCGCATTTGTGGGTTCTTTAAG 2400
Db 2341 GCTACACACTGCTTGACATATATGTTAGAGACACTCGCATTTGTGGGTTCTTTAAG 2400
OY 2401 AAAATCTGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460
Db 2401 AAAATCTGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460
OY 2461 TTCTCAGCAGAGCCGAAATTTGAATTTCCCTCATCTTTTAAAGATCATTTTACCAG 2520
Db 2461 TTCTCAGCAGAGCCGAAATTTGAATTTCCCTCATCTTTTAAAGATCATTTTACCAG 2520
OY 2521 GAGAGATTCAGACAGCTAGGTTGCTTCAATATGCTCTGACATTTGCTCCCTTTTG 2580
Db 2521 GAGAGATTCAGACAGCTAGGTTGCTTCAATATGCTCTGACATTTGCTCCCTTTTG 2580
OY 2581 TGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2640
Db 2581 TGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2640
OY 2641 TAAGAACTGTGATGATATCAACATTTAGGATTCAAAGAAATTTAGATTTAAGCTCA 2700
Db 2641 TAAGAACTGTGATGATATCAACATTTAGGATTCAAAGAAATTTAGATTTAAGCTCA 2700
OY 2701 CTGTGTAAGAGGAAACCAAGATATCAAGAACTGTGACATGCTGCCATCTCTGTGA 2760
Db 2701 CTGTGTAAGAGGAAACCAAGATATCAAGAACTGTGACATGCTGCCATCTCTGTGA 2760
OY 2761 GGCACAAACCAAGCAGGAGCCCAAGCATGTCTGAGATCTTAAATCAAGGAAACAGTG 2820
Db 2761 GGCACAAACCAAGCAGGAGCCCAAGCATGTCTGAGATCTTAAATCAAGGAAACAGTG 2820
OY 2821 TCATGAGTTGAATTCCTATATATGATGATGATGATGATGATGATGATGATGATG 2880
Db 2821 TCATGAGTTGAATTCCTATATATGATGATGATGATGATGATGATGATGATGATG 2880
OY 2881 GACACATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940
Db 2881 GACACATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940


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FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012.896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 690
LENGTH: 3923
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-690

Query Match      84.8%; Score 3036; DB 13; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGAGAAATAGCAAGTGCAGAGAGCTGGCATCAGAAAAACAGAGGGAGATTGTGT 60
DB 1 ACAGAGAAATAGCAAGTGCAGAGAGCTGGCATCAGAAAAACAGAGGGAGATTGTGT 60
QY 61 GCGTCGACCCGAGGAGACCCAGGAAGATCTGCATGTTGGGAGAGACCTGATGATACAGAG 120
DB 61 GCGTCGACCCGAGGAGACCCAGGAAGATCTGCATGTTGGGAGAGACCTGATGATACAGAG 120
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DB 121 GAATTACACACATATATCTAGTGTTCATGATGAACACCAATATTAATAGTGAAGAGCTA 180
QY 181 GTCCGCTGTGAGTCTCTCACTGACACAGAGGCTGGATCCATCGACGCGACTTTCTGAG 240
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DB 481 AATGCCCGGCGCCATCTTGGGTATGATGATGAGCTTGGCTTGGCTTGGCTTGGCTTGGCT 540
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DB 541 GAGGGAAGACATAGAAAATGAATGATGTCTTAAAGATGGGCAAGAAAACAGA 600
QY 601 TCCGTTGTGATATTTATTTGAAACGGGATTTACGATTTGAAATGAAGTCACAAAGTGAG 660
DB 601 TCCGTTGTGATATTTATTTGAAACGGGATTTACGATTTGAAATGAAGTCACAAAGTGAG 660
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DB 661 CATTTACCATGAGAGAAAACAGACGAGAAAATCTTGATGGCTTCACAAGCATGCAACA 720
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DB 721 AACAAAATGGAATATCTGTATGACATGAGCAGCAAGCTGGGGAGAGATTAACACAGGG 780
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DB 781 GCGAGAGGTGAGATTTGGCCCTGCTTAAATCTGATGATCTTACGATTTCTTGGG 840
QY 841 ATATTTCTAACCTCAAAACAAAGCTGTGTAATATGATCTTACGATTTCTTGGG 900
DB 841 ATATTTCTAACCTCAAAACAAAGCTGTGTAATATGATCTTACGATTTCTTGGG 900
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QY 1081 AACAGCTGGGAGCATCTCAAGATCTTCCAGGGTATTTACTTACTTACACACAGCATGA 1140
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DB 1321 ATTTACATATTTTGTGTTTCCAGTGCAGAAAGATGACTAAGCTTTATCCCTCCCTTGTGTT 1380
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DB 1381 GATTTTCTTCCAGTATTAATTAATGCTTACCTGTGACTGAGGTGTATACAGCAC 1440
QY 1441 AGCCTCTCCCATCCCTCCAGCCTTATCTGATCAGCATCAACCCCTCCATACAGCCT 1500
DB 1441 AGCCTCTCCCATCCCTCCAGCCTTATCTGATCAGCATCAACCCCTCCATACAGCCT 1500
QY 1501 AAACAAAATCTAATCTGTAATCTTGAACATGTGACAGCATTAATTTCTTGTGCTT 1560
DB 1501 AAACAAAATCTAATCTGTAATCTTGAACATGTGACAGCATTAATTTCTTGTGCTT 1560
QY 1561 GAGAGGCTCTTCTGCTCTCTTAATCTAGAAATGATGAAGTTTGAATTAAGTTGACTA 1620
DB 1561 GAGAGGCTCTTCTGCTCTCTTAATCTAGAAATGATGAAGTTTGAATTAAGTTGACTA 1620
QY 1621 TCTTACTTTCATGCAAGAGGAGACATATGAGATTCATCATGAGACAGACAATA 1680
DB 1621 TCTTACTTTCATGCAAGAGGAGACATATGAGATTCATCATGAGACAGACAATA 1680
QY 1681 CTAAAAGTGTAAATTTGATTAATAGATTTGAATTAATGAATCAAGAGCCACAGA 1740
DB 1681 CTAAAAGTGTAAATTTGATTAATAGATTTGAATTAATGAATCAAGAGCCACAGA 1740
QY 1741 GGGAAATTTATGGGGACGTTTGTAGCCGAGGATGGAAGCAAGGAGGAGACCTCA 1800
DB 1741 GGGAAATTTATGGGGACGTTTGTAGCCGAGGATGGAAGCAAGGAGGAGACCTCA 1800
QY 1801 TAGTATCTTATATATATATCTTCAATTTCTATCTCATGACAAATATCCAAAGCTTTT 1860
DB 1801 TAGTATCTTATATATATATCTTCAATTTCTATCTCATGACAAATATCCAAAGCTTTT 1860
QY 1861 CACAGAATTCATGACATGCAAAATCCCAAGGTAACTTTATCCATTTCAATGAGTGC 1920
DB 1861 CACAGAATTCATGACATGCAAAATCCCAAGGTAACTTTATCCATTTCAATGAGTGC 1920
QY 1921 GCTTTAGAAATTTGGCAAAATCATACGTGCTACATTAATCAACTTTGAGATGTGTTGCTC 1980
DB 1921 GCTTTAGAAATTTGGCAAAATCATACGTGCTACATTAATCAACTTTGAGATGTGTTGCTC 1980
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QY 1981 TTGAGTAAATGAAGAAATAGGGCACTTGTGAGCCACTTTAGGGTTCACTCCTGGC 2040
1981 TTGAGTAAATGAAGAAATAGGGCACTTGTGAGCCACTTTAGGGTTCACTCCTGGC 2040
QY 2041 AATTAAGAAATTTACAAAGAGCTACTGAGACCAAGTTGTTAAGAGCTCTGTGTGTGTGT 2100
2041 AATTAAGAAATTTACAAAGAGCTACTGAGACCAAGTTGTTAAGAGCTCTGTGTGTGTGT 2100
QY 2101 GT 2160
2101 GT 2160
QY 2161 TTTAAACAAGCAATGTTTTCAAAATGACATGAGCTGCCAATGATGTATCACCAACATAT 2220
2161 TTTAAACAAGCAATGTTTTCAAAATGACATGAGCTGCCAATGATGTATCACCAACATAT 2220
QY 2221 CTCATTATTTCTCCAGTAAATGTGATTAATATGTATGTATGTATGTATGTATGTATGTAT 2280
2221 CTCATTATTTCTCCAGTAAATGTGATTAATATGTATGTATGTATGTATGTATGTATGTAT 2280
QY 2281 TTCAACAAAAGCAAGCTGTGAAATGAGACCAACCAATATGCAATTAATCTTACCTACATCA 2340
2281 TTCAACAAAAGCAAGCTGTGAAATGAGACCAACCAATATGCAATTAATCTTACCTACATCA 2340
QY 2341 GCTACACACTGCTTACATATATTTGTAGAACACCTCCATTTTGGGTTCTCTTAAGC 2400
2341 GCTACACACTGCTTACATATATTTGTAGAACACCTCCATTTTGGGTTCTCTTAAGC 2400
QY 2401 AAAATATCTTGATTAAGTGTGAGCTGAGCTGTGATCAGCGGTTTGAATAATATTCAA 2460
2401 AAAATATCTTGATTAAGTGTGAGCTGAGCTGTGATCAGCGGTTTGAATAATATTCAA 2460
QY 2461 TTTCTCAGCAGAAAGCAAGTGTGAAATGCTTCTTGAAGATATTATACAGAGTTTG 2520
2461 TTTCTCAGCAGAAAGCAAGTGTGAAATGCTTCTTGAAGATATTATACAGAGTTTG 2520
QY 2521 GAGAGATTCAGACAGCTGAGCTGCTTACTAATGTCTGTAATCTTGTCCCTTTTG 2580
2521 GAGAGATTCAGACAGCTGAGCTGCTTACTAATGTCTGTAATCTTGTCCCTTTTG 2580
QY 2581 TGTTCATGATAGTCCATTAATTAATGTATCTTTGAACTGATGTATGAGAGAGATA 2640
2581 TGTTCATGATAGTCCATTAATTAATGTATCTTTGAACTGATGTATGAGAGAGATA 2640
QY 2641 TTAAGAACTGTAGTGTATCAACATTAGGATTCAAAGAAATTTAGATTAAAGTCAACA 2700
2641 TTAAGAACTGTAGTGTATCAACATTAGGATTCAAAGAAATTTAGATTAAAGTCAACA 2700
QY 2701 CTGATCAAAAGAACCAAGATATCAAAAGACTGTGAGCTGTCAATCGTCCCATCTGTGA 2760
2701 CTGATCAAAAGAACCAAGATATCAAAAGACTGTGAGCTGTCAATCGTCCCATCTGTGA 2760
QY 2761 GCCACAACCAAGAGAGAGCAAGCATGTCTGAGATCTTTAAATCAAGAAACCAAGT 2820
2761 GCCACAACCAAGAGAGAGCAAGCATGTCTGAGATCTTTAAATCAAGAAACCAAGT 2820
QY 2821 TATATAGTGAATTTCTCTATATATGATGTAGCTTCTGAGCATCTGTGGCTCTCTCTT 2880
2821 TATATAGTGAATTTCTCTATATATGATGTAGCTTCTGAGCATCTGTGGCTCTCTCTT 2880
QY 2881 GACACATATTAAGCTTCTAGCTTTGCTGACAGACTTTATCTTTCTCCACACATATG 2940
2881 GACACATATTAAGCTTCTAGCTTTGCTGACAGACTTTATCTTTCTCCACACATATG 2940
QY 2941 TTACCAATCT 3000
2941 TTACCAATCT 3000
QY 3001 CAAGCTTTTCTTCCATCCCAACCACTAAGTGAAT 3036
3001 CAAGCTTTTCTTCCATCCCAACCACTAAGTGAAT 3036

RESULT 8
US-10-205-823-316
; Sequence 316, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gordacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamakkar, Shubhangt
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205, 823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 316
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-316
Query Match 84.8%; Score 3036; DB 14; Length 3923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGAAAGAAATAGCAAGTCCGAGAGCTGTGCAATCAAGAAACAGAGGGAGATTGTGT 60
1 ACAGAAAGAAATAGCAAGTCCGAGAGCTGTGCAATCAAGAAACAGAGGGAGATTGTGTGT 60
DB 1 ACAGAAAGAAATAGCAAGTCCGAGAGCTGTGCAATCAAGAAACAGAGGGAGATTGTGTGT 60
QY 61 GCGTCAGCGAGGAGGAGACAGAGATCTGCATGGTGGGAGAGACTGTATACAGAG 120
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QY 121 GAATTAACAACATATAGT 180
121 GAATTAACAACATATAGT 180
DB 121 GAATTAACAACATATAGT 180
QY 181 GTCCGCTGTGAGTCTCTCTCAAGTACACAGGCTGTGATCACCATGACGAGCTTTCTGAG 240
181 GTCCGCTGTGAGTCTCTCTCAAGTACACAGGCTGTGATCACCATGACGAGCTTTCTGAG 240
DB 181 GTCCGCTGTGAGTCTCTCTCAAGTACACAGGCTGTGATCACCATGACGAGCTTTCTGAG 240
QY 241 TATCTAGTGTGAGGAGAAAGAAAGTACAGACATCTCAATGAGGAGGAGGAGAAATAGAAA 300
241 TATCTAGTGTGAGGAGAAAGAAAGTACAGACATCTCAATGAGGAGGAGGAGAAATAGAAA 300
DB 241 TATCTAGTGTGAGGAGAAAGAAAGTACAGACATCTCAATGAGGAGGAGGAGAAATAGAAA 300
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301 GCGTCGTGACTTTACCATCTGAGGCGACACATCTGCTGAATGAGATTAATTAACATCAC 360
DB 301 GCGTCGTGACTTTACCATCTGAGGCGACACATCTGCTGAATGAGATTAATTAACATCAC 360
QY 361 TAGAAACAGCAAGATGACAAATATATGTCTAAGTGTGAGTGTGAGTGTGAGTGTGAGT 420
361 TAGAAACAGCAAGATGACAAATATATGTCTAAGTGTGAGTGTGAGTGTGAGTGTGAGT 420
DB 361 TAGAAACAGCAAGATGACAAATATATGTCTAAGTGTGAGTGTGAGTGTGAGTGTGAGT 420

QY	421	CCCCCTTAAATATCCACACACACAGGAAAGCACAAAAGACACACAGATCCCTGGAGAA	480
Db	421	CCCCCTTAAATATCCACACACACAGGAAAGCACAAAAGACACAGATCCCTGGAGAA	480
QY	481	AATGCCGGCCCCCATCTTGGGGTCATTCGATGAGCCCTCGCGTGCCTGCTCCGCTGT	540
Db	481	AATGCCGGCCCCCATCTTGGGGTCATTCGATGAGCCCTCGCGTGCCTGCTCCGCTGT	540
QY	541	GAGGAGAGACATYTAGAAAATGAATGTGTCTTAAAGATGGCGAGGAAAACAGA	600
Db	541	GAGGAGAGACATYTAGAAAATGAATGTGTCTTAAAGATGGCGAGGAAAACAGA	600
QY	601	TCCTGTGGGATTTATTTATTTGAACGGGATTCACATTTGAAATGAAGCCAAAGTGAG	660
Db	601	TCCTGTGGGATTTATTTATTTGAACGGGATTCACATTTGAAATGAAGCCAAAGTGAG	660
QY	661	CATTACCAATGAGAGAAAACAGACAGAAAATCTTGATGGCTTCACAAGACATCAACA	720
Db	661	CATTACCAATGAGAGAAAACAGACAGAAAATCTTGATGGCTTCACAAGACATCAACA	720
QY	721	AACAAAATGGAAATACTGTGATGACATGAGGCAAGCCAACTGGGGAGAGATPACCAAGG	780
Db	721	AACAAAATGGAAATACTGTGATGACATGAGGCAAGCCAACTGGGGAGAGATPACCAAGG	780
QY	781	GCAGAGGGTCAGAGATTCCTGGCCCTGCTCCTTAACTGTGCGCTCATTAACCAATCATTT	840
Db	781	GCAGAGGGTCAGAGATTCCTGGCCCTGCTCCTTAACTGTGCGCTCATTAACCAATCATTT	840
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Db	841	ATATTCTTAACCCCTCAAAAACAAAGCTGTTGTAATTCGATCTCAGGGTCTCTTGAGG	900
QY	901	CCCAACATCTTCACATATATCCAGCCACACTATTTTAAATTTTGGTCCAGATCTGTA	960
Db	901	CCCAACATCTTCACATATATCCAGCCACACTATTTTAAATTTTGGTCCAGATCTGTA	960
QY	961	CTGTGACCTTCTACACTGTAGAAATTAACATTACTCATTTTGTCAAAAGACCTTGCTT	1020
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QY	1021	GCTGCTTAATTTATGTGCTGACTGTTTTCTCAAGAGAGTCTGGCCCAAGGGATCTGTG	1080
Db	1021	GCTGCTTAATTTATGTGCTGACTGTTTTCTCAAGAGAGTCTGGCCCAAGGGATCTGTG	1080
QY	1081	AACAGGCTGGGAAGCATCTCAAGATCTTTCAGGGTTATCTTACTAGACACAGCATGA	1140
Db	1081	AACAGGCTGGGAAGCATCTCAAGATCTTTCAGGGTTATCTTACTAGACACAGCATGA	1140
QY	1141	TCATTAGGGAATGAATTTATCAATCAACATATCTCTCAGTGCTTGTGGCCATCTGAAT	1200
Db	1141	TCATTAGGGAATGAATTTATCAATCAACATATCTCTCTGCTTGGCCATCTGAAT	1200
QY	1201	TCATTTCGCACCTTTGTGGCCCATCTCTCAAGACCTCAAAATGTCAATCAATATATCA	1260
Db	1201	TCATTTCGCACCTTTGTGGCCCATCTCTCAAGACCTCAAAATGTCAATCAATATATCA	1260
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Db	1261	GGATTAACTTTTTTTTTTAAACCTGGAGAAATTCATGTTAATGCACTANTGGAAATTTA	1320
QY	1321	ATTACATATTTTGTTTTCCAGTGCAGGAAGATGACAAAGCTTTAAATCCCTCCCTTGT	1380
Db	1321	ATTACATATTTTGTTTTCCAGTGCAGGAAGATGACAAAGCTTTAAATCCCTCCCTTGT	1380
QY	1381	GATTTTTTTTCCAGTAAAGTTAAATGCTTAACTCTGTACTGAGGCTGTATACAGAC	1440
Db	1381	GATTTTTTTTCCAGTAAAGTTAAATGCTTAACTCTGTACTGAGGCTGTATACAGAC	1440
QY	1441	AGCCTTCGCCATCCCTCAGCCCTTATCTGTCAATCACATTAACCCCTCCATACCACT	1500
Db	1441	AGCCTTCGCCATCCCTCAGCCCTTATCTGTCAATCACATTAACCCCTCCATACCACT	1500
QY	1501	AAACAAAATCTAATCTGTAAATCCCTGTAACCTGACAGCATATATTTCTCTGCT	1560

[illegible]

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Db 3001 CAAGCTTTTCTTCATCCCAACCACTAACCTGAAT 3036

RESULT 9
US-09-759-143-468
; Sequence 468 Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-468

Query Match 38.1%; Score 1364; DB 9; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 285 GGTGAGAAATAGAAAGGCTGCTGACTTACCATCTGAGGCCACACATCTGTGAATG 344
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Db 1373 AGATAATTAACTACATAGAGAAACAGCAAGATGCAATATATGCTTAAGTAGACATGT 1432
QY 405 TTTTGCACATTTTCACGCCCTTTAAATATCCACACACACAGAGACAAAGAGACAC 464
Db 1433 TTTTGCACATTTTCACGCCCTTTAAATATCCACACACACAGAGACAAAGAGACAC 1492
QY 465 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATGATGAGCTCGCCCTGT 524
Db 1493 AGAGATCCCTGGGAGAAATGCCCCGCCCATCTTGGGTCATGATGAGCTCGCCCTGT 1552
QY 525 GCTGGTCCCGCTTGAGAGGAAAGGACATTAAGAAATGATGATGTTCTTAAAGG 584
Db 1553 GCTGGTCCCGCTTGAGAGGAAAGGACATTAAGAAATGATGATGTTCTTAAAGG 1612
QY 585 TGGGAGAGAAACAGATCCCTGTGTGATATTTATTTGAACGGGATTCAGATTTGAAT 644
Db 1613 TGGGAGAGAAACAGATCCCTGTGTGATATTTATTTGAACGGGATTCAGATTTGAAT 1672
QY 645 GAAGTCACAAAGTGAGCATTTACCAATGAGAGAAACACAGCAAAATCTTGATGCTT 704
Db 1673 GAAGTCACAAAGTGAGCATTTACCAATGAGAGAAACACAGCAAAATCTTGATGCTT 1732
QY 705 CACAGACATGCAAAACAAAGAAATGGAATCTGATGACATGAGGAGGCAAGCTGGG 764
Db 1733 CACAGACATGCAAAACAAAGAAATGGAATCTGATGACATGAGGAGGCAAGCTGGG 1792
QY 765 AGGAGATTAACACAGGGGACAGAGGTCAGATTTGCGCCCTGCTTAACCTGGGCTC 824
Db 1793 AGGAGATTAACACAGGGGACAGAGGTCAGATTTGCGCCCTGCTTAACCTGGGCTC 1852
QY 825 ATTAACCAATCATTTCTATTTCTTAACCTCAAAACAAAGCTTTGATATGTCATCTC 884
Db 1853 ATTAACCAATCATTTCTATTTCTTAACCTCAAAACAAAGCTTTGATATGTCATCTC 1912
QY 885 TAGGGTTCTTTGGGGCCCAACATTCCTCATATATCCAGACACATCTTTAAATTT 944
Db 1913 TAGGGTTCTTTGGGGCCCAACATTCCTCATATATCCAGACACATCTTTAAATTT 1972
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Db 1973 AGTTCCAGATCTGTACTGTGACTGACCTTCTCAGCTGTAGATTAACATTAATCTTGTTC 2032
QY 1005 AAAGACCTTCTGTTGCTGCTGCTTAATATGAGCTGACTGTTTCTTAAGAGTGTCTG 1064
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QY 1065 GCCCAGGGATCTGTGAACAGGCTGGGAAACATCTGAAGATCTTTCAGAGGTATACTTA 1124
Db 2093 GCCCAGGGATCTGTGAACAGGCTGGGAAACATCTGAAGATCTTTCAGAGGTATACTTA 2152
QY 1125 CTAGCACACAGCATGATCATTAAGAGTGAATATGTAATCAACATCATCTCAGAGTCT 1184
Db 2153 CTAGCACACAGCATGATCATTAAGAGTGAATATGTAATCAACATCATCTCAGAGTCT 2212
QY 1185 TTGCCCATACTGAATTCATTTCCACCTTTTGCCCAATCTCAAGACCTCAAAATGTCA 1244
Db 2213 TTGCCCATACTGAATTCATTTCCACCTTTTGCCCAATCTCAAGACCTCAAAATGTCA 2272
QY 1245 TTGCATTAATATACAGAGATTAATCTTTTAAACCTGGAAGATTCATGATTAACAG 1304
Db 2273 TTGCATTAATATACAGAGATTAATCTTTTAAACCTGGAAGATTCATGATTAACAG 2332
QY 1305 CAGCTATGGAATTTATTAATATATTTGTTTTCAGTGAAGATGACTAAGTCCCTTA 1364
Db 2333 CAGCTATGGAATTTATTAATATATTTGTTTTCAGTGAAGATGACTAAGTCCCTTA 2392
QY 1365 TCCCTCCCTTTGTTGATTTTTCACATATTAAGATTAAGTTCATGCTTGTACTG 1424
Db 2393 TCCCTCCCTTTGTTGATTTTTCACATATTAAGATTAAGTTCATGCTTGTACTG 2452

OY	1425	AGCGGTGTAPACG -CAGAGCCCTCCCATCCCTCCAGCCCTATCTGATCATCACCATCA	1485
Db	2453	AGCGTGTATACGCCACACCCCTCTCCCATCCCTCCAGCCCTTATCTGTGATCATCCACATCAA	2512
OY	1484	CCCTCCCATACCACTTAAACAAATCTTAACTTGAAATTCCTTGAAATGTGACGACATA	1543
Db	2513	CCCTCCCAT -GCACCTTAAACAAATCTTAACTTGAAATTCCTTGAAATGTGACG -CATA	2570
OY	1544	CATTTCCTCTGCTGCTGAGAAAGCTCTTCCTTGTCTCTTAAATCTAGATGATGAAAGT	1603
Db	2571	CATTATCTCTCTGCTGCTGAGAAAGCTCTTCCTTGTCTCTTAAATCTAGATGATGAAAGT	2630
OY	1604	TTTGAATTAAGTTGACTATCTTACTTCTATGACGAAGAGGACACATATGATGATCATATC	1663
Db	2631	TTTGAATTAAGTTGACTATCTTACTTCTATGACGAAGAGGACACATATGATGATCATATC	2690
OY	1664	ACATGAGACACAAATTAATAAAGTGTATTTGATTAATAGATTAGATTAATATATGA	1723
Db	2691	ACATGAGACACAAATTAATAAAGTGTATTTGATTAATAGATTAGATTAATATATATGA	2750
OY	1724	AATGCAAGAGCCACAGAGGAGATGTTTATGCGGCACGTTTGAAGCCCTGGATGGAAGC	1783
Db	2751	AATGCAAGAGCCACAGAGGAGATGTTTATGCGGCACGTTTGAAGCCCTGGATGGAAGC	2810
OY	1784	AAAGGACAGGAACTCATATGATCTTATATATATTAATTAATCTTCAATTCCTATCTATGACA	1843
Db	2811	AAAGGACAGGAACTCATATGATCTTATATATATTAATTAATTAATCTTCAATTCCTATCTATGACA	2870
OY	1844	ATATCCACACAGCTTTTTCACAGAAATTCATGACAGCAAAATCCCAAAAGTAACTTATC	1903
Db	2871	ATATCCACACAGCTTTTTCACAGAAATTCATGACAGCAAAATCCCAAAAGTAACTTATC	2930
OY	1904	CATTTCATGTGTAGTGGCTTTAGAAATTTTGGCAAAATCATACTGTCACTATCTCAACT	1963
Db	2931	CATTTCATGTGTAGTGGCTTTAGAAATTTTGGCAAAATCATACTGTCACTATCTCAACT	2990
OY	1964	TTGAGATGTGTTTTCCTGTGTAGTTAATGGAAGAAATATGAGGACCTCTTGAGACCACT	2023
Db	2991	TTGAGATGTGTTTTCCTGTGTAGTTAATGGAAGAAATATGAGGACCTCTTGAGACCACT	3050
OY	2024	TAGGGTTCACCTCTGGCAATTAAGAATTTTACAAAGAGC	2061
Db	3051	TAGGGTTCACCTCTGGCAATTAAGAATTTTACAAAGAGC	3088
RESULT 10			
US-09-780-669-468			
; Sequence 468, Application US/09780669			
; Patent No. US20020051977A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Devin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yugu			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Stoik, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darrick			
; APPLICANT: Li, Samuel			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skelky, Yasir A.W.			
; APPLICANT: Hepler, William			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghen, Raymond L.			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
FILE REFERENCE: 210121.427C24			

	:	CURRENT APPLICATION NUMBER:	US-09/780,669	
:	:	CURRENT FILING DATE:	2001-02-09	
:	:	NUMBER OF SEQ ID NOS:	943	
:	:	SOFTWARE:	FASTSEQ for Windows Version 3.0	
:	:	SEQ ID NO	468	
:	:	LENGTH:	3112	
:	:	TYPE:	DNA	
:	:	ORGANISM:	Homo sapiens	
:	:	US-09-780-669-	468	
		Query Match	38.1%; Score 1364; DB 9; Length 3112;	
		Best Local Similarity	99.8%; Pded. No. 0;	
		Matches 1774; Conservative	0; Mismatches 1; Indels 3; Gaps 3;	
OY		285	GGTGAGAAATTAAGAAAAGCGCTGCATTACCATCTGAGGCCACACATCTGCTGAATGG	344
Db		1313	GGTGAGAAATAAAGAAAGCGCTGACTTACCATCTGAGCCACACATCTGCTGAATGG	1377
OY		345	AGATTAATTACATCACTAGAAAACAGCAAGATGACAATAATATGTCTAAGTAGCATGT	404
Db		1373	AGATTAATTACATCACTAGAAAACAGCAAGATGACAATAATATGTCTAAGTAGCATGT	1433
OY		405	TTTTCGACATTTCCAGCCCCCTTAATATATCCACACACAGSAGAACAAAAAGSAGAC	464
Db		1433	TTTTGCACATTTCCAGCCCCCTTAATATATCCACACACAGSAGAACAAAAAGSAGAC	1492
OY		465	AGAGATCCCTGGGAGAAATGCCGGCCGCATCTTGGGTCATCGATGAGCCTCGCCCTGT	524
Db		1493	AGAGATCCCTGGGAGAAATGCCGGCCGCATCTTGGGTCATCGATGAGCCTCGCCCTGT	1555
OY		525	GCCTGCTCCCGCTTGTGAGGAGAGACATTTAGAAAATGATGTGTCTTTAAAGA	584
Db		1553	GCCTGCTCCCGCTTGTGAGGAGAGACATTTAGAAAATGATGTGTCTTTAAAGA	1612
OY		585	TGGGAGAGAAAACAGATCCTGTTGTGATATTATTAGCGGGATTACAGATTGGAAT	644
Db		1613	TGGGAGAGAAAACAGATCCTGTTGTGATATTATTAGCGGGATTACAGATTGGAAT	1672
OY		645	GAATTCACAAAGTAGCATTTACCAATGAGAGAAAAACAGACGAGAAATCTTGATGGCTT	704
Db		1673	GAATTCACAAAGTAGCATTTACCAATGAGAGAAAAACAGACGAGAAATCTTGATGGCTT	1732
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Db		1733	CACAGACATGGCAACAAACAAATGATACGTGATACATGAGGGCGCCACACCTGGGG	1792
OY		765	AGGAGATTAACAACGGGGGAGAGGGTCAGGATTTGGGCCCTGCTGCTTAACTGTGCCTT	824
Db		1793	AGGAGATTAACAACGGGGGAGAGGGTCAGGATTTGGGCCCTGCTGCTTAACTGTGCCTT	1852
OY		825	ATTAACCAANTATTTCATATTTCTTAACCTCTAAACAAAGCTGTGTGAATTCGATCTC	884
Db		1853	ATTAACCAANTATTTCATATTTCTTAACCTCTAAACAAAGCTGTGTGAATTCGATCTC	1912
OY		885	TACGGTTCCTTCTGGGCCCAACATTTCTCATATATCCAGCACACTCATTTTAAATTT	944
Db		1913	TACGGTTCCTTCTGGGCCCAACATTTCTCATATATCCAGCACACTCATTTTAAATTT	1972
OY		945	AGTTCACAGATCTGTACTGTACCTTTCTACACTGTAGAAATTAACATTAATCTATTTGTT	1004
Db		1973	AGTTCACAGATCTGTACTGTACCTTTCTACACTGTAGAAATTAACATTAATCTATTTGTT	2032
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Db		2033	AAAGACCTTGCTGTGCTGCTTAATATGATGCTGACGTGTTTCCTAAGSAGTGTCTG	2092
OY		1065	GCCCAGGGGATCTGGAACAGGCTGGGAGACATCTCAAGATCTTTCCAGGGTTTACTTTA	1124
Db		2093	GCCCAGGGGATCTGGAACAGGCTGGGAGACATCTCAAGATCTTTCCAGGGTTTACTTTA	2152
OY		1125	CTAGACACAGCATGATCATTTAGGAGTGAATTAATCAATCAATCATCTCAGTGTCT	1184
Db		2153	CTAGACACAGCATGATCATTTAGGAGTGAATTAATCAATCAATCATCTCAGTGTCT	2212

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1305 CAGCTATGGGAATTTAATACATATTTTCCAGTGAAGATGACTAGTCCCTTA 1364
2333 CAGCTATGGGAATTTAATACATATTTTCCAGTGAAGATGACTAGTCCCTTA 2392
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2931 CATTCATGCTGAGTCTGCTTTAAGATTTTGGCAATCATGCTGACCTTATCTCAAGT 2990
1964 TTGAGATGCTGCTGCTTTAAGATTTTGAAGAAATAGGACACTTGTGAGCAGCTT 2023
2991 TTGAGATGCTGCTGCTTTAAGATTTTGAAGAAATAGGACACTTGTGAGCAGCTT 3050
2024 TAGGTTCACTCTGTCATTAAGATTTTACAAAGAGC 2061
3051 TAGGTTCACTCTGTCATTAAGATTTTACAAAGAGC 3088

RESULT 11

US-09-822-827-468
Sequence 468, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-827-468

Query Match 38.1%; Score 1364; DB 9; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

285 GGTGAGAAATTAAGAAAGGCTGCTGACTTTTACATCTGAGCGCACACATCGTGAATG 344
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1433 TTTTGACATTTCCAGCCCTTTAATATTCACACACAGAGAGCAACAAAGAGCAC 1492
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2093 GCCCAGGAGTCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGAGGTTATCTTA 2152
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Db 2213 TTGCCATACCTAAATTTATTTCCACTTTGTGGCCATCTCAAGACCTCAAAATGCA 2272
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Oy 1365 TCCCTCCCTTTGTGTGATTTTTTTTTTCCAGTAAAGTTAAAGTCAAGCTTATACG 1424
Db 2393 TCCCTCCCTTTGTGTGATTTTTTTTTTCCAGTAAAGTTAAAGTCAAGCTTATACG 2452
Oy 1425 AGCGTATATACG-CACAGCCTTCGCCATCCCTCCAGCCTTATCTGTCATCAGCA 1483
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Oy 1484 CCCCCCATACACCTAAACAAATCTAACTGTAAATCTCTGAACATGTCAGACATA 1543
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Oy 1724 AATGCAAGAGCCACAGAGAGATGTTATGGGACGCTTTGAAGCCTGGAGTGAAGC 1783
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Oy 1904 CATTTCAATGAGTGGCTTTAGAAATTTGGCAATCATAGTGGCTATATCAACT 1963
Db 2931 CATTTCAATGAGTGGCTTTAGAAATTTGGCAATCATAGTGGCTATATCAACT 2990
Oy 1964 TTGAGATGTGTTTCTCTTGTAGTTAATTTGAAGAAATAGGGCACTTTGAGCCACT 2023
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Oy 2024 TAGGGTCACTCCCTGGCAATTAAGAAATTTAACAAGAGC 2061
Db 3051 TAGGGTCACTCCCTGGCAATTAAGAAATTTAACAAGAGC 3088

APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurrell, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-793-468
Query Match 38.1%; Score 1364; DB 10; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
Oy 285 GGTGAGAAATAGAAAGGCTGCTGACTTTACATCTGAGGCGACACATCTGCTGAATG 344
Db 1313 GGTGAGAAATAGAAAGGCTGCTGACTTTACATCTGAGGCGACACATCTGCTGAATG 1372
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Db 1373 AGATAATATACATCATCTGAAGACAGCAAGATGCAATATATATATATATATATAT 1432
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Oy 765 AGGAGATTAACACAGGCGAGAGGCTCAGATTTGCGCCCTGCTAACTGTGCGTTC 824
Db 1793 AGGAGATTAACACAGGCGAGAGGCTCAGATTTGCGCCCTGCTAACTGTGCGTTC 1852
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Db 1913 TAGGTTCCCTTGCGGCCAACATCTCCATATATCCAGCACACTCATTTTAAATATTT 1972

QY 945 AGTCCCAATCTGTACTGTGACCTTTCTACACTGTAGAAATAACATTACTCATTTTGTTC 1004

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QY 1005 AAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1064

Db 2033 AAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2092

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Db 2571 CATTATTCCTTCTGCTGAGAGCTCTCTCTCTCTTAAATCTAGAAATGATGTAAGT 2630

QY 1604 TTTGAATTAAGTGTACTATCTTACTCATGCAAGAGGACACATATGACATTCATC 1663

Db 2631 TTTGAATTAAGTGTACTATCTTACTCATGCAAGAGGACACATATGACATTCATC 2690

QY 1664 ACATGAGACAGCAAACTAATAAGTAAATTTGATATATAAGTTAGATTAATATATGTA 1723

Db 2691 ACATGAGACAGCAAACTAATAAGTAAATTTGATATATAAGTTAGATTAATATATGTA 2750

QY 1724 AATGCAAGACCCACAGAGGAAATGTTATGAGGACAGTTTGTAAAGCTGGAGTGAAGC 1783

Db 2751 AATGCAAGACCCACAGAGGAAATGTTATGAGGACAGTTTGTAAAGCTGGAGTGAAGC 2810

QY 1784 AAGGACGAGGAACTCATATGATCTTATATATATATATCTTCTCTATCTCTATCA 1843

Db 2811 AAGGACGAGGAACTCATATGATCTTATATATATATATCTTCTCTATCTCTATCA 2870

QY 1844 ATATCAACAGGTTTTCACAGAAATTCATGACAGTGAATCCCAAGGAAACCTTATTC 1903

Db 2871 ATATCAACAGGTTTTCACAGAAATTCATGACAGTGAATCCCAAGGAAACCTTATTC 2930

QY 1904 CATTTCATGCTGAGTCCGCTTTAGAAATTTTGGCAATTCATGCTCATTATCTCACT 1963

Db 2931 CATTTCATGCTGAGTCCGCTTTAGAAATTTTGGCAATTCATGCTCATTATCTCACT 2990

QY 1964 TTGAGATGTGTTTGTCTTGTAGTAAATGAAGAAATAGGACATCTTGTGAGCCACT 2023

Db 2991 TTGAGATGTGTTTGTCTTGTAGTAAATGAAGAAATAGGACATCTTGTGAGCCACT 3050

QY 2024 TAGGTTCACTCCTGCGCAATTAAGATTTACAAAGAGC 2061

Db 3051 TAGGTTCACTCCTGCGCAATTAAGATTTACAAAGAGC 3088

RESULT 13

US-09-895-814-468

; Sequence 468, Application US/09895814

; Publication No. US20020193296A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yugu

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Horal, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals de Bassols, Carlota

; APPLICANT: Roy, Teresa

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C26

; CURRENT APPLICATION NUMBER: US/09/895,814

; NUMBER OF SEQ. ID NOS: 990

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 468

; LENGTH: 3112

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-895-814-468

Query Match 38.1%; Score 1364; DB 10; Length 3112;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 285 GGTGCAAAATTAAGAGGCTGCTGACTTATACCATCTGAGGCCACACATCTGCGGAATGG 344

Db 1313 GGTGCAAAATTAAGAGGCTGCTGACTTATACCATCTGAGGCCACACATCTGCGGAATGG 1372

QY 345 AGATTAATTAACATCACTAGAAACAGCAAGATGCAATTAATGCTAAAGTATGACATGT 404

Db 1373 AGATTAATTAACATCACTAGAAACAGCAAGATGCAATTAATGCTAAAGTATGACATGT 1432

QY 405 TTTTGCACATTTCCAGCCCCCTTTAAATATCCACACACACAGGAGCACAAAAGAGCAC 464

Db 1433 TTTTGCACATTTCCAGCCCCCTTTAAATATCCACACACAGGAGGACAAAAGAGAGCAC 1492

QY 465 AGAGATCCCTGGGAGAAATGCCCGGCGCATCTGSGTCATGAGACCTGCGCCTGT 524

Db 1493 AGAGATCCCTGGGAGAAATGCCCGGCGCATCTGSGTCATGAGACCTGCGCCTGT 1552

QY 525 GCGTGTCCCGCTTGTGAGGAGAGGACATTAGAAATGAAATGATGATGTCTTCTTAAGGA 584

Db 1553 GCGTGTCCCGCTTGTGAGGAGAGGACATTAGAAATGAAATGATGATGTCTTCTTAAGGA 1612

QY 585 TGGGACAGAAACAGATCCTGTTGTGATATTTATTTGAACGGGATTAACAGATTGAAAT 644

Db 1613 TGGGACAGAAACAGATCCTGTTGTGATATTTATTTGAACGGGATTAACAGATTGAAAT 1672

OY	645	GAAAGCAAAAGTGAAGCTTTACCATGAGAGAAAACGACGAGAAAAATCTTGATGGCTT	704
Dd	1673	GAAGTGCACAAAGTGAAGCTTAACCATGAGAGAAAACGACGAGAAAAATCTTGATGGCTT	1732
OY	705	CACAAGACATCACAACAAAATAATGAGATTACTGTGATGACATGAGAGCGCCAGCTGGGG	764
Dd	1733	CACAAGACATCACAACAAAATAATGAGATTACTGTGATGACATGAGAGCGCCAGCTGGGG	1792
OY	765	AGGAGATTACCACGGGGGACAGAGGTCAGGATTCTGGGCCCTGCTAACTGTGCGTTG	824
Dd	1793	AGGAGATTACCACGGGGGACAGAGGTCAGGATTCTGGGCCCTGCTAACTGTGCGTTG	1852
OY	825	ATAACCAATCATTTTCATATTTCTAACCCCTCAAACAAAGGCTGGTTGAATPFCGATGTC	884
Dd	1853	ATAACCAATCATTTTCATATTTCTAACCCCTCAAACAAAGGCTGGTTGAATPFCGATGTC	1912
OY	885	TACGGTTCCTTCTGGGCCCAACATTTCCATATATCCAGCCACACTATTTTTAATATTT	944
Dd	1913	TACGGTTCCTTCTGGGCCCAACATTTCCATATATCCAGCCACACTATTTTTAATATTT	1972
OY	945	AGTTCCACGATCTGTACTGTACCTTTCTACAGTGTAGAATPAACATTTCTATTTGTTT	1004
Dd	1973	AGTTCCACGATCTGTACTGTACCTTTCTACAGTGTAGAATPAACATTTCTATTTGTTT	2032
OY	1005	AAAGACCCCTTGCTGTGCTGCCCTAATATGTAGCTGACGCTTTTTCCTAAGSAGTGTCTG	1064
Dd	2033	AAAGACCCCTTGCTGTGCTGCCCTAATATGTAGCTGACGCTTTTTCCTAAGSAGTGTCTG	2092
OY	1065	GCCCCAGGGGATCTGTGAACAGGCTGGGACAGCATCTCAAGATCTTTCAGSGTTATCTTA	1124
Dd	2093	GCCCCAGGGGATCTGTGAACAGGCTGGGACAGCATCTCAAGATCTTTCAGSGTTATCTTA	2152
OY	1125	CTACACACACACATGATCATTTACGAGAGATTTTCTPATACATCATCTCTCAGTGTCT	1184
Dd	2153	CTACACACACACATGATCATTTACGAGAGATTTTCTPATACATCATCTCTCAGTGTCT	2212
OY	1185	TTGGCCCATCTGAANAATTCATTTCCOACTTTTGTGCCAYTTCGCAAGACCTCAAAATGTCA	1244
Dd	2213	TTGGCCCATCTGAANAATTCATTTCCOACTTTTGTGCCAYTTCGCAAGACCTCAAAATGTCA	2272
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Dd	2273	TTCCATTPAATPNCACAGGATTAACCTTTTTTAACTGGAGAAATTCANATGTTACNTG	2332
OY	1305	CAGCTATGGAATTTAATTACATATTTTGTTCAGTAGCAAAAGATGACTAAGTCCTTTA	1364
Dd	2333	CAGCTATGGAATTTAATTACATATTTTGTTCAGTAGCAAAAGATGACTAAGTCCTTTA	2392
OY	1365	TTCCCTCCCCTTTGTTTGAATTTTTTTCACAGTATAAGTTAAATAGCTTAGCTGTACTG	1424
Dd	2393	TTCCCTCCCCTTTGTTTGAATTTTTTTCACAGTATAAGTTAAATAGCTTAGCTGTACTG	2452
OY	1425	AGGCTGTATACAG-CACAGCCTCCGCCATCCGACGACCTTATCTGTGCATCACACATCAA	1483
Dd	2453	AGGCTGTATACAGCAGCCTCCGCCATCCGACGACCTTATCTGTGCATCACACATCAA	2512
OY	1484	CCCTCCCATPACACCTPAAACAAAATCTAACTTAATCTCTTGACATGTCSAGACATA	1543
Dd	2513	CCCTCCCATPACACCTPAAACAAAATCTAACTTAATCTCTTGACATGTCSAGACATA	2570
OY	1544	CATTATTTCCCTTCTGCGTGAGAAAGCTTCCCTGTGCTTAATCTAGATGATGTAAAGT	1603
Dd	2571	CATTATTTCCCTTCTGCGTGAGAAAGCTTCCCTGTGCTTCTTAATCTAGATGATGTAAAGT	2630
OY	1604	TTTGAATPAAGTTGACTATCTTACTTCATGCAAAAGAGGACACATATGAGATTATCATCT	1663
Dd	2631	TTTGAATPAAGTTGACTATCTTACTTCATGCAAAAGAGGACACATATGAGATTATCATCT	2690
OY	1664	ACATGAGACAGCAAAATCTATAAAGTGTATTTGATTATAGAGATTAGATPAATATATGA	1723
Dd	2691	ACATGAGACAGCAAAATCTATAAAGTGTATTTGATTATAGAGATTAGATPAATATATGA	2750

OY	1724	AATCGAAGAGCCACAGAGAGGAAATGTTTATGCGGACGTTTGTAACCTGGGATGTGAAGC	178
Db	2751	AATCGAAGAGCCACAGAGAGGAAATGTTTATGCGGACGTTTGTAACCTGGGATGTGAAGC	2810
OY	1784	AAAGCAGGGAACCTCATAGTATCTTATATATATATATCTTCATTTCTATCTATACACA	1843
Db	2811	AAAGCAGGGAACCTCATAGTATCTTATATATATATATCTTCATTTCTATCTATACACA	2870
OY	1844	ATATCCAAACAGCTTTTACAGAAATTCATGCAGTCCAAATCCCAAAGTAACCTTTATC	1905
Db	2871	ATATCCAAACAGCTTTTACAGAAATTCATGCAGTCCAAATCCCAAAGTAACCTTTATC	2930
OY	1904	CATTTCATGATGAGAGTGCCTTTAGCAATTTTGGCAATCATACTGCTCACTATCTCACT	1963
Db	2931	CATTTCATGATGAGAGTGCCTTTAGCAATTTTGGCAATCATACTGCTCACTATCTCACT	2990
OY	1964	TTGAGATGCTGTTTGCTCTGTAGTTAATTGAAGAATAAGGCACTCTTGAGGCCACTT	2022
Db	2991	TTGAGATGCTGTTTGCTCTGTAGTTAATTGAAGAATAAGGCACTCTTGAGGCCACTT	3050
OY	2024	TAGGCTCAGCTCGCCAAATTAAGAATTTACAAAGC	2061
Db	3051	TAGGCTCAGCTCGCCAAATTAAGAATTTACAAAGC	3088
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	US-10-144-678A-468		
	Sequence 468, Application US/10144678A		
	Publication No. US20030157089A1		
	GENERAL INFORMATION:		
	APPLICANT: Xu, Jiangchun		
	APPLICANT: Dillon, Davin C.		
	APPLICANT: Mitcham, Jennifer L.		
	APPLICANT: Harlocker, Susan L.		
	APPLICANT: Jiang, Yuxin		
	APPLICANT: Henderson, Robert A.		
	APPLICANT: Kalos, Michael D.		
	APPLICANT: Fanger, Gary R.		
	APPLICANT: Retter, Marc W.		
	APPLICANT: Stolk, John A.		
	APPLICANT: Day, Craig H.		
	APPLICANT: Vedvick, Thomas S.		
	APPLICANT: Carter, Darrick		
	APPLICANT: Li, Samuel X.		
	APPLICANT: Wang, Aljun		
	APPLICANT: Skeiky, Yasir A. W.		
	APPLICANT: Hepler, William T.		
	APPLICANT: Hural, John		
	APPLICANT: McNeill, Patricia D.		
	APPLICANT: Houghton, Raymond L.		
	APPLICANT: Vinals y de Bassols, Carlota		
	APPLICANT: Foy, Teresa M.		
	APPLICANT: Watanabe, Yoshihiro		
	APPLICANT: Deng, Ta		
	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND		
	TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER		
	FILE REFERENCE: 210121.427C28		
	CURRENT APPLICATION NUMBER: US/10/144, 678A		
	CURRENT FILING DATE: 2002-08-12		
	NUMBER OF SEQ ID NOS: 1033		
	SOFTWARE: FASTSEQ for Windows Version 3.0		
	SEQ ID NO 468		
	LENGTH: 3112		
	TYPE: DNA		
	ORGANISM: Homo sapiens		
	US-10-144-678A-468		
	Query Match	38.1%;	Score 1364; DB 12; Length 3112;
	Best Local Similarity	99.8%;	Pred. NO. 0;
	Matches 1774; Conservative	0;	Mismatches 1; Indels 3; Gaps 3;
OY	285	GGTAGGAATTAAGAAAGCTGCTGACTTATACATCTGAGGCACACATCTGCTGAATAG	344


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; APPLICANT: Watanabe, Yoshitiro
; APPLICANT: Weagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FASTED for Windows Version 3.0
; LENGTH: 3112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-468

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Query Match      38.1%; Score 1364; DB 13; Length 3112;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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QY	285	GCTGAGAAATGAAGAGCTGCTGACCTTACCATCTGAGGCCACACATCTGCTGAATGG	344
DB	1313	GGTGAAGATTAAGAAAGCTGCTGACTTACCCTTGAGGCCACACATCTGCTGAATGG	1372
QY	345	AGATAATTACATCTAGAAACAGCAGATGACATATTAATGCTAGTAGTGCATGT	404
DB	1373	AGATTAATTACATCTAGAAACAGCAGATGACATATTAATGCTAGTAGTGCATGT	1432
QY	405	TTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGACACAAAAAGAGCAG	464
DB	1433	TTTTCACATTTCCAGCCCTTTAAATATCCACACACAGAGACACAAAAAGAGCAG	1492
QY	465	AGAGATCCCTGGGAGAAATGCCGGCCGCACTTTGGGTATCGATGAGCCTCGCCCTGT	524
DB	1493	AGAGATCCCTGGGAGAAATGCCGGCCGCACTTTGGGTATCGATGAGCCTCGCCCTGT	1552
QY	525	GCTGTGCTCCGCTTTGTAGGAGAGACATTAAGAAATGAATTGATGCTTCTTAAGGA	584
DB	1553	GCTGTGCTCCGCTTTGTAGGAGAGACATTAAGAAATGAATTGATGCTTCTTAAGGA	1612
QY	585	TGGGAGAGAAACAGATCTGTGTGATATTATTGTAACGGGATTAACAGATTTGAAT	644
DB	1613	TGGGAGAGAAACAGATCTGTGTGATATTATTGTAACGGGATTAACAGATTTGAAT	1672
QY	645	GAAGTCACAAAGTGAAGCATTTACCAATGAGAGAAAAACAGAGAAAAATCTTGATGCTT	704
DB	1673	GAAGTCACAAAGTGAAGCATTTACCAATGAGAGAAAAACAGAGAAAAATCTTGATGCTT	1732
QY	705	CACAAGACATGCAACAACAATAATGGAATTAATGATGATGACATGAGGAGCCAGCTGGGG	764
DB	1733	CACAAGACATGCAACAACAATAATGGAATTAATGATGATGACATGAGGAGCCAGCTGGGG	1792
QY	765	AGGAGATTAACCAAGGGGAGAGGGTCAAGATTTGGCCCTCTGCTAACTGAGCGCTTC	824
DB	1793	AGGAGATTAACCAAGGGGAGAGGGTCAAGATTTGGCCCTCTGCTAACTGAGCGCTTC	1852
QY	825	ATAACCAATCATTTCAATTTTCAACCCCTCAAAAACAAGCTGTGTAATCTGATGCTC	884
DB	1853	ATAACCAATCATTTCAATTTTCAACCCCTCAAAAACAAGCTGTGTAATCTGATGCTC	1912
QY	885	TACGGTTCCTTCTGGGGCCCAACATTTCCATATATCCAGCACACTCTTTTAAATATT	944
DB	1913	TACGGTTCCTTCTGGGGCCCAACATTTCCATATATCCAGCACACTCTTTTAAATATT	1972
QY	945	AGTTCACAGATCTGATGACCTTTCTACATGTAAGTAATTAACATTAATCTATTTGTTTC	1004
DB	1973	AGTTCACAGATCTGATGACCTTTCTACATGTAAGTAATTAACATTAATCTATTTGTTTC	2032
QY	1005	AAAGACCTTGTGCTGCTTAATATAGTAGTACGCTTTTTCCTAAGAGAGTTCG	1064
DB	2033	AAAGACCTTGTGCTGCTTAATATAGTAGTACGCTTTTTCCTAAGAGAGTTCG	2092
QY	1065	GCCAGAGGATCTGTGAACAGAGCTGGGAAGCATCTCAAGATCTTCCAGGGTAACTTA	1124

DB	2093	GCCAGGGGATCTGTGAACAGGCTGGGAAGCATCTCAAGATCTTCCAGGGTAACTTA	2152
QY	1125	CTAGCACACAGATGATCTTACGGAGGAATTAATCTATCAATCAATCATCTGCTGCT	1184
DB	2153	CTAGCACACAGATGATCTTACGGAGGAATTAATCTATCAATCAATCATCTGCTGCT	2212
QY	1185	TTGCCATACAGAAATTCATTTCCACATTTTGTGCCATTCACAGACCTCAAAATGTCA	1244
DB	2213	TTGCCATACAGAAATTCATTTCCACATTTTGTGCCATTCACAGACCTCAAAATGTCA	2272
QY	1245	TTCCATTAATATACAGATTAATCTTTTATTAATACCTGAGAGAAATTAATGTTACATG	1304
DB	2273	TTCCATTAATATACAGATTAATCTTTTATTAATACCTGAGAGAAATTAATGTTACATG	2332
QY	1305	CAGCTATGGAATTAATTAATATATTTGTTTCCAGTGAAGATGATCAAGCTTCA	1364
DB	2333	CAGCTATGGAATTAATTAATATATTTGTTTCCAGTGAAGATGATCAAGCTTCA	2392
QY	1365	TCCCTCCCTTTGTTGATTTTTCAGATATAAGTTAAATGCTTAGCCTGTACTG	1424
DB	2393	TCCCTCCCTTTGTTGATTTTTCAGATATAAGTTAAATGCTTAGCCTGTACTG	2452
QY	1425	AGGCTGATACAG-CACAGCCTCCCATCCCATCCCATCCCATCTGATCATCACATCA	1483
DB	2453	AGGCTGATACAG-CACAGCCTCCCATCCCATCCCATCCCATCTGATCATCACATCA	2512
QY	1484	CCCCCTCCATACACCTTAACAAATTAATCTTAATCTTGAACATGTCAGAGATA	1543
DB	2513	CCCCCTCCAT-CCACCTTAACAAATTAATCTTAATCTTGAACATGTCAGAGATA	2570
QY	1544	CATTATTCCTTGTGCTGAGAGAGCTCTTCTGCTCTTAATCTAGAAATGATTAAGT	1603
DB	2571	CATTATTCCTTGTGCTGAGAGAGCTCTTCTGCTCTTAATCTAGAAATGATTAAGT	2630
QY	1604	TTTGAATAGTTGATCTTACTTCAATGCAAAAGAGGACATGATGATTAATCATC	1663
DB	2631	TTTGAATAGTTGATCTTACTTCAATGCAAAAGAGGACATGATGATTAATCATC	2690
QY	1664	ACATGAGACAGCAATTAATAAGTGAATTTGATTAATAGAGTTTGAATTAATATGA	1723
DB	2691	ACATGAGACAGCAATTAATAAGTGAATTTGATTAATAGAGTTTGAATTAATATGA	2750
QY	1724	AATGCAAGAGCCACAGAGGGAATTTTATGCGGACGCTTTGTAAAGCTGGATGTGAAC	1783
DB	2751	AATGCAAGAGCCACAGAGGGAATTTTATGCGGACGCTTTGTAAAGCTGGATGTGAAC	2810
QY	1784	AAAGGAGGAGACCTCATAGTATCTTAATTAATTAATCTGCTATCTATATACA	1843
DB	2811	AAAGGAGGAGACCTCATAGTATCTTAATTAATTAATCTGCTATCTATATACA	2870
QY	1844	ATATCAACAAGCTTTTCACAGAAATTCAGCAGTGCAGAAATCCCAAGAGTAACCTTATC	1903
DB	2871	ATATCAACAAGCTTTTCACAGAAATTCAGCAGTGCAGAAATCCCAAGAGTAACCTTATC	2930
QY	1904	CATTTCATGATGATGGCTTTTACAATTTTGGCAATCAATCTGCTATCTATCACT	1963
DB	2931	CATTTCATGATGATGGCTTTTACAATTTTGGCAATCAATCTGCTATCTATCACT	2990
QY	1964	TTGAGATGTGTTTCTCTGTTAGTTAAATGGAAGAAATAGGGCACTCTTGAGACCACTT	2023
DB	2991	TTGAGATGTGTTTCTCTGTTAGTTAAATGGAAGAAATAGGGCACTCTTGAGACCACTT	3050
QY	2024	TAGGTTCACTCTGCGCAATTAAGAAATTAACAAAGAGC	2061
DB	3051	TAGGTTCACTCTGCGCAATTAAGAAATTAACAAAGAGC	3088

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 Job time : 836.096 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 21:39:38 ; Search time 7516.98 Seconds
(without alignments)
11581.589 Million cell updates/sec

Title: US-09-402-713a-6
Perfect score: 3582
Sequence: 1 acagaagaatacgcaagtcg.....tgattcttgcatacaattt 3582

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estov:*
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6: em_estov:*
7: em_estov:*
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9: gb_est1:*
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13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
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19: em_gss_hum:*
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27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	14.9	542	28	AQ318297 RPC11-10
2	452	12.6	546	28	AQ318289 RPC11-10
3	367	10.2	402	9	AA578773 nb24a04.s
4	323	9.0	654	28	AQ319247 RPC11-10

Result No.	Score	Query Match	Length	DB ID	Description
5	319	8.9	346	10	AW948945 QV4-FT000
6	293	8.2	304	13	BQ372852 CM4-FT010
7	287	8.0	856	9	A1557225 PT2.1.15
8	280	7.8	700	13	BQ373258 MR0-FT017
9	247	6.9	319	13	BQ371438 RC6-FN011
10	238	6.6	290	10	BF373619 MR0-FT017
11	238	6.6	304	13	BQ38234 CM2-NN011
12	214	6.0	326	10	BF658371 RC5-FT019
13	214	6.0	394	28	AQ206972 HS.3238.B
14	213	5.9	332	10	BF658286 RC5-FT019
15	198	5.5	282	10	BF373581 MR0-FT017
16	194	5.4	323	13	BQ38235 CM2-NN011
17	172	4.8	189	13	BQ372602 QV4-FT000
18	167	4.7	167	10	BF373406 IL2-FT015
19	152	4.2	197	13	BQ372624 QV4-FT000
20	146	4.1	332	13	BQ372858 CM4-FT010
21	142	4.0	441	10	BF658890 RC5-FT019
22	121	3.4	572	13	BQ292350 PM0-AN008
23	86	2.4	657	9	A1557495 PT2.1.7-H
24	83	2.3	245	13	BQ373093 RC2-FT012
25	62	1.7	451	28	AQ246715 HS.2059.B
26	61	1.7	376	28	AQ069980 HS.3027-B
27	51	1.4	111	13	BQ373237 RC2-FT012
28	44	1.2	863	28	BZ190572 CH230-330
29	36	1.0	610	28	BH076212 RPC1-24-2
30	35	1.0	598	28	AZ323381 IM0044P06
31	35	1.0	602	28	AZ323366 IM0044P05
32	35	1.0	960	29	CNS02000 Tetraodon
33	34	0.9	1166	14	CD498534 CD434-B05
34	33	0.9	505	28	BH082184 RPC1-24-3
35	33	0.9	868	28	BH084129 RPC1-24-3
36	33	0.9	909	29	CNS015X0 Tetraodon
37	33	0.9	189	10	BE552517 UI-M-AKO-
38	32	0.9	200	28	AZ758563 IM0550D10
39	32	0.9	266	28	AZ965467 2M0235N02
40	32	0.9	272	29	FR0047998 BE953161 UI-M-CD1-
41	32	0.9	429	10	AZ037336 RPC1-23-2
42	32	0.9	551	28	AZ308663 IM0011E22
43	32	0.9	577	28	AZ308663 IM0011E22
44	32	0.9	581	10	BG086866 H3131E09-
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
RPC11-108A20.TV RPC1-11 Homo sapiens genomic clone RPC1-11-108A20,
genomic survey sequence.

ACCESSION
AQ318297
VERSION
AQ318297.1 GI:4050267
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Other_GSSs: RPC11-108A20.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetlgr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong

QY 2810 GGAAACCATGTCATGAGTTGAA 2832
|||||
Db 23 GGAAACCATGTCATGAGTTGAA 1
|||||

RESULT 3
AA578773 402 bp mRNA linear EST 12-SEP-1997
LOCUS nh24a04.s1 NCL_CGAP_Prl Homo sapiens cDNA clone IMAGE:953262, mRNA
DEFINITION
sequence.
ACCESSION AA578773
VERSION AA578773.1 GI:2356957
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquí, M.D.,
Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrp/image/image.html
Insert length: 565 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 373.
Location/Qualifiers
1. 402
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:953262"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCL_CGAP_Prl"
/note="Vector: PAMP10; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dt)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
/000 microdissected, histologically normal prostate
epithelial cells. Double-stranded cDNA was ligated to
EcoRI adaptors, 5 cycles of PCR applied to the cDNA with
an adaptor-specific primer, and the resulting PCR product
subcloned into PAMP10 by the UDG-cloning method (Life
Technologies). Average insert size is 600 bp. NOTE: Not
directionally cloned. This library was constructed by
David Krizman."

BASE COUNT 128 a 86 c 84 g 104 t
ORIGIN
Query Match 10.2%; Score 367; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 6.9e-151;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 TATTTGAACGGGATTACAGATTGAATGAGTCAACAAAGTGAGCATTTACCATGAGAG 676
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Db 36 TATTTGAACGGGATTACAGATTGAATGAGTCAACAAAGTGAGCATTTACCATGAGAG 95
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QY 677 AAACAGACGAGAAATCTTGATGCTTCAACAGACATGCAACAAACAAATGGAATACT 736
|||||
Db 96 AAACAGACGAGAAATCTTGATGCTTCAACAGACATGCAACAAACAAATGGAATACT 155
|||||

QY 737 GTGATGACATGAGGACCAAGCTGGGAGAGAGATTAACACGCGGAGAGAGGTCAGATT 796
|||||

Db 156 GTGATGACATGAGGACCAAGCTGGGAGAGAGATTAACACGCGGAGAGGTCAGATT 215
QY 797 CTGGCCCTGCTGCTTAACCTGTCCTTCAATACCAATATTTCAATTTCAACCTCA 856
|||||
Db 216 CTGGCCCTGCTGCTTAACCTGTCCTTCAATACCAATATTTCAATTTCAACCTCA 275
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QY 857 AAACAAAGCTGTTGTAATATGATCTACAGGTTCTTGGGCCCAACATTTCCATA 916
|||||
Db 276 AAACAAAGCTGTTGTAATATGATCTACAGGTTCTTGGGCCCAACATTTCCATA 335
|||||

QY 917 TATCCAGCACACTCAATTTTAAATATTAATTAATGTTCCAGATCTGATGATCTTTTACA 976
|||||
Db 336 TATCCAGCACACTCAATTTTAAATATTAATTAATGTTCCAGATCTGATGATCTTTTACA 395
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QY 977 CTGTAGA 983
Db 396 CTGTAGA 402
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RESULT 4
AQ319247/c 654 bp DNA linear GSS 06-MAY-1999
LOCUS RPCI11-108L4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-108L4,
DEFINITION genomic survey sequence.
ACCESSION AQ319247
VERSION AQ319247.1 GI:4052212
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
TITLE use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@ligr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.bufileo.edu/ordering>) or from
Research Genetics (<http://inforesgen.com>). BAC end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: r7
Class: BAC ends.
Location/Qualifiers
1. 654
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7541355"
/db_xref="taxon:9606"
/clone="RPCI-11-108L4"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"

BASE COUNT 213 a 100 c 139 g 202 t
ORIGIN
Query Match 9.0%; Score 323; DB 28; Length 654;
Best Local Similarity 100.0%; Pred. No. 1.8e-131;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1540 CATACATTAATTCCTTCTGCTGAGAGCTCTCTCTTCTTAATCTAGAAATGATGTA 1599
|||||
Db 332 CATACATTAATTCCTTCTGCTGAGAGCTCTCTCTTCTTAATCTAGAAATGATGTA 273
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```
OY 1600 AAGTTTGAAATAGTTGACTATCTTACTTCATGCAAGAGGACACATATGAGATTCAT 1659
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DB 272 AAGTTTGAAATAGTTGACTATCTTACTTCATGCAAGAGGACACATATGAGATTCAT 213
|||||
OY 1660 CATACATGAGACAGCAAAATCTAAAGTGTATTTGTTATAGAGTTTGATTAATAT 1719
|||||
DB 212 CATACATGAGACAGCAAAATCTAAAGTGTATTTGTTATAGAGTTTGATTAATAT 153
|||||
OY 1720 ATGAATGCAAGAGCCACAGAGGAGAAATGTTATGCGCAGCTTTGATAGCCTGGAGTGTG 1779
|||||
DB 152 ATGAATGCAAGAGCCACAGAGGAGAAATGTTATAGCGCAGCTTTGATAGCCTGGAGTGTG 93
|||||
OY 1780 AAGCAAGGCGAGGAGACTCATATGATCTTATATATATATCTTCAATTTCTATCTCAT 1839
|||||
DB 92 AAGCAAGGCGAGGAGACTCATATGATCTTATATATATATCTTCAATTTCTATCTCAT 33
|||||
OY 1840 CACATATCCAAACAGCTTTTCA 1862
|||||
DB 32 CACATATCCAAACAGCTTTTCA 10
|||||

RESULT 5
AM948945 346 bp mRNA linear EST 31-MAY-2000
LOCUS QV4-FT0004-130500-212-d11 FT0004 Homo sapiens cDNA, mRNA sequence.
DEFINITION AM948945
ACCESSION AM948945
VERSION AM948945.1 GI:8126719
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 346)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURN. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4t2-QV4-FT0004-130
500-212-d11&t3=2000-05-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 344.
location/Qualifiers
1..346
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0004"
/note="Organ: prostate,tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
```

```
BASE COUNT 104 a 81 c 63 g 98 t
ORIGIN
Query Match 8.9%; Score 319; DB 10; Length 346;
Best Local Similarity 100.0%; Pred. No. 1,2e-129;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2612 CTTGAACTGATGCTCATAGAGAGAAATATTAAGAACTGTGATATATCAATAGGGA 2671
|||||
DB 28 CTTGAACTGATGCTCATAGAGAGAAATATTAAGAACTGTGATATATCAATAGGGA 87
|||||
OY 2672 TTCAAAGAAATATTAAGATTTAAGCTCACACGCGCAAAAGAACCAAGATCAAGAACT 2731
|||||
DB 88 TTCAAAGAAATATTAAGATTTAAGCTCACACGCGCTAAAGAACCAAGATCAAGAACT 147
|||||
OY 2732 CTGAGCTGCATCGCTCCCATCTGTGAGCCACAAACAGCAGAGACCCAGCATGT 2791
|||||
DB 148 CTGAGCTGCATCGCTCCCATCTGTGAGCCACAAACAGCAGAGACCCAGCATGT 207
|||||
OY 2792 CTGAGATCTTAAATCAAGAAACCAAGTGTATGATGTAATTCCTATTATGAGATCT 2851
|||||
DB 208 CTGAGATCTTAAATCAAGAAACCAAGTGTATGATGTAATTCCTATTATGAGATCT 267
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OY 2852 AGCTTGTGGCATCTCGGCTCTCTCTTGAACATATATAGCTTCTGCTTCCCA 2911
|||||
DB 268 AGCTTGTGGCATCTCTGCTCTCTCTTGAACATATATAGCTTCTGCTTCCCA 327
|||||
OY 2912 CGACTTTATCTTTTCTCC 2930
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DB 328 CGACTTTATCTTTTCTCC 346
|||||

RESULT 6
BQ372852 304 bp mRNA linear EST 21-MAY-2002
LOCUS BQ372852
DEFINITION CM4-FT0103-230600-211-c09 FT0103 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ372852
VERSION BQ372852.1 GI:21048366
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 304)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURN. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-FT0103-
230600-211-c09&t3=2000-06-23&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 304.
location/Qualifiers
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/mol_type="mRNA"
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BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Matches	Score	DB	Length	304:
68 a	97 c	8.2%	100.0%	0: Mismatches	0: Indels	0: Gaps	0: Gaps	0: Gaps
2742	ATCGTCCCATCTCTGTGAGCCACACCAACAGCAGCAGCCACGATGTCTGAGATCT	2801	12	ATCGTCCCATCTCTGTGAGCCACACCAACAGCAGCAGCCACGATGTCTGAGATCT	71	2802	TAAATCAAGAAACCAAGTGCATGATGTAATTCCTATTATGATGATCAGCTTGGCC	2861
72	TAAATCAAGAAACCAAGTGCATGATGTAATTCCTATTATGATGATCAGCTTGGCC	131	2862	CATCTCGGCTCTCTCTGTGACATATNTACTTCTAGCCTTTCCTCCAGACTTTTAT	2921	132	CATCTCGGCTCTCTCTGTGACATATNTACTTCTAGCCTTTCCTCCAGACTTTTAT	191
2922	CTTTTCTCCACACATCGCTTACCAATCCCTCTCTGCTGTTGCTTGGACTTCCCA	2981	192	CTTTTCTCCACACATCGCTTACCAATCCCTCTCTGCTGTTGCTTGGACTTCCCA	251	2982	CAGAAATTTCAAGACATCTCAAGTCTTTCTTCATCCCAACCACTAACCCTGA	3034
252	CAGAAATTTCAAGACATCTCAAGTCTTTCTTCATCCCAACCACTAACCCTGA	304	252	CAGAAATTTCAAGACATCTCAAGTCTTTCTTCATCCCAACCACTAACCCTGA	304	252	CAGAAATTTCAAGACATCTCAAGTCTTTCTTCATCCCAACCACTAACCCTGA	304
RESULT 7	AI557225	856 bp	linear	EST 09-AUG-1999				
LOCUS	PT2.1.15_B05.r	tumor2	Homo sapiens	CDNA 3', mRNA sequence.				
DEFINITION	AI557225							
ACCESSION	AI557225.1	GI:4489588						
VERSION	EST.							
KEYWORDS	Homo sapiens (human)							
SOURCE	Homo sapiens							
ORGANISM	Eukaryotes: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:							
REFERENCE	Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.							
AUTHORS	Huang,G.M., Ng,W.L., Parkas,J., He,L., Liang,H.A., Gordon,D., Yu,J.							
TITLE	Prostate cancer expression profiling by cDNA sequencing analysis							
JOURNAL	Genomics 59 (2), 178-186 (1999)							
MEDLINE	99339982							
PUBMED	10409429							
COMMENT	Contact: Guyang Matthew Huang							
	Leroy Hood							
	University of Washington							
	Department of Molecular Biotechnology, Box 357730, University of							
	Washington, Seattle, WA 98195							
	Tel: 5106280100							
	Fax: 5106280108							
	Email: huanggm@yahoo.com.							
FEATURES	location/Qualifiers							
source	1..856							
	/organism="Homo sapiens"							
	/mol_type="mRNA"							
	/db_xref="taxon:9606"							
	/clone_lib="tumor2"							
	/note="Organ: Prostate; Vector: pBluescript; Directional							
	cDNA library was constructed using lambda ZP II kit							
	(Stratagene). mRNA was extracted from a frozen prostate							

BASE COUNT	237 a	191 c	180 g	214 t	34 others
ORIGIN	tumor tissue (Mayo Clinics) *				
Query Match	8.0%; Score 287; DB 9; Length 856;				
Best Local Similarity	100.0%; Pred. No. 1,5e-115;				
Matches 287;	Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
OY	1540	CATACATTTATTCCTTTCGCTGAGACGCTCTCTCTGCTTAAATCTGAAATGATGTA	1599		
DB	205	CATACATTTATTCCTTTCGCTGAGACGCTCTCTCTGCTTAAATCTGAAATGATGTA	264		
OY	1600	AAGTTTGAAATACCTGACTATCTTACTTCAATGAAAGGAGCAGATATGATTCAT	1659		
DB	265	AAGTTTGAAATACCTGACTATCTTACTTCAATGAAAGGAGCAGATATGATTCAT	324		
OY	1660	CATACATGAGACAGCAAAATCTAATAAGTGAATTTGATTATAGAGTTAGATTAATAT	1719		
DB	325	CATACATGAGACAGCAAAATCTAATAAGTGAATTTGATTATAGAGTTAGATTAATAT	384		
OY	1720	ATGAATGCAAGAGCCACAGAGGAATGTTATGGGACAGTTTGAAGCCTGGGATGTG	1779		
DB	385	ATGAATGCAAGAGCCACAGAGGAATGTTATGGGACAGTTTGAAGCCTGGGATGTG	444		
OY	1780	AAGCAAGGCGAGGACCTCATATGATCTTATATATATATCTTCAT	1826		
DB	445	AAGCAAGGCGAGGACCTCATATGATCTTATATATATATCTTCAT	491		
RESULT 8					
LOCUS	B0373258	700 bp	mRNA	linear	EST 21-MAY-2002
DEFINITION	MR0-F0176-040900-202-g07 F0176 Homo sapiens cDNA, mRNA sequence.				
ACCESSION	B0373258				
VERSION	B0373258.1	GI:21048772			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 700)				
	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.J.F., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
MEDLINE	20202663				
PUBMED	10737800				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?file=MR0&t2=MR0-F0176-040900-202-g07&t3=2000-09-04&t4=1) Seq primer: puc 18 forward High quality sequence start: 19 High quality sequence stop: 625. Location/Qualifiers 1..700 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult"				
FEATURES					
source					

/clone.lib="FT0176"
/note="Organ: prostate,tumor; Vector: puc18; Site:1: Smai;
Site:2: Smai; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 201 a 122 c 156 g 221 t
ORIGIN

Query Match 7.8%; Score 280; DB 13; Length 700;
Best Local Similarity 99.3%; Pred. No. 1.9e-112;
Matches 430; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2405 TACTTCATTAGTCTCAGTCTGGGCTGTGCATCAGCGGTTTGAAATATTCATCT 2464
|||||
DB 450 TACTTCATTAGTCTCAGTCTGGGCTGTGCATCAGCGGTTTGAAATATTCATCT 391
|||||
OY 2465 CAGCAGAACCCAGAAATTTGAATTCCTTCATCTTTAGGAATCATTTACCAGGTTTGAGA 2524
|||||
DB 390 CAGCAGAACCCAGAAATTTGAATTCCTTCATCTTTAGGAATCATTTACCAGGTTTGAGA 331
|||||
OY 2525 GGATTCAGACAGCTCAGGCTGCTTCTCATAATGCTCTGAATCTGCTCTTGTGTT 2584
|||||
DB 330 GGATTCAGACAGCTCAGGCTGCTTCTCATAATGCTCTGAATCTGCTCTTGTGTT 271
|||||
OY 2585 CATGGATAGTCCATTAATTAATGTTATCTTGAATGCTCATAGAGAGAAATATAG 2644
|||||
DB 270 CATGGATAGTCCATTAATTAATGTTATCTTGAATGCTCATAGAGAGAAATATAG 211
|||||
OY 2645 AACTCTGATGATATTCACATTAAGGATTCAGAAATATTTAGATTAGCTCACACTGG 2704
|||||
DB 210 AACTCTGATGATATTCACATTAAGGATTCAGAAATATTTAGATTAGCTCACACTGG 151
|||||
OY 2705 TCAAAAGGAACCAAGATTCAGAAAGACTGTGAGTGTGATGCTCCCATCTGTGAGCCA 2764
|||||
DB 150 TCAAAAGGAACCAAGATTCAGAAAGACTGTGAGTGTGATGCTCCCATCTGTGAGCCA 91
|||||
OY 2765 CAACCAACAGCAGAGACCCCAACGATGTCTGAGATCCTTAATCAAGAAACAGATGTCAT 2824
|||||
DB 90 CAACCAACAGCAGAGACCCCAACGATGTCTGAGATCCTTAATCAAGAAACAGATGTCAT 31
|||||
OY 2825 GAGTTGAAATTCCTC 2837
|||||
DB 30 GAGTTGAAATTCCTC 18
|||||

RESULT 9 319 bp mRNA linear EST 21-MAY-2002
B0371438
LOCUS B0371438
DEFINITION RC6-FN0116-200700-011-D08 FN0116 Homo sapiens cDNA, mRNA sequence.
ACCESSION B0371438
VERSION B0371438.1 GI:21046952
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/ICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&ct=RC6-FN0116-
200700-011-D08&ct=2000-07-20&ct=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 319.
Location/Qualifiers
1. 319

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone.lib="FN0116"
/note="Organ: prostate,normal; Vector: puc18; Site:1: Smai;
Site:2: Smai; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 85 a 74 c 67 g 93 t
ORIGIN

Query Match 6.9%; Score 247; DB 13; Length 319;
Best Local Similarity 100.0%; Pred. No. 8.5e-98;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2293 GCTGGAATGGACACCAACCAATATGCAATATGCAATGCTACGATGACGACTGC 2352
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DB 27 GCTGGAATGGACACCAACCAATATGCAATATGCAATGCTACGATGACGACTGC 86
|||||
OY 2353 TTGACATATATTTAGGAAGCAGCTGCTGTTGTTGTTCTTTAGCAAAATATCTTGA 2412
|||||
DB 87 TTGACATATATTTAGGAAGCAGCTGCTGTTGTTGTTCTTTAGCAAAATATCTTGA 146
|||||
OY 2413 TTAGTCTCAGCTGGGCTGTGCATCAGCGGTTTGAAATATTCATTTCTAGCGAA 2472
|||||
DB 147 TTAGTCTCAGCTGGGCTGTGCATCAGCGGTTTGAAATATTCATTTCTAGCGAA 206
|||||
OY 2473 GCCGAATTTGAATTCCTCATCTTTAGGAATCATTTACAGGTTGGAGAGATTCAG 2532
|||||
DB 207 GCCGAATTTGAATTCCTCATCTTTAGGAATCATTTACAGGTTGGAGAGATTCAG 266
|||||
OY 2533 ACAGCTC 2539
|||||
DB 267 ACAGCTC 273
|||||

RESULT 10 290 bp mRNA linear EST 24-NOV-2000
BF373619
LOCUS BF373619
DEFINITION MRO-FT0175-310800-106-h09 FT0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF373619
VERSION BF373619.1 GI:11335644
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MM0&t2=MM0-FT0175-310800-106-h09&t3=2000-08-31&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 290.
Location/Qualifiers
1. 290
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0175"
/note="Organ: prostate.tumor; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 78 a 73 c 53 g 86 t
ORIGIN
Query Match 6.6%; Score 238; DB 10; Length 290;
Best Local Similarity 100.0%; Pred. No. 8.3e-94;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 762 GGGAGAGATTAACACGGGGCAGAGGGTGTGAGATTGCGCTGCTTAACGTGGG 821
|||||
DB 21 GGGAGAGATTAACACGGGGCAGAGGGTGTGAGATTGCGCTGCTTAACGTGGG 80
822 TTCATTAACCAATTCATTAATTTCTAACCCCTCAACAAAGAGCTGTAAATGTGAT 881
|||||
DB 81 TTCATTAACCAATTCATTAATTTCTAACCCCTCAACAAAGAGCTGTAAATGTGAT 140
882 CTCACGCTTCCTCTGGGCCCAACATTCCTCATATATATCCAGCACATCTATTATATA 941
|||||
DB 141 CTCACGCTTCCTCTGGGCCCAACATTCCTCATATATATCCAGCACATCTATTATATA 200
942 TTTAGTCCCAAGATCTGTAAGTGTGACCTTTTACACTGTAGATAAATTACTATT 999
|||||
DB 201 TTTAGTCCCAAGATCTGTAAGTGTGACCTTTTACACTGTAGATAAATTACTATT 258
RESULT 11 304 bp mRNA linear EST 20-MAY-2002
B0338234
LOCUS B0338234
DEFINITION CM2-NN0116-100700-257-e11 NN0116 Homo sapiens cDNA, mRNA sequence.
ACCESSION B0338234
VERSION B0338234.1 GI:20996652
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
1 (bases 1 to 304)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'hare

TITLE 'M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t2=CM2-NN0116-100700-257-e11&t3=2000-07-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 304.
Location/Qualifiers
1. 304
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN0116"
/note="Organ: nervous.normal; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 66 a 98 c 45 g 95 t
ORIGIN
Query Match 6.6%; Score 238; DB 13; Length 304;
Best Local Similarity 99.7%; Pred. No. 8.2e-94;
Matches 288; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2745 GTCCCATCTCTGTGAGCCACACCAACAGACAGACCAAGCATGCTGAGATCTTAA 2804
|||||
DB 1 GTCCCATCTCTGTGAGCCACACCAACAGACAGACCAAGCATGCTGAGATCTTAA 60
2805 ATCAAGAAACAGATGATGATTAATTTCTATTATATGATGCTAGCTTGTGCCAT 2864
|||||
DB 61 ATCAAGAAACAGATGATGATTAATTTCTATTATATGATGCTAGCTTGTGCCAT 120
2865 CTCGTGCTCTCTCTTGACACATATTAGCTTCTAGACCTTTCCTCCACGATTTATCTT 2924
|||||
DB 121 CTCGTGCTCTCTCTTGACACATATTAGCTTCTAGACCTTTCCTCCACGATTTATCTT 180
2925 TTCTCCACACATCGTTACCAATTCCTCTCTCTGCTGTGCTTGGACTTCCGACAA 2984
|||||
DB 181 TTCTCCACACATCGTTACCAATTCCTCTCTCTGCTGTGCTTGGACTTCCGACAA 240
2985 GAATTTCAAGACTCTCAAGTCTTTTCTTCATCCACACACAACTG 3033
|||||
DB 241 GAATTTCAAGACTCTCAAGTCTTTTCTTCATCCACACACAACTG 289
RESULT 12 226 bp mRNA linear EST 16-JAN-2001
BF858371
LOCUS BF858371
DEFINITION RCS-FT0193-211100-012-E11 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF858371
VERSION BF858371.1 GI:12246115
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 226)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
JOURNAL MEDLINE PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC5&t2=RC5-FT0193-21100-012-E11&t3=2000-11-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 226.
Location/Qualifiers
1..226
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0193"
/note="Organ: prostate tumor; Vector: puc18; Site: 1: SmaI, Site: 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 79 a 29 c 59 g 59 t
ORIGIN
Query Match 6.0%; Score 214; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.5e-83;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 809 CCTAAGTCGCGCTCATTAACCAATCATTTTCATTTTCAACCTCAAAACAAAGCTGT 868
DB 226 CCTAAGTCGCGCTCATTAACCAATCATTTTCATTTTCAACCTCAAAACAAAGCTGT 167
QY 869 TGTAAATATGATCTACAGGTTCTCTGGGCCCAACATCTCATATATCCAGCCCA 928
DB 166 TGTAAATATGATCTACAGGTTCTCTGGGCCCAACATCTCATATATCCAGCCCA 107
QY 929 CTCATTTTAAATATTTAGTTCCAGATCTGATGTAACCTTTCTACACTAGAAATAC 988
DB 106 CTCATTTTAAATATTTAGTTCCAGATCTGATGTAACCTTTCTACACTAGAAATAC 47
QY 989 ATTACATTTTGTTCAAAGACCTTGCTGTGC 1022
DB 46 ATTACATTTTGTTCAAAGACCTTGCTGTGC 13
RESULT 13
AO206972/c 394 bp DNA linear GSS 17-SEP-1998
LOCUS
DEFINITION
HG_3238_B1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=21 Row=N, genomic survey
sequence.
ACCESSION
AO206972

VERSION AO206972.1 GI:3617542
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 394)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764
JOURNAL MEDLINE PUBMED
COMMENT
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence tagged Connector
Plate: 3238 row: N column: 21
Class: BAC ends
High quality sequence stop: 394.
Location/Qualifiers
1..394
/organism="Homo sapiens"
/mol_type="genomic DNA"
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/clone_plate="Plate=3238 Col=21 Row=N"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pbe10BAC11; BAC clones in E-Coli DH10B"
BASE COUNT 134 a 62 c 93 g 103 t 2 others
ORIGIN
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Best Local Similarity 99.4%; Pred. No. 3.2e-83;
Matches 314; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 905 ACATTTCTCCATATATCCAGCACACTATTTTATATATTTAGTCCAGATCTGACTGT 964
DB 381 ACATTTCTCCATATATCCAGCACACTATTTTATATATTTAGTCCAGATCTGACTGT 322
QY 965 GACCTTTCTACAGTGTAATTAACATTAATCTGATTTGTTCAAAGACCTTGCTGCTG 1024
DB 321 GACCTTTCTACAGTGTAATTAACATTAATCTGATTTGTTCAAAGACCTTGCTGCTG 262
QY 1025 CCTAATATGATGACGTGTTTCTTAAGAGAGTCTGCGCCAGGGATCTGTGACA 1084
DB 261 CCTAATATGATGACGTGTTTCTTAAGAGAGTCTGCGCCAGGGATCTGTGACA 202
QY 1085 GCGTGGAGACATCTCAAGATCTTTCACAGGTTTACTTACTAGACACAGATGATCAT 1144
DB 201 GCGTGGAGACATCTCAAGATCTTTCACAGGTTTACTTACTAGACACAGATGATCAT 142
QY 1145 TAGGAGAGATTTTCAATCAATCATCATCTCGTGTGCGCCATAGGAATTCAT 1204
DB 141 TAGGAGAGATTTTCAATCAATCATCATCTCGTGTGCGCCATAGGAATTCAT 82
QY 1205 TTCCCACTTTTGTGCC 1220
DB 81 TTCCCACTTTTGTGCC 66
RESULT 14
BF858286 332 bp mRNA linear EST 16-JAN-2001
LOCUS
DEFINITION
RC5-FT0193-201100-012-D06 FT0193 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF858286

VERSION BF858286.1 GI:12246030
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 332)
Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC5&t2=RC5-FT0193-201100-012-D06&t3=2000-11-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 332.
Location/Qualifiers
1..332
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0193"
/note="Organ: prostate; tumor: Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 90 a 84 c 64 g 94 t
ORIGIN
Query Match 5.9%; Score 213; DB 10; Length 332;
Best Local Similarity 100.0%; Pred. No. 9.2e-83;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 763 GGAGAGATACACGAGGAGAGAGGATTCGCGCCCTGCTTAACGTGCGCT 822
DB 61 GGAGAGATACACGAGGAGAGGAGGATTCGCGCCCTGCTTAACGTGCGCT 120
QY 823 TCATTAACCAATCATTTCTATTTCTAACCTTCAAAACAAGCTGTTGAATATCTGATC 882
DB 121 TCATTAACCAATCATTTCTATTTCTAACCTTCAAAACAAGCTGTTGAATATCTGATC 180
QY 883 TCTAGGCTCTTCTGGGGCCAAACATTCATATATTCAGGACACACTATTTTAAAT 942
DB 181 TCTAGGCTCTTCTGGGGCCCAACATTCATATATTCAGGACACACTATTTTAAAT 240
QY 943 TTAGTCCAGATCTGTACTGTGACCTTTCTAC 975
DB 241 TTAGTCCAGATCTGTACTGTGACCTTTCTAC 273
RESULT 15
BF373581/c 282 bp mRNA linear EST 24-NOV-2000
LOCUS BF373581

DEFINITION MR0-FT0175-210800-101-d05 FT0175 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF373581
VERSION BF373581.1 GI:11335606
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 282)
Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR0&t2=MR0-FT0175-210800-101-d05&t3=2000-08-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 35
High quality sequence stop: 282.
Location/Qualifiers
1..282
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0175"
/note="Organ: prostate; tumor: Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 85 a 51 c 70 g 76 t
ORIGIN
Query Match 5.5%; Score 198; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 4.1e-76;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 775 CACGGGCGAGAGGCTGAGATTCGCGCCCTGCTTAACGTGCGCTTCAACCAAT 834
DB 262 CACGGGCGAGAGGCTGAGATTCGCGCCCTGCTTAACGTGCGCTTCAACCAAT 203
QY 835 CATTCATATTTCTAACCTTCAAAACAAGCTGTTGAATATCTGATCTCTACGTTCT 894
DB 202 CATTCATATTTCTAACCTTCAAAACAAGCTGTTGAATATCTGATCTCTACGTTCT 143
QY 895 TCTGGGCCCAACATTCATATATTCAGGACACACTATTTTAAATATTAGTCCACA 954
DB 142 TCTGGGCCCAACATTCATATATTCAGGACACACTATTTTAAATATTAGTCCACA 83
QY 955 TCTGTACTGTGACCTTTC 972
DB 82 TCTGTACTGTGACCTTTC 65

Mon Sep 29 08:56:35 2003

us-09-402-713a-6.olg.rst

Page 10

Search completed: September 27, 2003, 11:35:49
Job time : 7519.98 secs
